# EvolDir

July 1, 2017

Month in Review

## Foreword

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

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

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

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# Conferences

## AarhusU ModelingGenomics Sep18-20 Deadline

The 3rd Probabilistic Modeling in Genomics Conference (ProbGen17) will be held at Aarhus University, Denmark, from 18-20 Sept 2017.

The conference will cover probabilistic models, algorithms, and statistical methods across a broad range of applications in genetics and genomics. We invite abstract submissions on a range of topics including Population Genetics, Functional Genomics, Systems and Structural Biology, Methods for Genome-wide Association Studies, Causal inference in genetic studies, Assembly and Variant Identification, Phylogenetics, Natural Selection and Quantitative Genetics. Alongside invited speakers, oral presentations will be selected from submitted abstracts. We particularly encourage abstract submissions from junior investigators, including postdoctoral fellows and graduate students.

We have provisional capacity for only 200 participants; due to space limitations, registration will proceed on a first-come-first-served basis. We already have participants from Denmark, France, Germany, US and the UK. ***IMPORTANT DEADLINE: Early bird registration & ABSTRACT submission will close on June 23. ***

Probgen was held previously in Cold Spring Harbor (2015), and Oxford (2016). It evolved from the success of previous similarly-themed workshops held at the HHMI Janelia Farm Research Campus (2013) and Merton College, Oxford (2014).

The conference talks and poster sessions will be held at the new Moesgaard Museum for archaeology and ethnography (MOMU) situated just 5 km out of Aarhus. Aarhus is most easily accessible from either Aarhus (AAR) or Billund (BLL) Airport that serves most major European cities.

The meeting will begin with an informal mixer on the evening of Sunday 17 September 2017 at Hotel Comwell [http://www.comwellaarhus.dk/] in central Aarhus. Talks will take place from Monday 18 September until lunchtime on Wednesday 20 September.

The conference venue webpage: www.moesgaardmuseum.dk/en/ The conference webpage can be found at http://conferences.au.dk/probgen17/ Please send enquiries to probgen17@birc.au.dk

We would appreciate if you could circulate this announcement to your local colleagues and collaborators.

Kind regards Thomas

On behalf of the organizers:

Ida Moltke, University of Copenhagen Thomas Mailund, Aarhus University Thomas Bataillon, Aarhus University Mikkel H. Schierup, Aarhus University

Thomas Bataillon <tbata@birc.au.dk>

## Austin SMBE 2017 Jul2-6 RegistrationAccommodation

SMBE 2017 On-Site Registration Accommodation

Regular Registration Fees Ending Soon

For those that haven't registered for SMBE 2017, please note that the regular registration fees will end on Friday, June 16th, with the onsite rate starting after this date. This increase applies across all categories of registration.

Register Here

We'd also like you to note that rooms in the J.W. Marriott - the official meeting hotel - are now becoming limited. We would recommend booking your hotel room today to ensure you secure your place at the centre of SMBE 2017.

You can book your room directly through our registration system, even if you completed your registration at an earlier date. Just log back in to the registration system to add accommodation to your booking. Student accommodation is also available.

Book Accommodation

SMBE 2017 <SMBE2017@mci-group.com>

## Barcelona RECOMB CG Oct4-6 DeadlineExtension

RECOMB Comparative Genomics 2017

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

The 15th RECOMB-CG conference will be held in the Centre for Genomic Regulation (CRG), Barcelona, Spain, on October 04-06 2017. With this Call for Papers we invite high-quality original full papers on topics related to the conference theme. The conference will also have a poster session. A detailed call for posters will be published later on the conference web page:

http://www.crg.eu/en/event/15th-recomb-comparative-genomics-satellite-workshop TOPICS Papers are solicited on, but not limited to, the following topics: §genome evolution §genome rearrangements §genome variation, diversity and dynamics §phylogenomics §comparative tools for genome assembly §population genomics §comparison of functional networks §comparative epigenomics §paleogenomics §cancer evolution genomics §epidemiology §gene identification and/or annotation

IMPORTANT DATES §Paper Submission Deadline: June 18, 2017 §Author Notification: July 14, 2017 §Final Version Due: July 28, 2017 §Conference: October 04-06, 2017

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

Accepted papers will be published in the conference proceedings, a volume in the Lecture Notes in Bioinformatics (LNBI) series. In addition, authors of selected papers will be invited, but not required, to submit a significantly extended version of their papers to PeerJ, BMC Bioinformatics, or BMC Genomics. Papers submitted to PeerJ will be assigned to an Academic Editor of the journal and will be reviewed according to the normal PeerJ standards. Papers submitted to BMC Bioinformatics or BMC Genomics will be handled by the Program Committee co-chairs. Authors who choose to publish their extended manuscripts in one of these journals will have to pay the journal's publication fees. Authors are encouraged to submit their manuscripts in PDF format according to the LNBI series guidelines:

http://www.springer.com/us/computer-science/lncs/conference-proceedings-guidelines Submitted papers must be within 15 pages (in the LNBI format), with optionally a clearly marked appendix containing supplementary material made available to the reviewers. All submissions must be made online, through the EasyChair submission system, at the following address:

https://easychair.org/conferences/?conf=recombcg17 Authors need to register on that web site before submitting. A standard PDF file must be received by midnight on June 18, 2017 (any time zone) in order for a submission to be considered. Re-submission of already submitted papers will be possible until midnight June 18, 2017 (any time zone).

CONFIRMED KEYNOTE SPEAKERS - Iria Fernández Silva (Department of Biochemistry, Genetics and Immunology, School of Biology, University of Vigo ES) - Toni Gabaldón (Centre for Genomic Regulation, Barcelona ES) - Iñaki Ruiz-Trillo (ICREA Research Professor at Institut de Biologia Evolutiva [CSIC-IBE], Barcelona ES) - Wes Warren (McDonnell Genomics Institute, Washington University School of Medicine USA)

ORGANIZING COMMITTEE Tomàs Marquès-Bonet (UPF) tomas.marques@upf.edu Roderic Guigó Serra (CRG) roderic.guigo@crg.eu Laura Prat Busquets (CRG Conference Officer) laura.prat@crg.eu

PROGRAM COMMITTEE (PARTIAL) Max Alekseyev (George Washington University) Lars Arvestad (Stockholm University) Anne Bergeron (UQAM) Marilia Braga (Bielefeld University) Cedric Chauve (Simon Fraser University) Leonid Chindelevitch (Simon Fraser University) Miklós CsÅ±rös (University of Montréal) Ingo Ebersberger (Goethe University Frankfurt) Nadia El-Mabrouk (University of Montréal) Guillaume Fertin (University of Nantes) Katharina Jahn (ETH Zurich) Asif Javed (Genome Institute of Singapore) Kevin Liu (Michigan State University) Ketil Malde (Institute of Marine Research, Norway) Joao Meidanis (UNICAMP, co-chair) István Miklós (Rényi Institute, Hungarian Academy of Sciences) Siavash Mirarab (UCSD)

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## Bialowieza Poland ProgrammingforEvolBiol Sep16-20

The dealine for 3rd Programming for Evolutionary Biology Conference 16-20 Sept 2017, BiaÅ$^3$owieÅ¿a, Poland has been extended. We now accept abstracts till 31st July.

The Programming for Evolutionary Biology (PEB) conference brings together biologists broadly interested in applying bioinformatic tools to answer evolutionary and ecological questions.

It aims to serve as a platform for discussing the ongoing projects and related bioinformatic pitfalls. The meeting consists of plenary talks by renowned specialists in the field, contributed talks by the participants (works in progress are more than welcome!) and workshops.

This year, we are fortunate to be joined by an outstanding list of Plenary Speakers: Mark Blaxter from University of Edinburgh, Stuart Baird from Czech Academy of Sciences, Katja Nowick from University of Leipzig. The workshops will be provided by PrzemysÅ$^3$aw Biecek, a data scientist and R enthusiast from University of Warsaw.

The fee, including meals, accommodation, and transportation from Warsaw airport and back, is 250 euro.

More info: pebconference.info

Looking forward seeing you in Bialowieza!

On behalf the organising committee, Agnieszka Kloch

– dr Agnieszka Kloch ZakÅ$^3$ad Ekologii WydziaÅ$^3$ Biologii, Uniwersytet Warszawski ul. Åwirki i Wigury 101, 02-089 Warszawa budynek CNBCh (Cent3), pok. 4.47 tel. (22) 55 26 603 http://perlism.org/akloch/ "akloch@biol.uw.edu.pl" <akloch@biol.uw.edu.pl>

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## Biddeford Maine GRCEvolutionaryGenomics Jul16-21

There is still time to register for the* Gordon Research Conference -*

*Ecological & Evolutionary Genomics at the University of New England, Biddeford, Maine USA. *

*See the full program: (http://www.grc.org/-programs.aspx?id=13136)*

Connecting Genomic Diversity to Organisms and Environments: Gaining Insights from Advances in Technology, Theory, and Applications

The 2017 Gordon Research Conference on Ecological and Evolutionary Genomics will highlight recent advances in our understanding of the genomic basis of adaptation and the interaction between organisms and the dynamic environments they live in. This meeting will highlight a combination of empirical studies, recent theoretical advances and emerging technologies. Topical areas such as population genomics, phylogenomics, adaptation, the genomic basis of development, and functional genomic responses to the environment will highlight how the rapidly advancing field of genome biology can inform our understanding of the evolutionary and ecological processes that shape biodiversity. The conference will highlight the analysis of large, complex data sets and emerging technologies driving the expanding scale of these data.

Co-chairs, Felicity Jones (Max Plank Institute, Tubingen) and Michael Pfrender (University of Notre Dame) along with co-Vice Chairs, Christian Landry (Université Laval) and Angela Douglas (Cornell University) invite you to join us on the ocean-side campus of the University of New England in Biddeford, Maine for a stimulating conference. We are assembling a diverse group of established and early career investigators to discuss their latest work. Many sessions will include talks by speakers chosen from among the submitted abstracts. The organizers are actively seeking funds to assist students and others attending the meeting. Applications for attendance will be accepted on a first-come-first serve basis until the meeting is full. Don't delay! Gordon Conferences are famous for fostering in depth interactions that yield new insights in a collegial atmosphere. Please plan on joining us in Biddeford in 2017.

Join us for this great conference. Inquiries can be directed to Michael Pfrender (michael.pfrender.1@nd.edu).

Best regards,

Michael Pfrender & Felicity Jones Co-Chairs

Angela Douglas & Christian Landry Co-Vice Chairs

Michael E. Pfrender, Director Genomics & Bioinformatics Core Facility Associate Professor Department of Biological Sciences 109B Galvin Life Science Center Notre Dame, IN 46556 USA

Ph#: 574-631-0591 (O)

Pfrender Lab (http://www.nd.edu/ ˜ mpfrende/-) Eck Institute for Global Health (http://-globalhealth.nd.edu/) Environmental Change Initiative (http://environmentalchange.nd.edu) Genomics and Bioinformatics Core Facility (http://genomics.nd.edu < http://daphnia.cgb.indiana.edu/ >)

Michael Pfrender <Michael.Pfrender.1@nd.edu>

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## Cambridge UK AnimalEvoDevo Sep17-18

Symposium on Animal Development and its Evolutionary Variation 17th - 18th September 2017 Department of Zoology University of Cambridge Cambridge, UK (Apologies for cross posting)

Dear Friends and Colleagues,

We wanted to bring your attention to a meeting taking place on 17-18 September in Cambridge (UK) on the subject of Animal Development and its Evolutionary Variation. The meeting is intended in part as a celebration of the contributions of Prof Michael Akam to this field.

On 17th September there will be an evening drinks celebration at the Department of Zoology. On 18th September there will be a day long scientific symposium held at the Department of Zoology. The symposium will be followed by a celebratory dinner in Trinity College.

The list of confirmed speakers is detailed below.

Keynote speakers

Sean Carroll (University of Wisconsin-Madison, USA)

Matt Scott (Carnegie Institution for Science, USA)

Speakers / Titles

Detlev Arendt (EMBL, Heidelberg, Germany) "Evolution of the centralised nervous system: a cell type perspective"

Nadia Bakalenko (St Petersburg State University, Russia) "Antisense transcripts in the nereid Hox clusters"

Erik Clark (University of Cambridge, UK) "Making stripes elegantly"

Cassandra Extavour (Harvard University, USA) "From soma to germ line: Origin, evolution and molecular mechanisms of the oskar gene"

Jack Green (University of Marseille, France) "How do organs change size during evolution? The cellular and genetic basis of ovipositor enlargement in Drosophila suzukii"

Robert Kelsh (University of Bath, UK) "Pigment cells and their progenitors in the neural crest"

Alfonso Martinez-Arias (University of Cambridge, UK) "What in vitro studies teach us about the evolution of axial elongation in vertebrates"

Christen Mirth (Monash University, Australia) "Plasticity in body size and shape: how environmental conditions modify development to generate phenotypic variation."

Tassos Pavlopoulos (Howard Hughes Medical Institute, Janelia Farm, USA) "Arthropod limb morphogenesis and diversification: lessons from a crustacean"

Mariana Wolfner (Cornell University, USA) "Not your average peep-show: molecules and physiology that mediate post-mating changes in female Diptera"

To register for the event please follow the following link:

http://onlinesales.admin.cam.ac.uk/conferences-and-events/department-of-zoology/symposium-on-animal-development-and-its-evolutionary-variation
In case of any queries regarding registration please contact: Paula McPhee, Department of Zoology, University of Cambridge Tel: +44 1223 336621 Email: admin@zoo.cam.ac.uk

Please forward this email to any other interested parties. We hope to see you in September!

Sincerely,

Claudio Alonso Michalis Averof Paul Brakefield James Castelli-Gair David Stern Max Telford

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/-telford/telford.html Open access journal EvoDevo: http://www.evodevojournal.com/ "Telford, Max" <m.telford@ucl.ac.uk>

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## DurhamU DiversityConservation Sep14-15

Update: Conservation of Adaptive Potential and Functional Diversity

14-15 September 2017, Durham University, UK

A discussion meeting to explore the potential for new paradigms and next generation sequencing to facilitate the more effective conservation of adaptive potential and functional diversity.

Plenary speakers include Rasmus Nielsen (Berkeley, USA), Bob Wayne (UCLA, USA), Paul Hohenlohe (Idaho, USA), Chris Jiggins (Cambridge, UK), Simone Sommer (Ulm, Germany), Oscar Gaggiotti (St. Andrews, UK), Barbara Mable (Glasgow, UK), Violeta Munoz Fuentes (EMBL-EBI, UK), Victor Soria-Carrasco (Sheffield, UK), Chris Funk (Colorado, USA), Rob Fleischer (Smithsonian, USA), and Mike Bruford (Cardiff, UK)

There will also be a series of shorter talks chosen from among the submitted abstracts and a poster session.

Abstract Submission: If you would like to be considered for presenting a talk or poster, please send an abstract in the following format: From the top of the page provide the title of the presentation, then the full list of author names, name of speaker (if for a talk), list of affiliations, contact email address, choice of talk vs poster (required), and finally the abstract (250 word maximum). All should be single-spaced and in 12pt Times Roman font.

Abstract deadline: 15 July 2017.

Please send abstracts to: cap.meeting@durham.ac.uk

Meeting sponsored by Springer-Nature and the Genetics Society.

Registration and further information available at:

https://www.dur.ac.uk/conference.booking/-details/?id=761 "HOELZEL, RUS A.R." <a.r.hoelzel@durham.ac.uk>

## Ecuador HerpetologyGenomics Jul24-28

**Deadline for submitting abstracts coming soon!**

Symposium "Applying genomic-scale approaches to the study of Neotropical amphibians and reptiles"

We invite you to participate in an exciting symposium addressing challenges in the application of high-throughput sequencing technologies in amphibian and reptiles research at the XI Latin American Congress of Herpetology (24-28 July 2017) in Quito, Ecuador.

Genomic-scale approaches are increasing in popularity as high-throughput sequencing techniques become more accessible and affordable. These techniques can allow us to investigate evolutionary and ecological questions with a novel approaches.

Nevertheless, the use of genomic data brings many challenges across the different stages of a research project, which include adequate sampling and preservation methods during fieldwork, museum curation, data processing, and bioinformatic analyses.

The symposium will include work on phylogenetics, environmental DNA, physiology, metagenomics, microbiomes, disease research, and gene expression applied to amphibians and reptiles.

Submission deadline for abstracts: 8 June 2017. Abstract submission: http://www.latinherps.ec/instructions/ Registration: http://www.latinherps.ec/instructions/ We hope to see you in Ecuador!

Symposium organisers:

Karen Siu-Ting Dept. of Herpetology, Natural History Museum, Lima, Peru School of Biotechnology, Dublin City University, Ireland

Jeff Streicher Herpetology Division, Natural History Museum, London, UK.

email: genomics.latinherps@gmail.com

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**Fecha limite para enviar resumenes es pronto! **

Simposio: "Aplicacion de enfoques de escala genomica al estudio de anfibios y reptiles neotropicales "

Los invitamos a participar a un interesante simposio sobre los desafíos en la aplicacion de tecnologías de secuenciacion de alto rendimiento en la investigacion de anfibios y reptiles que se dara en el XI Congreso Latinoamericano de Herpetología (24-28 de julio de 2017) en Quito, Ecuador.

Los enfoques de escala genomica estan aumentando en popularidad a medida que las tecnicas de secuenciacion de alto rendimiento se tornan mas accesibles. Estas tecnicas nos permiten investigar preguntas evolutivas y ecologicas en anfibios y reptiles con enfoques nuevos.

Pero el uso de datos genomicos trae muchos retos a traves de las diferentes etapas de un proyecto de investigacion, los cuales incluyen metodos adecuados de muestreo y preservacion durante el trabajo de campo, curaduría, procesamiento de datos y analisis bioinformaticos.

El simposio incluira trabajos en filogenetica, ADN ambiental, fisiología, metagenomica, microbiomas, investigacion de enfermedades y expresion genica aplicada a anfibios y reptiles.

Fecha límite de envío de resÃºmenes: 8 de junio de 2017. Envío de resÃºmenes: http://www.latinherps.ec/instructions/ Inscripcion: http://www.latinherps.ec/instructions/ Los esperamos en Ecuador!

Organizadores del simposio:

Karen Siu-Ting Departamento de Herpetología, Museo de Historia Natural, Lima, PerÃº School of Biotechnology, Dublin City University, Ireland

Jeff Streicher Herpetology Division, Natural History Museum, London, UK.

email: genomics.latinherps@gmail.com

Genomics Symposium LACH <genomics.latinherps@gmail.com>

agalychnica@gmail.com

## Marseilles 21stEvolBiol Sep26-29 FirstAcceptedAbstracts

Dear All

the AEEB is hosting" the 21st evolutionary biology meeting at Marseilles" Web site

aeeb.fr

the list of first accepted abstract is available

The meeting will take place September 26-29

The Dead Line is june 30

Best regards

Pierre

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

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## Montpellier Galaxy Jun26-30 RegisterByJun16

2017 Galaxy Community Conference (GCC2017) 26-30 June 2017 Montpellier, France https://gcc2017.sciencesconf.org/ https://gcc2017.sched.com/ https://galaxyproject.org/ –

The Galaxy Community Conference (GCC) brings together researchers working in and supporting data intensive life science research. There is no better place to share your work and learn from others that are addressing diverse questions and facing common challenges in data intensive biology. GCC participants work across the tree of life, around the world, and represent universities, research organizations, industry, medical schools and research hospitals.

GCC2017 will be in Montpellier, France, 26-30 June and features two days of presentations, discussions, poster sessions, lightning talks, computer demos, keynotes, and birds-of-a-feather meetups, all about data-intensive biology and the tools that support it. GCC2017 also features data and coding hackathons, and two days of training covering 16 different topics. GCC2017 will be held at Le Corum Conference Centre in the heart of Montpellier, just 10km from the Mediterranean.

** Registration closes 16 June. Costs start at 75€per day for postdocs and students. **

If you work in data intensive life science research then GCC2017 is an ideal opportunity to present your work. Lightning talk and birds-of-a-feather submission are still open, and there is limited space available for late poster and computer demo submissions.

About Galaxy: Galaxy is an open, web-based platform for data-intensive biomedical analysis used by tens of thousands of researchers around the world. It supports ad hoc exploration and analysis through scalable and repeatable data analysis pipelines for large research studies. Galaxy is available in over 90 free and publicly accessible web servers, on public and national cloud infrastructures, and is locally installed at hundreds, if not thousands, of research organisations around the world.

We hope to see you in Montpellier!

Au revoir,

The GCC2017 Organising Committee

Dave Clements <clements@galaxyproject.org>

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## Pittsburgh ThreeRiversEvolution Sep9 CallForAbstracts

Hello evolution community,

We are excited to announce the first annual Three Rivers Evolution Event (TREE), a new regional conference serving Western Pennsylvania and the surrounding areas, sponsored in part by the American Society of Naturalists. Researchers of all stages and institution types are welcome. TREE will take place on Saturday, September 9th, 2017 at the University of Pittsburgh and include multiple sessions of talks, a poster session, and a keynote lecture presented by Dr. Cynthia Beall of Case Western University. Abstract submission closes July 14th, and we encourage those interested in presenting talks or posters to apply. Please see our website for more information.

bit.do/tree2017

Thank you for your time and consideration and we hope to see you in September!

The TREE organizing committee

Dr. Wynn Meyer

Dr. Caroline Turner

Dr. Martin Turcotte

Melissa Plakke

Sebastian Echeverri

Contact us at biotree2017@gmail.com

biotree2017@gmail.com

## Prague CichlidScience Sep04-07 EXTENDEDdeadlineJun30

We would like to announce the extended registration deadline for the Cichlid Science conference.

Cichlid Science 2017 - research meeting focused on cichlid fishes.

We would like to invite scientists (and enthusiasts) to the upcoming Cichlid Science meeting held in Prague (Czech Republic) on 4th - 7th September. The main goal of the meeting is to bring together scientists from various research fields studying cichlid fishes.

The previous meetings in Basel (2010), Leuven (2012), Bangor (2013) and Graz (2015) covered wide range of aspects of cichlid biology including (but not only) contributions on speciation, adaptive evolution, behavioural or parasitology research, and we hope to continue the tradition.

More info here: http://web.natur.cuni.cz/zoologie/CichlidScience2017/ We look forward to meeting you in Prague.

cichlid.science@natur.cuni.cz

zuzmus@gmail.com

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## PuertoRico EvolBiol Nov14-16

International Conference on Recent Advances in Biological Sciences, 14-16 November 2017, Puerto Rico

Dear colleagues,

The Barranquitas campus of Inter American University of Puerto Rico (IAUPR BC) is proud to welcome delegates to our hosting of International Conference on Recent Advances in Biological Sciences, 14-16^th November 2017. Please find more information at: http://www.br.uipr.edu/icrabs2017/ The plenary speakers of the conference are:

Liam Dolan, University of Oxford,UK

Cassandra Extavour, Harvard University, USA

Mark Cock, CNRS-Station Biologique, France

Karen Sears, University of Illinois, USA

We invite talks and poster presentations in different areas of biological sciences.

Deadline for early-bird registration is 30^th July 2017. Abstract submission ends on 30^th August 2017.

Facebook: https://www.facebook.com/International-Conference-on-Recent-Advances-in-Biological-Sciences-420062228345736/?ref=bookmarks We look forward to seeing you in Puerto Rico.

On behalf of the organizing committee,

Alok Arun

Organizing Secretary Assistant Professor, Inter American University of Puerto Rico PO Box 517 Barraqnuitas 00794 Puerto Rico, USA

alok_arun@br.inter.edu

Alok Arun <alok_arun@br.inter.edu>

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## Shenzhen 1stAsiaEvoConf Apr18-20 CallForSymposia

http://www.asianevo.org/html/programme/topics.html Dear Colleagues:

We are inviting proposals for symposia for the 1st Asian Evolutionary Conference to be held at Shenzhen, China on April 18th-20th. The currently confirmed speakers include, Shigeru Kuratani (RIKEN), Wen-Hsiung Li (Academia Sinica), Manyuan Long (University of Chicago), Nori Satoh (Okinawa Institute of Science and Technology), Zhonghe Zhou (Institute of Vertebrate Paleontology and Paleoanthropology), Xing Xu (Institute of Vertebrate Paleontology and Paleoanthropology).

We launch this platform to connect Asian researchers to the rest of the world for their common interest in evolution. We expect the conference to promote cross-disciplinary collaboration among countries, particularly to nurture the new generation of evolutionary scientists.

The selected symposia will receive substantial financial support to cover at most three invited speakers' registration, travel and accommodation. To encourage young researchers to attend the conference, we will also offer fellowships for five postdocs and five PhD students.

The symposium submission deadline is August 15th, 2017. More details of the conference can be found at http://www.asianevo.org/html/index.html Qi Zhou

Conference Committee: - Hiroshi Akashi, Department of Population Genetics, National Institute of Genetics at Japan - Shu-Miaw Chaw, Biodiversity Research Center, Academia Sinica - Qiaomei Fu,Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences - Naoki Irie, University of Tokyo - Antonia Monteiro, National University of Singapore - Kinya Ota, Academia Sinica - Uma Ramakrishnan, National Centre for Biological Sciences at India - Chau-Ti Ting, National Taiwan University - Zhiheng Wang, Peking University - Xing Xu, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences - Jr-Kai Yu, Institute of Cellular and Organismic Biology, Academia Sinica - Guojie Zhang, BGI & Kunming Institute of Zoology - Qi Zhou, Zhejiang University

Zhou Qi <zhouqi1982@zju.edu.cn>

## Torun Poland EvoLang Apr16-19

The 12th International Conference on the Evolution of Language invites substantive contributions relating to the evolution of human language.

Submissions may be in any relevant discipline, including, but not limited to: anthropology, archeology, artificial life, biology, cognitive science, genetics, linguistics, modeling, paleontology, physiology, primatology, philosophy, semiotics, and psychology. Please see the Call for Papers for details:

https://www.facebook.com/EvoLang2018/-
http://evolang.cles.umk.pl/call-papers Slawomir Wacewicz Nicolaus Copernicus University, Torun http://www.cles.umk.pl http://www.maius.umk.pl/ang/?pid=1&spid=123

Slawomir Wacewicz <wacewicz@umk.pl>

## UAlmeria Biodiversity Sep27-30

Dear all,

Nature and Oceans of Americas and Botanical Garden of University "Marta Abreu" de las Villas, Cuba in collaboration with Andalusian Center for the Assessment and Monitoring of Global Change (CAESCG), University of Almería is also glad to announce the 2nd Symposium on Biodiversity and Nature Conservation: Dissemination and transfer of knowledge among all society sectors.

The second annual Symposium will take place on September 27th-30th, 2017 at the University of Almeria, Spain.

This will become a great venue for a diversity of researchers, managers, conservationists, environmental journalists and general public, so we hope to attract a diverse group.

Information about our meeting:

Our goal is to better integrate all society sectors focused on conservation. We plan to continue annual workshops at Almería as this site is both beautiful and unique. This will be our 2nd annual meeting and we have been attracting scientists from all over the country and overseas.

Registrations are now open.

Abstract and extended registration are due on Jun 20th, 2017.

Symposium has a limited capacity of students.

Website with further information: www.conserbio.wordpress.com < http://www.conserbio.wordpress.com/ >

ConserBio < http://www.conserbio.wordpress.com/ > www.conserbio.wordpress.com Bienvenidos a la página del II Congreso de Biodiversidad y Conservación de la Naturaleza

Link to meeting information: http://www.facebook.com/infoconserbio/ < http://www.facebook.com/ >

Facebook - Log In or Sign Up < http://www.facebook.com/ > www.facebook.com Create an account or log into Facebook. Connect with friends, family and other people you know. Share photos and videos, send messages and get updates.

For further information, please feel free to contact us:

infoconserbio@gmail.com

The organizing committee

marga lopez rivas <margaflor13@hotmail.com>

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## UNewEngland Biddeford GenomicsAdaptation Jul16-21

*Gordon Research Conference -*

*Ecological & Evolutionary Genomics *

*(http://www.grc.org/programs.aspx?id=3D13136 < http://www.grc.org/programs.aspx?id=3D13136 >)*

Connecting Genomic Diversity to Organisms and Environments: Gaining Insights from Advances in Technology, Theory, and Applications

The 2017 Gordon Research Conference on Ecological and Evolutionary Genomics will highlight recent advances in our understanding of the genomic basis of adaptation and the interaction between organisms and the dynamic environments they live in. This meeting will highlight a combination of empirical studies, recent theoretical advances and emerging technologies. Topical areas such as population genomics, phylogenomics, adaptation, the genomic basis of development, and functional genomic responses to the environment will highlight how the rapidly advancing field of genome biology can inform our understanding of the evolutionary and ecological processes that shape biodiversity. The conference will highlight the analysis of large, complex data sets and emerging technologies driving the expanding scale of these data.

Co-chairs, Felicity Jones (Max Plank Institute, Tubingen) and Michael Pfrender (University of Notre Dame) along with co-Vice Chairs, Christian Landry (Universite Laval) and Angela Douglas (Cornell University) invite you to join us on the ocean-side campus of the University of New England in Biddeford, Maine for a stimulating conference. We are assembling a diverse group of established and early career investigators to discuss their latest work. Many sessions will include talks by speakers chosen from among the submitted abstracts. The organizers are actively seeking funds to assist students and others attending the meeting. Applications for attendance will be accepted on a first-come-first serve basis until the meeting is full. Don't delay! Gordon Conferences are famous for fostering in depth interactions that yield new insights in a collegial atmosphere. Please plan on joining us in Biddeford in 2017.

Application Deadline

Applications for this meeting must be submitted by *June 18, 2017*. Please apply early, as some meetings become oversubscribed (full) before this deadline. If the meeting is oversubscribed, it will be stated here. *Note*: Applications for oversubscribed meetings will only be considered by the Conference Chair if more seats become available due to cancellations.

Join us for this great conference. Inquiries can be directed to Michael Pfrender (michael.pfrender.1@nd.edu).

Best regards,

Michael Pfrender & Felicity Jones Co-Chairs

Angela Douglas & Christian Landry Co-Vicechairs

Michael E. Pfrender, Director Genomics & Bioinformatics Core Facility Associate Professor Department of Biological Sciences 109B Galvin Life Science Center Notre Dame, IN 46556 USA

Ph#: 574-631-0591 (O)

Pfrender Lab (http://www.nd.edu/ ˜ mpfrende/-) Eck Institute for Global Health (http://-globalhealth.nd.edu/) Environmental Change Initiative (http://environmentalchange.nd.edu) Genomics and Bioinformatics Core Facility (http://genomics.nd.edu < http://daphnia.cgb.indiana.edu/ >)

"mpfrende@nd.edu" <mpfrende@nd.edu>

# GradStudentPositions

## BangorU PollenBiodiversity

Exploring the ecology of airborne pollen biodiversity using environmental DA analysis and identifying links to hay fever

We are advertising for a PhD opportunity to be hosted in the Molecular Ecology & Fisheries Genetics Laboratory (MEFGL), at Bangor University (http://mefgl.bangor.ac.uk/) to commence in October 2017. The PhD has been made possible via the availability of the ERC Industrial Strategy CASE Studentship scheme and strong links with project partner, the ational Botanic Garden of Wales. The studentship will form part of the ERC EVISIO Doctoral Training Programme (http://www.envision-dtp.org/), a PhD consortium partnership between Bangor, ottingham and Lancaster Universities, alongside numerous environmental bodies, aimed at equipping the next generation of Environmental Biologists with advanced skills.

Project rationale: In addition to providing benefits to society, biodiversityâ€also brings costs. The aerial biosphere includes ecologically complexâ€mixtures of pollens that negatively affect human health. Almost a quarterâ€of people display allergic reactions to tree and grass pollen, causingâ€symptoms ranging from hay fever to asthma, with associated socio-â€economic costs. Identifying tree pollens can be achieved using microscopy,â€but the process is challenging. evertheless, since most grass pollens lookâ€the same, we need to devise novel ways to identify different species toâ€understand which species of grass contribute to allergies. This studentshipâ€has three components. The first aims to use an environmental DA (eDA) approach to enhance the way that we assess aerial tree pollen mixtures. Secondly, to use modelling approaches to compare and contrast the aerial transit of tree and grass pollens in relation to biology/ecology and finally, to identify which species of grass pollen are linked with hay fever. The PhD will form a distinct component within a larger ERC funded study "PollerGE" (http://pollergen.bangor.ac.uk/) and provide an opportunity to work with an interdisciplinary team of scientists from a range of UK Universities, the UK Met Office and the CASE Partner, ational Botanic Garden of Wales (BGW - home of the Wales Plant DA Barcode library). The successful candidate will become a highly skilled, interdisciplinary graduate working at the interface between molecular ecology and environmental epidemiology with the potential to make substantial advances to our understanding of UK flora pollination dynamics and interactions with the allergic response. Co-supervision will be provided by atasha De-Vere/Gareth Griffith/Mat Hegarty (BGW and Aberystwyth), Carsten Skjøth (Worcester), Ben Wheeler/ick Osborne (Exeter/Sydney) and the UK Met Office. Training will be provided in the main areas of molecular ecology, genomics, taxonomy, bioinformatics, modelling; multidisciplinarity skills and epidemiology, complemented by a host of additional opportunities for postgraduate development. Fieldwork will occur within the UK, with opportunities for travel/collaborations in Europe and Australia.

Applicants should hold a minimum of a UK Honours Degree at 2:1 level or equivalent in subjects such as Biology, Environmental or atural Sciences, with a strong motivation to study eDA biodiversity- environment interactions. Eligibility requirements and application portal can be found at http://www.envision-dtp.org . If you are interested in applying, we would strongly recommend contacting Prof. Simon Creer in the first instance (http://mefgl.bangor.ac.uk/staff/si.php; s.creer@bangor.ac.uk; Twitter @spideycreer) and he will be on hand to assist with any questions related to the project, important information on the application process and life in the group.

Closing date for applications: 2nd of July 2017 with interviews predicted to take place between 13th-14th July and look forward to hearing from you!

Rhif Elusen Gofrestredig 1141565 - Registered Charity o. 1141565

Georgina Brennan <g.l.brennan@bangor.ac.uk> Georgina Brennan <g.l.brennan@bangor.ac.uk>

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## Barcelona HumanPopulationGenomics

Ph. D. Scholarship

An FPI Ph. D. scholarship is available within the "Population genomics and demographic history of the Roma (Gypsy) populations" project, in the Population Genetics Program, Institute of Evolutionary Biology (CSIC-UPF), Barcelona. Candidates should have a strong background in population genetics and bioinformatics. Familiarity with the Linux environment, one or more programming languages, and R are desirable. Candidates must be organized, level-headed, focused team players. To learn more about the IBE and the research groups were the successful candidate will integrate, please visit http://www.ibe.upf-csic.es/, http://biologiaevolutiva.org/fcalafell/, and http://biologiaevolutiva.org/dcomas/, and feel free to contact Francesc Calafell (francesc.calafell@upf.edu) for further details. Candidates should send a CV and the contact details for two references to Francesc Calafell (francesc.calafell@upf.edu) before July 15th, 2017.

Francesc Calafell, Ph.D. Institut de Biologia Evolutiva (CSIC-UPF) Dr. Aiguader 88, 08003 Barcelona - Catalonia - Spain Tel: +34-933.160.842 http://biologiaevolutiva.org/fcalafell/ Francesc Calafell <francesc.calafell@upf.edu>

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## CNAG-CRG Barcelona PopGenomicsBioinformatics

The CNAG-CRG is one of the major Genome Sequencing Centers in Europe. It is integrated in the Centre for Genomic Regulation (CRG), an international biomedical research institute of excellence classified in the 9th position (Q1 indicator, Health sector) by the SCImago Institution Rankings (SIR) World Report 2014.

The CNAG-CRG is actively involved in collaborative research projects on a number of specific topics: Disease Gene Identification, Cancer Genomics, Genomics of Infectious Diseases, Model Organism Genomics and Synthetic Biology Genomics of Model Organisms. Researchers at CNAG-CRG actively participate in several H2020 consortia, lead one ERC Synergy grant and are involved in major international initiatives in Genomics (ICGC, IRDiRC, iHEC, GA4GH).

We offer a PhD position to work at the CNAG-CRG on the analysis of whole-exome sequencing and GWAS data to evaluate the role of common and rare genetic variants as possible contributors to dimensional scores of ADHD, led by the team leader of Population Genomics Dr Oscar Lao.

The position requires a candidate with high knowledge in bioinformatics, with strong focus on next generation sequencing/exome sequencing. Advance knowledge on population genetics and genetic epidemiology is also desirable.

The duration of the contract is for three years.

Requirements:

- A BSc or MSc degree in Biology, Biomedical Sciences, Bioinformatics or a related field.
- An advanced knowledge of at least a high-performance language for numerical computation (C, C++, JAVA, Phyton or Perl), as well as a good working knowledge of statistical packages such as R.
- A good working knowledge of Unix systems, in particular large Unix clusters.
- Good spoken and written English.

- May not have resided or carried out her/his main activity (work, study, etc) for more than 12 months in the last 3 years in Spain at the moment the candidate signs her/his contract.

- The candidate should be within the first four years (full-time equivalent) after obtaining her/his BSc or MSc degree.

- The candidate must be eligible for a national PhD fellowship.

Application procedure:

Interested candidates should submit a CV and a brief statement of experience and interests before June 30^th to the recruitment portal through the following link: http://www.crg.eu/en/content/jobs/cnag-jobs MiND EU funding project

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Thanks you in advance!

Nadezhda Alexandrovich

HR Department

Centre for Genomic Regulation (CRG)

C/ Dr. Aiguader, 88

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08003 Barcelona, Spain

Phone. +34 93 316 01 75 (ext. 1175)

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cid:image002.jpg@01D16366.3140F650

Please consider the environment before printing this email

Nadezhda Alexandrovich <Nadezhda.Alexandrovich@crg.eu>

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## ETHZurichEawag ImmuneDefenseEvolution

A PhD student position is offered in the group of aquatic ecology at ETH Zurich (Swiss Federal Institute of Technology Zurich) / Eawag (Swiss Federal Institute of Aquatic Research), in Switzerland, to assess evolutionary potential of innate immune traits of the freshwater snail Lymnaea stagnalis.

Host immune capabilities that counter harmful parasites are considered important determinants for fitness. However, knowledge on the evolutionary potential of immune traits in the wild is limited. This project will examine the extent of genetic variation as well as genetic architecture of snail immunity in natural populations under stress of parasite infections. The project will combine field work, classical quantitative genetic breeding designs, and modern genomics and transcriptomics technologies. The goals of the project are (1) to quantify additive genetic variance and covariance of immune defense traits under field conditions, (2) to determine their genetic architecture by testing whether the traits are polygenic or not and which candidate loci contribute to trait variation, and (3) to test the relative importance of various genetic and non-genetic factors in determining the expression of immune genes by calculating variance components for them. Extensive transcriptomic datasets, previously obtained from L. stagnalis, are available to initiate this project. The work will be conducted in collaboration with Dr. Philine Feulner (Eawag), Prof. Coen Adema (University of New Mexico) and the Genetic Diversity Centre at ETH (http://www.gdc.ethz.ch/).

General information about the research group can be found at http://www.ae.ethz.ch/ We invite highly motivated students with a good background in evolutionary ecology and molecular methods to apply for the position. A MSc or equivalent degree is required. Earlier experience with the study system is not required. The project is funded by ETH Zurich for 3 years. The project will be integrated with ongoing investigations of natural selection on immune function.

Earliest starting date: September 1, 2017

Qualified persons are invited to apply by email. Please attach a single PDF file including a letter of motivation, CV, and names plus contact information of two references to otto.seppaelae@env.ethz.ch. Subject line should read “PHD-Position 2017”. Evaluation of applications starts July 21, 2017. Top candidates will be interviewed.

Dr. Otto Seppälä

Otto.Seppaelae@eawag.ch

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## HumboldtU Berlin EvolutionaryGenomics

The Garfield Lab for Evolutionary Biology at the IRI for Life Sciences/Humboldt University of Berlin has an opening for a PhD student in the field of evolutionary genomics/developmental biology.

Our group focuses on understanding the evolution of developmental gene expression from a population genetics perspective. We are currently recruiting for a project aimed at understanding how gene regulatory networks evolve between closely related species of sea urchin using a combination of ’omics’ methods, including single-cell sequencing, and computational analyses of DNA sequence evolution. The position offers training primarily in experimental biology, though students interested in computational and analytical methods are also encouraged to apply.

PhD candidates will have a Masters degree in Molecular Biology, Evolution, Genetics, or a related field and an interest in understanding evolutionary processes as well as the molecular mechanisms underlying development. Previous experience with modern genomics methods (e.g. high-throughput sequencing) is encouraged but not required. Strong communication and organisational skills are a must. Recruitment is through the IRI Graduate School, which offers numerous training opportunities as well as close interactions with our partner institutions (Charité and the Max Delbrück Center for Molecular Medicine) and collaborators at the nearby Museum of Natural History.

We offer a competitive salary according to German E13 TVöD/Bund (65%). Contracts are 3 years in duration with the possibility of extension. While the working language of the laboratory is English, some knowledge of German (or a willingness to learn) is encouraged. The position requires a flexible commitment of ˜3 hours of teaching per week during the academic semester.

Applications, including a motivation letter, CV, and contact details for two academic references should be sent as a single PDF to info@garfieldlab.org. Applications will be considered until the position is filled with the successful candidate starting in late August (exact starting date is flexible).

For more information, please visit our website at www.garfieldlab.org . David Garfield, PhD

Research Group Leader IRI Life Sciences Humboldt-Universität zu Berlin Philippstr. 13 (Haus 18, Rm. 224) 10115 Berlin, Germany

Office: +49 (0)30 2093-92382 Fax: +49 (0)30 2093-47908 info: www.garfieldlab.org email: david.garfield@hu-berlin.de

David Garfield <david.garfield@hu-berlin.de>

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## ImperialCollege London EvolutionaryBiol

The Quantitative and Modelling Skills in Ecology and Evolution (QMEE) CDT is pleased to announce 5 further NERC-funded PhD studentships plus 1 institutional PhDs starting in October 2017. These projects are in partnership with industry, charities and other stakeholder organisations, including CASE projects providing an additional pounds 1000 stipend to the student each year.

Funded by NERC, QMEE is led by a consortium of 5 research organisations (Imperial College London, University of Reading,Cefas, Centre for Ecology & Hydrology, ZSL) with complementary expertise in quantitative ecology and evolution, working in partnership with government, industry and charities. Individual research projects will be supplemented by innovative cohort training solving real-world problems for non-academic stakeholders.

Partners on advertised projects include the Zoological Society of London, Cefas, Microsoft, the British Honey Company, Nature Metrics, CABI, Medicine and Healthcare products Regulatory Agency (MHRA), UK Atomoic Energy Authority, ClimateEdge, the Biodiversity Consultancy Ltd, JNCC, Royal Horticultural Society, The Woodland Trust, and IBM. For the full list of 16 advertised projects visit our website.

To view example projects, instructions on how to apply and information on eligibility please visit our website.

Applications received before 31st July 2017 will be given priority.

For any questions, please contact Ibi Wallbank, Departmental Manager, at qmee.cdt@imperial.ac.uk

Findaphd.com advert: https://www.findaphd.com/search/PhDDetails.aspx?CAID=3289 Please forward this opportunity to anyone you think may be interested!

"Wallbank, Ibi H" <i.wallbank@imperial.ac.uk>

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## INRA Avignon AphidAdaptation

PhD thesis proposal : Non host resistance and genetic/heritable resistance: how Aphis gossypii, the melon aphid, does adapt?

Supervisor Nathalie Boissot INRA-GAFL (Avignon, https://www6.paca.inra.fr/gafl_eng/), Nathalie.Boissot@inra.fr for more details

The paradigm for plant-pathogen interactions is based on the evolution of molecular patterns of pathogens recognized by the plant (1)): pathogens adapt to immune reaction of plants, either the immune reaction concern the entire plant species and act against the pathogen at the scale species, it is non host resistance, or the immune reaction concern specific plant accessions, what we call genetic resistance or heritable resistance. Like pathogens, aphids deliver into the plant effectors via their adapted mouthparts, the stylets. Aphids establish a compatible relationship with the plant when these stylets reach the phloem in which they feed. Does the paradigm for plants/pathogens coevolution portable to plants/aphids interaction as proposed recently (2), especially in the Melon-Aphis gossypii system? An alternate hypothesis is that aphid specializing on Cucurbit and/or adapted to NLR resistance present in melon use the particularity of the phloemic system, which is dual, in Cucurbits (3).

(1) Jones D.G., Dangl J.L. ,2006, The plant immune system. Nature 444:323-32 (2) Dangl J.L., Horvath D.M., Staskawicz B.J,2013, Pivoting the plant immune system from dissection to deployment. Science 341:746-751 (3) Zhang B.C., Tolstikov V., Turnbull C., Hicks L.M., Fiehn O., 2010, Divergent metabolome and proteome suggest functional independence of dual phloem transport systems in cucurbits. PNAS 107:13532-13537

WORKPACKAGES 1A / Establish in which phloem of Cucurbitaceous plants feed in A. gossypii clones specializing on Cucurbits. This could be tested on Cucurbits belonging to three genera of Cucurbitaceaous: Cucumis melo, Cucurbita pepo and Citrullus lanatus.

1B / Determine whether the punctures of non-Cucurbits aphids not-specializing on Cucurbits cause clogging of the fascicular and/or extra-fascicular phloem on a non-Vat melon plant.

1C / Determine whether the punctures of the specializing clones on Cucurbits which elicit the Vat resistance (ie avirulent clone) lead to clogging of the fascicular phloem and/or extra fascicular on melon Vat plants.

2A / Characterize the diversity of candidate genes for their involvement in the adaptation of A. gossypii to Cucurbits. Establish the phylogeny and confront it with the membership of the breed of hosts of the individuals analyzed. Seek for the traces of selection in these genes.

2B / Identify the avirulence gene in A. gossypii eliciting the Vat resistance. Characterize its diversity, establish the frequency of the allele (s) conferring virulence in natural populations.

METHODOLOGY PROPOSITIONS To determine in which phloem feed the aphids specializing on Cucurbits, adapted or not to the Vat-1 resistance, we will collaborate with the team of Sylvie Dinant at the IJPB (http://www-ijpb.versailles.inra.fr/en/). We will take advantage of the difference in flow velocity in the two types of phloem in Cucurbits, coupled with the use of fluorochromes (Zhang et al., 2010) that can be tracked even in honeydew produced by aphids.

We will use the particular phenotype of aphid-elicited resistance to viruses to identify among an established set of candidate proteins the aphid effector for avirulence. Candidate proteins will be expressed in planta via the use of a viral expression vector. If the candidate protein is the elicitor of resistance, replication of the virus will be blocked in Vat-1 melons but will occur in non-Vat-1 melons. This work will be carried out in collaboration with Cécile Desbiez, (http://www6.paca.inra.fr/pathologie_vegetale_eng/).

We will sample on Cucurbits winged individuals at spring, these aphid populations are known to contain wide diversity (Thomas et al., 2012). Each individual will be characterized on the basis of the 8 SSR markers used routinely in the laboratory and assigned to one of the genetic groups established on the basis of the 2095 genotypes that we have described to date. The candidate genes studied will be sequenced in individuals with non-redundant multilocus genotypes, we will establish phylogenies and selective traces of selection. This work will be carried out in collaboration with Flavie Vanlerberghe, (http://www6.montpellier.inra.fr/cbgp_eng/).

Boissot Nathalie <nathalie.boissot@inra.fr>

## INRA France PopulationGenomicsEuropeanBeech

European beech (Fagus sylvatica L.) is a keystone tree species in European forests, making up 14-18% of total forest cover and with a range spanning from Greece to Sweden.

Beech is the focus of multiple, long-lasting and intensive international research programs in ecology and population genetics. Despite this, little is known about the genetic bases of the adaptation of this species to environmental variation, no genomic reference is available and patterns of genomic diversity are virtually unexplored.

Based on genome sequencing and re-sequencing data, obtained on natural populations and provenance tests throughout Europe, we propose to study patterns of adaptive diversity in coding and promoter regions, to: (a) determine patterns of genomic diversity determined by adaptive processes at multiple geographical scales, from stand to region to range; (b) estimate intensity of selection, through a combination of analytical and modelling approaches; (c) model and predict the ability of European beech to cope with climate change through adaptation.

See links:

https://ivanscottiforestpopgen.blog/2017/05/19/a-phd-thesis-on-the-popu lation-genomics-of-european-beech/

http://www6.paca.inra.fr/-ecologie_des_forets_mediterraneennes/Sujet-de-these-propose/Sujet-de-doctorat-propose-projet-BEECHGENOMES

For more information, please contact Ivan Scotti (ivan.scotti[at]inra.fr)

Thank you very much in advance, Ivan

Ivan Scotti INRA, UR 0629 ≪ Ãcologie des Forets Mediterraneennes ≫ Site Agroparc, Domaine Saint Paul - 84914 AVIGNON Cedex 9 - FRANCE ivan.scotti@inra.fr - Phone +33(0)432722956 - twitter @ittocsnavi http://www6.paca.inra.fr/-ecologie_des_forets_mediterraneennes ——

“To consult the statistician after an experiment is finished is often merely to ask him to conduct a post mortem examination. He can perhaps say what the experiment died of.” (R. A. Fisher)

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Ivan Scotti <ivan.scotti@inra.fr>

## JagiellonianU DrosophilaEvolution

A full PhD position in biology is open for applications in the Institute of Environmental Sciences, Jagiellonian University in Krakow, Poland (http://www.eko.uj.edu.pl/index.php/en/)

Project title: Cell size and performance of ectotherms across environmental gradients in temperature and oxygen availability - testing the theory of optimal cell size on Drosophila melanogaster

Funding agency: National Science Centre, Poland

Project leader: Dr. Marcin Czarnoleski, Life History Evolution group

Duration: 3 years (36 months), starting 1 October 2017

Scholarship: 2 200 PLN (Polish Zloty) monthly for 3 years (this is what exactly a student will receive, no taxes are subtracted from scholarships)

Additional funding possibilities at IES JU: a student can independently appply for a PhD scholarship and for one-year internal grants for young researchers, both funded by the Institute

Formal requirements:

- application deadline: 26 June 2017

- application (email to marcin.czarnoleski@uj.edu.pl) should include CV, motivation letter and contact emails to two persons who are ready to provide a reference letter

- applicants will be interviewed (September 2017, possible online interview)

- applicants have to formally become students of a PhD program in the Institute . The recruitment for this program will be carried out in September 2017 (please follow information on http://www.binoz.uj.edu.pl/studia/-phd_biology/about-the-studies)

Expectations from a candidate:

- predispositions to work as a team member

- background in physiological ecology and evolutionary ecology

- background in basics of cell biology/physiology

- predispositions to manage large experiments, animal stocks, execute histological and microscopic procedures, perform laboratory measurements

Short project outline

1) The main question to be addressed in the project What is an evolutionary significance cell size differences and how an adaptive value of cell size varies with environmental conditions?

2) Background information Following the theory of optimal cell size, a body that consists of many small cells gains increased capacity to deliver oxygen and fuel to cells, but small cells are also costly due to the need to spend energy on their maintenance. We predict that small cells help ectotherms in warm, food-rich but oxygen-poor environments, but they harm ectotherms in cold, food-poor and oxygen-rich environments. A warm ectotherm has speeded metabolism that requires oxygen and fuel, and small cells should help to meet these challenges. In cold and oxygen-rich environment, where organisms do not need super-fast cellular transport but should save energy, large and economic cells would be advantageous.

3) Description of work Laboratory experiments on Drosophila melanogaster will explore how cell size differences between different lines of flies correspond to organismal performance during activity (flight endurance and intensity, egg laying) and during rest (oxygen consumption) at different thermal and oxygen conditions. Generally, by raising ambient temperature, we will test whether small cells help flies to perform in warm and low-oxygen conditions. We will use lines with mutations in cell cycle generated by genetic engineering, lines with evolved cell size differences during evolutionary experiment, and lines with plastic changes in cell size. Histological methods with automated methods of image analysis will be used to measure cell size differences among flies. Confocal microscopy will be used to measure differences in the architecture of a tracheal system.

Dr. Marcin Czarnoleski

Jagiellonian University Institute of Environmental Sciences Gronostajowa 7, Krakow 30-387 Poland phone: (+48)126646873 email: marcin.czarnoleski@uj.edu.pl

Dr hab. Marcin CzarnoÂ³êski

Instytut Nauk o Ârodowisku Uniwersytet Jagiellon̄ski ul. Gronostajowa 7, Kraków 30-387

"UrodziÂ³em siê z rodziców ubogich, od dziecka pociÂ±g czujÂ±c do myÂbyt penetrujÂ±cego" StanisÂ³aw Lem, Cyberiada

marcin.czarnoleski@uj.edu.pl

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## LudwigMaximiliansU ButterflySpeciation

PhD: Behavioural isolation in Heliconius butterflies

We are seeking a highly motivated PhD student to investigate mate choice and speciation in the tropics. The student will focus on behavioural and genetic/genomic aspects of reproductive isolation in Heliconius butterflies.

The student will be supervised by Dr Richard Merrill (https://richmerrill.wordpress.com), and funded as part of his DFG Emmy Noether grant. The project is focused on understanding the genetic basis and evolution of differences in visual mate recognition between divergent Heliconius taxa. Heliconius butterflies are well known for their bright warning patterns, which males also use as a mate recognition cue. Although the genetic basis of the colour pattern cues is now known in great detail, we know relatively little about the genetic basis of the corresponding preference behaviours. In addition, we still know little of how colour pattern cues may influence female mating decisions.

The project would suit someone keen to combine fieldwork and behavioural experiments in the tropics with molecular lab work and genomic analysis.

Methodological approaches could include mate choice assays, QTL and/or gene expression analyses, but could also involve additional field, lab or insectary experiments depending on the candidate's interests.

The successful candidate will be based in the Division of Evolutionary Biology, Ludwig-Maximilians-Universitat, Munich. Across the division, we take an integrative approach to the study of evolutionary processes (http://www.evol.bio.lmu.de/), and apply a large range of methodologies including fieldwork, population genetic modelling, large genomic approaches, experimental evolution work and functional characterization. The student will also likely spend considerable time at the Smithsonian Tropical Research Institute in Panama, in collaboration with Dr Owen McMillan's research group. Both at LMU and STRI (http://www.stri.si.edu), the student will be part of vibrant international communities of scientists. The researcher will join a collaborative and driven community of Heliconius biologists (http://www.heliconius.org).

Further information (including relevant publications) can be found at (https://richmerrill.wordpress.com), and questions should be directed to Richard Merrill (merrill@biologie.uni-muenchen.de). Applications should be sent to the same address, and include a CV, a letter of motivation and the names and contact details of two referees before 21^th June 2017. Please use the subject header: "HELICONIUS SPECIATION PHD".

Dr. Richard Merrill Emmy Noether Group Leader Division of Evolutionary Biology Faculty of Biology Ludwig-Maximilians-Universitat Munchen Grosshaderner Strasse 2 82152 Planegg-Martinsried phone: +49 (0)89 / 2180-74160 (Panama: (+507) 64267029) https://richmerrill.wordpress.com @dickmerrill

Richard Merrill <merrill@biologie.uni-muenchen.de>

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## MaxPlanck BeetleMolEvol

The MPI for Chemical Ecology, Department of Entomology, has an opening for a PhD student (m/f) on a DFG-funded project

Project Description: The charismatic longhorned beetles (Coleoptera: Cerambycidae) are part of the most diverse group of wood-feeding (xylophagous) animals on Earth. Larvae of these beetles have evolved to thrive on a highly challenging and sub-optimal environment - wood material - where they have to cope with the structural polysaccharides of the plant cell wall which make the bulk of their food. Earlier research indicated that cerambycid beetle larvae break down cellulose, hemicelluloses and pectins themselves by producing plant cell wall degrading enzymes (PCWDEs), independent of symbionts. Yet, the corresponding genes and the way they evolved remain elusive in this group of beetles. By combining gene discovery by sequencing beetle midgut transcriptome using RNA-Seq, to phylogenetic analyses and rapid screening of enzymatic activity by expressing the corresponding cDNAs in heterologous expression systems, this project aims to identify and characterize the genes encoding PCWDEs and to determine their evolutionary history in Cerambycidae. This research will provide information on how host plants and feeding behavior have shaped the composition of these gene families during the evolution of Cerambycidae; and on how PCWDEs contributed to build and maintain the biodiversity of this family of beetles. This project also opens the exciting possibility that screening the gut transcriptome of longhorned beetles represents an alternative to microorganisms for the discovery of new and better PCWDEs for use in industrial biotechnology, in particular for the improvement of biofuel production from plant biomass.

We are looking for a motivated student with a University degree (M.Sc. or equivalent) with a focus on bioinformatics and molecular evolution, with a strong will to work in the wet lab. We expect good verbal and written communication skills. Experience working with RNA-Seq data (assembly and analysis) and molecular evolution methodologies (phylogenetic analyses among othersâ euro Â) is required. Knowledge of different wet lab techniques (e.g. PCR; DNA, RNA and protein extraction; Western Blot; Enzyme assays; insect cell and/or bacterial cultures) is a plus.

We offer excellent technical equipment and close supervision in an international environment. A structured PhD program is offered by our graduate school (IMPRS) which provides interdisciplinary training by seminars, lectures and scientific workshops. The payment and benefits are based on the TVoD guidelines and the appointment is for 3 years with possibility of extension. Application deadline: July 1st.

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

Application: Questions concerning the project or the position are welcome and should be addressed to Dr. Yannick Pauchet. To apply, please email a statement of motivation, CV and a letter of reference as a single PDF file to ypauchet [at] ice.mpg.de. (end)

Yannick Pauchet <ypauchet@ice.mpg.de>

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## NanyangTechU HumanPopGenomics

Title: Nanyang Technological University, Singapore, Human Population Genomics

A PhD position is available at Nanyang Technological University, Asian School of the Environment (http://www.ase.ntu.edu.sg/).

The main research interests are Human demographic history and genome diversity.

The PI is a founding member of the GenomeAsia 100K consortium (http://www.genomeasia100k.com/), and the research project will be a collaboration with the consortium project.

Candidates must have strong interests and passions on population genetics, genomics, or bioinformatics.

To learn more about the Institute and admission, please visit http://www.ntu.edu.sg/, and feel free to contact Hie Lim Kim (HLKIM@ntu.edu.sg).

Candidates should send a CV including research interests to HLKIM@ntu.edu.sg.

Hie Lim Kim, PhD

Asian School of the Environment, Nanyang Technological University

Hie Lim Kim Ph.D. | Assistant Professor | Asian School of the Environment, SCELSE | Nanyang Technological University

60 Nanyang Drive, SBS-B3N-27, Singapore 637551 Tel: (65) 6908-3375 | Email: HLKIM@ntu.edu.sg

"Kim Hie Lim (Asst Prof)" <HLKIM@ntu.edu.sg>

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## Rothamsted AphidGenetics

A full Waitrose - BBSRC CTP funded PhD position is open to work on population genetics and the evolution of resistance in aphids. The project is a collaboration between Rothamsted Research, University of Warwick, and G's, a leading lettuce producer.

"Using landscape genomics to improve management of insect pest species"

Insect pests have a widespread negative impact in agriculture, resulting in very large economic loses. Monitoring and surveillance of pest species is fundamental to control their populations and reduce the damage they inflict on crops. This is because an early detection improves the chances of controlling them before they spread out and increase their population size. However, studying the migration of small insects can be problematic due to the difficulty of tracking individuals. In addition, resistance to pest control methods, whether to insecticide or to host-plant resistant cultivars, is becoming an increasingly important issue. Inferring the population structure of pest species and the connectivity across populations and landscapes is key to understand migration patterns, which can be used to inform pest surveillance and control schemes. This fully-funded project provides an exciting opportunity to apply population genomics and evolutionary concepts to improve insect pest management and understand the evolution of resistance.

The project will use /Nasonovia ribisnigri/, the currant-lettuce aphid, as a model system to evaluate how landscape genomics can be used to improve aphid surveillance and control the spread of resistance alleles. The currant-lettuce aphid, /Nasonovia ribisnigri/, is a major pest of lettuce crops responsible for large economic losses. One of the most efficient way to reduce aphid infestations and damage is growing host-resistant lettuce cultivars that stop aphids from colonising the plant. However, the capacity of breaking the host-plant resistance mechanism (Rb) has recently evolved in some biotypes. In these circumstances, surveillance and monitoring of crops becomes of great importance to produce early warning information that would improve targeted control of /N. ribisnigri /before aphids enter the lettuce head. However, the paradox is that whilst winged aphids are quick to colonise the lettuce crop in spring they are unusually scarce in both water traps and suction traps.

Understanding the migration patterns of the species is, therefore, fundamental to design efficient methods of capture and control. For this, the project will use genomics to infer the population structure and the levels of gene flow between populations of /N. ribisnigri/ at different geographic scales and different landscapes. This knowledge will be used to develop surveillance methods that maximise the observation of individuals of the species at the early stages of their migration into the crops. Furthermore, these results combined with the development of genome-wide markers for the Rb phenotype will provide fundamental information about the evolution and spread of resistance across the UK.

*Application deadline is the 10 July and the starting date is October 2017. *

Informal enquiries to ramiro.morales-hojas@rothamsted.ac.uk are very welcome.

Application procedure and further information can be found at:

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=84993&LID=1573 Eligibility: UK citizens and EU citizens who have resided in the UK for 3 or more years.

Ramiro Morales-Hojas

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Dr. Ramiro Morales-Hojas Molecular Ecologist / Entomologist Rothamsted Insect Survey Agroecology Department

e-mail: ramiro.morales-hojas@rothamsted.ac.uk; r.moraleshojas@gmail.com web-site: https://sites.google.com/site/ramiromoraleshojas/ web-site: http://www.rothamsted.ac.uk/insect-survey r.moraleshojas@gmail.com

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## SGN Frankfurt AvianEvolutionaryGenoimics

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) explores the interactions between biodiversity, climate, and society. Senckenberg BiK-F invites applications for a

PhD position in Evolutionary Genomics of Birds

(50 %) There is an exciting opportunity for a talented and motivated applicant to join the working group of Prof. Dr. Axel Janke.

Your profile: • Master degree in Biology, Genetics, Evolution and speciation in birds at the genomic level • Strong interest and proven skills in evolutionary, population or phylo-genetics • Experience in analyzing genomic data • Very good written and oral communication skills in English • Interest to be involved in an international and interdisciplinary group to expand the work to species distribution modeling, paternal inference and conservation genetics

Salary and benefits are according to a full time public service position in Germany (TV-H E 13, 50%). The contract should start on October 1st, 2017 and will initially be limited until September 30th, 2020. The Senckenberg Biodiversity and Climate Research Centre supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung. Please send your application, mentioning the reference of this job offer (ref. #11-17016) before June, 30th 2017 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your Master degree to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de

For scientific enquiries please get in contact with Prof. Dr. Axel Janke, axel.janke@senckenberg.de

Mit freundlichen Grüßen /Best Regards

Maria di Biase Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß Â§22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

Besucheradresse: Voltastraße 1, 60486 Frankfurt am Main (5. Obergeschoss)

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting) - 1313 di-Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid Kröncke Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Senckenberg forscht für Ihr Leben gern! www.200jahresenckenberg.de recruiting <recruiting@senckenberg.de> recruiting <recruiting@senckenberg.de>

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## SheffieldHallamU GenomicAnalysis

PhD position in genomic analysis with Dr Lucy Crooks at Sheffield Hallam University, Department of Biosciences and Chemistry.

I have funding for a UK/EU PhD student to start on October 2nd.

This is a bioinformatics project of data analysis as opposed to 'wet-lab'. The area is disease genomics with a focus on schizophrenia.

Next generation sequencing enables us to detect nearly all the genetic variants in an individual. The difficulty for determining the cause of disease is that there are hundreds of thousands of variants per person. A GWAS of nearly 37,000 patients and over 100,000 controls associated 108 loci with schizophrenia but these only explain 3% of the disease risk. There are clearly more variants to be found. The aim of the project is to develop and apply a different approach to work with moderate-sized patient groups. The idea is firstly to filter the variants in one patient by combining biological knowledge and pathogenicity predictions from databases to a shortlist that are likely to be contributing to disease. Using gene expression data to define differential expression in the brain will particularly be investigated. Secondly, to look for a common process from the aggregated variants across a set of patients, with the assumption that each may have a different variant.

Schizophrenia has a lifetime prevalence of 0.5-1% and it is ranked as the 12th highest worldwide cause of disability. It is a chronic condition that can impact on your ability to think, your emotions and behaviour. People with schizophrenia are often unable to connect and properly function in the society around them. Identifying genetic variants and the process involved in schizophrenia should lead to people being diagnosed quicker and more targeted treatments, which would improve patient prognosis and wellbeing. The developed method should be of broad interest for identifying variants in other diseases and relevant to interpreting results from the NHS 100,000 genomes project.

You will work with variant calls from existing exome sequences and publically available gene expression data. You will need to use a Linux server and programme in a language such as Perl. These are skills I can teach you, but it is essential that you have a logical mind and are good at solving novel problems. You should consider this position if you are good at maths or statistics. I particularly encourage you to apply if you have experience in large-scale data analysis or programming in a language such as Perl. You should have at least a 2.1 Honours degree in either a biological subject with a maths or statistics component, physics, or computer science.

You would be a part of the Sheffield Bioinformatics Hub, which includes several researchers from the University of Sheffield and their PhD students. The Hub provides support, opportunities for seminars and discussion and to learn from other members. Sheffield is a lovely city, there are plenty of green spaces and the Peak District is nearby. Living costs are reasonable and many students like the city so much that they stay on here.

Closing date for applications is 30th June.

For further details, including how to apply please go to http://www.findaphd.com?pj=86852 If you are interested in the studentship and would like to discuss it with me, please contact me at L.Crooks@shu.ac.uk

Departmental website https://www.shu.ac.uk/about-us/our-people/staff-profiles/lucy-crooks
Sheffield Bioinformatics Hub website http://bioinformatics.group.shef.ac.uk/

“L.Crooks@shu.ac.uk” <L.Crooks@shu.ac.uk>

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## UExeter WesternSydneyU InsectExptEvolution

PhD in Lifespan and healthy ageing, with Prof John Hunt and Prof David Hosken.

This PhD will harness the power of experimental evolution in two insect systems (Drosophila simulans and the decorated cricket, Gryllodes sigillatus) to examine the importance of dietary adaptation in the evolution of lifespan and healthy ageing.

This is a collaboration between the University of Exeter (UK) and Western Sydney University (Australia) for a fully-funded PhD studentship to commence in January 2018 or soon thereafter. Applicants should be based in the UK or EU and must have a MSc. Publications in the primary international literature would be beneficial. For eligible students the studentship will cover UK/EU tuition fees plus an annual tax-free stipend of at least 14,553 for 3.5 years full-time, or pro rata for part-time study. The student would be based in the Centre for Ecology & Conservation at the Penryn Campus in Cornwall (University of Exeter) and the School of Science and Health at the Hawkesbury Campus (Western Sydney University).

Academic Supervisors: Professor David Hosken, University of Exeter Professor John Hunt, Western Sydney University

For further information contact David Hosken: d.j.hosken@exeter.ac.uk

Prof DJ Hosken University of Exeter, Cornwall Tremough, Penryn TR10 9FE UK

D.J.Hosken@exeter.ac.uk http://biosciences.exeter.ac.uk/staff/index.php?web_id=david_hosken “Hosken, David” <D.J.Hosken@exeter.ac.uk>

## 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: http://luvs.hi.is/-phd_position_evolution_reproductive_barriers_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 Hólar University College, Iceland, will also participate in the project.

Application deadline is July 15th 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.

Applicants should send 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 to Sigurdur S. Snorrason (sigsnor@hi.is). They should also send a i) CV, ii) transcripts of university diplomas, iii) courses taken at bachelor and masters level, iv) degree project thesis and v) 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 Palsson 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:

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To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

## UMontpellier GenomicConvergence

ERC-funded PhD position

The ConvergeAnt project: Tracking molecular convergence in ant-eating mammal genomes.

We invite applications for a PhD position funded by the European Research Council (ERC) for 36 months at the University of Montpellier (France).

Co-supervisors. Dr. Frédéric Delsuc (frederic.delsuc@umontpellier.fr) and Dr. Benoit Nabholz (benoit.nabholz@umontpellier.fr).

Research Unit. Institut des Sciences de l'Evolution de Montpellier, UMR 5554, CNRS, IRD, EPHE, Université de Montpellier, Montpellier, France.

Host Laboratory. Genome Department, Team "Phylogeny and Molecular Evolution" (http://www.isem.univ-montp2.fr/recherche/equipes/phylogenie-et-evolution-moleculaire/personnel/).

Background. Despite its widespread occurrence across the tree of life, many questions still remain unanswered concerning the fascinating phenomenon of convergent evolution. Our objectives with this project are to provide new insights on a textbook example of adaptive evolutionary convergence represented by mammalian myrmecophagous species, in which similar phenotypes evolved independently in several lineages. The acquisition of a myrmecophagous diet almost exclusively composed of ants and/or termites has indeed evolved independently in five placental lineages with armadillos (Cingulata), anteaters (Pilosa), aardvarks (Tubulidentata), pangolins (Pholidota) and aardwolves (Carnivora). However, large-scale comparative genomic studies of myrmecophagous placentals are still lacking. In this ConvergeAnt PhD project, we propose taking advantage of the unique set of convergently evolved characters associated with the ant-eating diet to investigate the molecular mechanisms underlying phenotypical adaptation by analyzing the genomes of myrmecophagous placentals.

Tasks. The main objectives of this PhD project are to reveal the genomic adaptations underlying the convergent evolution of myrmecophagous phenotypes in armadillos, anteaters, aardvarks, pangolins, and aardwolves. The fundamental evolutionary questions we aim to answer by the completion of this project are: (1) Which genomic adaptations have evolved in response to the selective constraints imposed by the myrmecophagous life-style? (2) Do the same genomic adaptations underlie the convergent phenotypes seen in independent ant-eating mammalian lineages? (3) How widespread is adaptive convergent molecular evolution in ant-eating placental genomes? To this aim we will analyse genomic data that are currently produced within the project in the form of both RNAseq experiments and whole genome sequences. We will first focus on candidate genes likely to be involved in the convergent adaptation to the myrmecophagous diet. For these genes, we will perform detailed analyses of molecular evolution based on site- and branch-wise estimations of the non-synonymous to synonymous substitution ratio (dN/dS) in order to investigate the potential occurrence of convergent selective pressures in myrmecophagous lineages. We will then evaluate the extent of genome-wide adaptive convergent molecular evolution in myrmecophages by performing genome-wide survey of convergent and divergent amino acid substitutions using site-heterogeneous mixture models. The aim is to identify genes presenting an excess of adaptive convergent substitutions in myrmecophagous lineages by contrast with non myrmecophagous lineages. Finally, we will investigate the potential parallel evolution of specific gene families such as olfactory and taste receptors. Gene repertoires will be statistically compared among myrmecophagous species to identify potential convergent expansions and/or losses relative to other mammalian species with different diets. Overall, the project will build upon recent experimental and theoretical advances on detecting convergent evolution at the molecular level.

Candidate profile. Mandatory requirements include a Master's degree in evolutionary biology, bioinformatics skills, experience in working with genomic data (whole genome assembly, RNAseq), and good knowledge of phylogenetics and molecular evolution methods. Basic programming skills (Bash/Perl/Python scripting) are a prerequisite, advanced programming skills will be a plus. A high degree of initiative and motivation, and dedication to the project are also expected. There are no conditions of nationality, but as the successful candidate will be part of an international team, good English skills and capacity for teamwork are highly desirable. The successful candidate will have a genuine interest to interact with other project members working on morphological evolution and microbiome evolution in mammals.

Applications. Candidates must send electronically their application before June 30th, 2017 in the form of a single PDF file including a

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## UNevada Reno PlantPopulationGenetics

The Parchman lab at the University of Nevada, Reno is recruiting a PhD student to conduct population genetic and genomic analyses on a suite of native plants in the Great Basin Desert. The student would be advised by Dr. Thomas Parchman (Department of Biology; http://parchmanlab.com) and co-advised by Dr. Elizabeth Leger (Department of Natural Resources and Environmental Sciences; http://www.ag.unr.edu/leger/Leger/Home.html). This work, funded by a USDA NIFA grant, aims to determine the phenotypes and evolutionary histories that enhance seedling establishment and to analyze the genetic structure and diversity of native plant populations to inform restoration practices. Ideal applicants would have strong interest in plant evolutionary genetics and some or all of the following qualifications (or a strong desire to learn these skills): 1) Molecular genetic laboratory experience, 2) Programming experience in R, Unix, and/or Perl (or Python), 3) interest in the ecology and evolutionary biology of Great Basin native plants 4) Past experience or strong interest in restoration ecology and restoration genetics.

UNR has a strong interdisciplinary PhD program in Ecology, Evolution, and Conservation Biology (http://environment.unr.edu/eecb/). Graduate students accepted into the EECB program are guaranteed financial support through Teaching Assistantships (TAs), which includes health insurance and an out-of-state tuition waiver. For this position, funds are additionally available for a number of semesters will be available through Research Assistantships (RAs). The successful applicant could begin the PhD program as soon as Fall 2017, with the possibility of joining the lab sooner as a technician.

University of Nevada, Reno (UNR) is a Tier I research university located in a spectacular environment at the confluence of the Great Basin and the Sierra Nevada Mountains. The faculty and graduate students at UNR are highly interactive and include an internationally known group of evolutionary biologists and ecologists. The Parchman lab has recently been renovated, and is equipped with ample (and new) molecular and computational resources for modern genome sequence analysis. We are also located in an ideal setting for field-based projects in the Great Basin and Sierra Nevada regions, allowing enviable access to spectacular montane and desert ecosystems. Reno is only 40 minutes from Lake Tahoe, offers a high quality of living, an excellent climate, and is a large enough city to offer diverse activities and amenities. World class rock climbing, skiing, and mountain biking opportunities are in extremely close proximity.

Interested applicants should send a CV, copies of transcripts, and a statement of research experience and interests to Tom Parchman (tparchman@unr.edu) and Elizabeth Leger (eleger@cabnr.unr.edu). Consideration will begin immediately and applications will be reviewed until the position is filled.

Thomas L. Parchman Assistant Professor Department of Biology, MS 314 University of Nevada, Reno Max Fleishman Agriculture Building 1664 N. Virginia Street Reno, NV 89557-0314 tparchman@unr.edu

Thomas Parchman <tparchman@unr.edu>

## UNewSouthWales Phylogenetics

A PhD position: Climate Change: phylogenetic comparative analysis, meta-analysis and computational modelling UNSW has announced another round of prestigious PhD scholarship (http://www.2025.unsw.edu.au/apply). We have been lucky enough to have been awarded one of these.

This project comes with $40,000 per year stipend and $10,000 of research funding per year (for full 4 years). It is open to both Australian and international applicants.

The topic is broad intentionally to attract an outstanding student: Climate change is impacting ecosystems worldwide. Many plant and animal species will not survive unless their distributions shift. However, not all species are moving and we don't systematically understand why.

This is a key challenge for understanding climate impact. In this project students will tackle important knowledge gaps: Can we use functional traits to predict species' ability to shift distributions? Which biotic and abiotic factors are important in determining species range? Do different processes act at northern vs southern limits?

And, are distributions shaped by extreme climate events, or by the average conditions at a site? We will tackle a range of questions relating to climate change using phylogenetic comparative methods, meta-analysis and computational modelling (our supervisor team members are experts in these areas).

Given the generous stipend and project funding, an applicant is expected to be very competitive. We expect an applicant to have at least one peer-reviewed publication or an equivalent publication or experience which demonstrate their outstanding abilities.

Supervisory team: A/Prof Shinichi Nakagawa (http://www.i-deel.org/) A/Prof Will Cornwell (http://willcornwell.org/) Dr Daniel Falster (http://danielfalster.com/) If you would like to be considered, send your CV, cover letter, and contact information to three references to Vera Banschikoff – v.banschikoff@unsw.edu.au – by 24 June 2017. For more information on the scholarship program, see https://research.unsw.edu.au/ unsw-scientia-phd-scholarship-scheme.

Dr Shinichi Nakagawa (Associate Professor / ARC Future Fellow) Deputy Director of Research, Evolution & Ecology Research Centre, EERC (Visiting Scientist at Garvan Institute of Medical Research) Room 5102, Biological Sciences Building (E26) School of Biological, Earth and Environmental Sciences, BEES The University of New South Wales Randwick NSW 2052, Sydney, Australia Mobile: 0422 655 854 Office : 0293 859 138 Website: http://www.i-deel.org/ Shinichi Nakagawa <s.nakagawa@unsw.edu.au>

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## Unife FEM ConsGenomicsAlpineGrouse

A fully-funded 3-year PhD position is available for an enthusiastic student with a background in conservation, population or evolutionary genetics, to analyse patterns of genomic variation in three Alpine grouse species for conservation and management purposes.

The student will spend approximately half their time in the two collaborating research groups, those of Giorgio Bertorelle (University of Ferrara, Italy - UNIFE), and Heidi C. Hauffe (Fondazione Edmund Mach, Trento, Italy - FEM). Barbara Crestanello in the Hauffe group, and expert in tetraonid conservation genetics and genomics, will act as an additional supervisor.

The student will register at UNIFE, and academic training include seminars and courses, as well as participation in national and international conferences.

Brief project description: This project will focus on three charismatic alpine bird species of conservation and management concern for which data on mtDNA and STR markers for more than 200 individuals per species are already available from Trentino and surrounding regions. The main goals of the project are to a) type SNP markers for a subset of the above samples using GBS; b) compare the power of mtDNA/STRs and SNPs to reconstruct demographic history; c) identify if and how different ecological niches, reproductive systems, and hunting pressures affect the genomic variation; d) translate the results into efficient management and conservation strategies; e) use available technologies to develop SNP sets that can be used for future cost-effective conservation genomic investigations.

Informal enquiries for further details of the aims of the project should be sent to barbara.crestanello@fmach.it, heidi.hauffe@fmach.it, or giorgio.bertorelle@unife.it.

The position is for candidates with a degree equivalent to an Italian "Magistrale" degree (Master), and in an appropriate subject (e.g. Biology, Biotechnology, Mathematics). A keen interest in data analysis as applied to conservation, and preferably, at least 6 months' experience in a basic molecular biology laboratory, are requested. Good English skills are necessary, but knowledge of Italian is not essential (although it obviously helps for living in Italy!).

The formal online application form will be available around mid June at the site www.unife.it/studenti/dottorato/concorsi. However, interested candidates are welcome to send already to giorgio.bertorelle@unife.it an application letter, stating the applicant's motivation for the position, experience and skills related to the requirements listed above, a full CV, and contact information (including email addresses) for 2 potential referees. Please send your application file as a single pdf.

Ferrara is an ancient Medieval and Renaissance town located in North-Eastern Italy, 50 km North of Bologna and 100 km south of Venice. Far from being shrouded in the past, Ferrara is a cyclist- and pedestrian-friendly sustainable town where young people can experience a high quality of life, take advantage of well-maintained infrastructures, and pleasantly blend in. More information can be found at http://www.unife.it/international/student-life The campus of the Fondazione Mach is located in San Michele all'Adige 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. See also: https://www.visittrentino.info/en, and http://www.fmach.it.– –

Giorgio Bertorelle Department of Life Sciences and Biotechnology University of Ferrara Phone +39 0532 455743 Fax: +39 0532 249761

Bertorelle Giorgio <ggb@unife.it>

## UOtago NewZealand EvolutionaryGenomics

Evolutionofthe New Zealand bird fauna

APhDposition in evolutionary genomics is available to study aspects of the evolution of New Zealand's unique bird fauna with Dr Michael Knapp at the University of Otago, Dunedin, New Zealand.

NewZealand'sisolation and mammal predator free environment has lead to the evolution of a unique bird fauna. It includes model species to study the evolution of island gigantism, flightlessness and alpine adaptations, to name just a few and is therefore uniquely suited to shed light on the ecological and molecular processes that underlie such evolutionary adaptations.

ThisPhDproject is part of our Royal Society funded research programme, which uses genomic data to address key questions of bird evolution and conservation in New Zealand's unique environment. It offers the flexibility for the PhD student to decide on the direction of the PhD studies within the framework of our research programme. Possible question include for example the response of the New Zealand bird fauna to past and predicted future climate change, and the evolutionary basis of island gigantism and flightlessness.

TheidealPhD student will have skills in molecular ecology/population genetics and/or bioinformatics and genome data analyses.

TheUniversity of Otago is one of the most research-intensive Universities in New Zealand with a world-class reputation in the life sciences. It provides an environment that allows its students to undertake internationally recognised research, in a diverse and vibrant postgraduate environment and has been ranked as one of the 15 most beautiful campuses in the world. The PhD student will be hosted by the Department of Anatomy, a diverse and research-oriented department with expertise ranging from genomics to biomedical sciences.

Fordetails and instructions on how to apply, please visit: http://www.otago.ac.nz/anatomy/study/postgraduate/opportunities/index.html Theproject is listed under "Evolution of the New Zealand bird fauna".

Forfurther questions please contact Dr. Michael Knapp (michael.knapp@otago.ac.nz).

Pleaseapply by 18/June/2017.

michael.knapp@otago.ac.nz

## UOtago NewZealand MarineBiodiversity

Evaluating marine biodiversity in New Zealand using environmental DNA

A PhD position studying marine biodiversity in New Zealand is available with Dr Michael Knapp at the University of Otago, Dunedin, New Zealand.

A key to efficient, ecosystem-based management of marine resources is the availability of suitable tools to measure patterns in biodiversity. Current methods are costly, labour intensive and rely on surveys of a limited number of indicator species and sites to provide an estimate of biodiversity and ecosystem health. Consequently, their capacity for resolving the complexity of marine communities at an ecosystem level is highly compromised.

This PhD project will establish, test and apply an innovative, high-throughput and cost efficient strategy for quantifying marine biodiversity using environmental DNA (eDNA) extracted from marine water samples. It will include evaluating and analysing the biodiversity in marine protected areas around New Zealand and its implications for marine conservation efforts.

This PhD project is part of a National Science Challenge funded research programme, which uses environmental DNA techniques to evaluate marine biodiversity in New Zealand.

The ideal PhD student will have skills in molecular ecology, marine ecology, population genetics and/or bioinformatics and metabarcoding data analyses.

The University of Otago is one of the most research-intensive Universities in New Zealand with a world-class reputation in the life sciences. It provides an environment that allows its students to undertake internationally recognised research, in a diverse and vibrant postgraduate environment and has been ranked as one of the 15 most beautiful campuses in the world. The PhD student will be hosted by the Department of Anatomy, a diverse and research-oriented department with expertise ranging from genomics to biomedical sciences.

For details and instructions on how to apply, please visit: http://www.otago.ac.nz/anatomy/study/-postgraduate/opportunities/index.html The project is listed under "Evaluating marine biodiversity in New Zealand".

For further questions please contact Dr. Michael Knapp (michael.knapp@otago.ac.nz).

Please apply by 18/June/2017.

"michael.knapp@otago.ac.nz"
<michael.knapp@otago.ac.nz>

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## UPisa CiliateSystematicsGenomics

Available 3 PhD positions on the topic "Integrative systematics and metagenomics for the study of ciliates and their bacterial symbionts".

We are actively looking for competitive, highly motivated, not-Italian candidates

Candidates having any combination of the following expertise are especially welcome:

Ciliate biology, Protistology, evolutionary biology, ciliate or protist cell culturing, bacterial symbiont biology, traditional morphology and morphometric, taxonomy, systematics, evolution, host-symbiont interaction and co-evolution, silver nitrate and protargol cell staining, scientific hand drawing for taxonomic purposes, Scanning Electron Microscopy, Transmission Electron Microscopy, ecology, in vivo experiments with protist, advanced statistics, microbial ecology, molecular biology, molecular systematics, Next Generation Sequencing, bioinformatics, Linux, metagenomics assembly programs, metagenomic analysis, transcriptomics, comparative genomics, phylogenomics, metabolic pathway reconstruction, Rickettsiales and/or Verrucomicrobiales biology and genomics, microbiome characterization and analysis, bacterial and parasitic fish disease, wastewater treatment

Deadline for the application 19^th July at 1.00 p.m. Italian time (bureaucratic procedure is a bit complex)

All interested scholars are invited to contact each of us for any information, advice, or also for an "informal" pre-evaluation of their own Curriculum Vitae.

Our contacts are:

Letizia Modeo, email: letizia.modeo@unipi.it

Giulio Petroni, email: giulio.petroni@unipi.it

Please consider that probably one candidate will be selected to work mainly in Integrative Systematics while the other mainly in Metagenomics.

Please also note that scholars who already get a PhD outside Italy or students who will defend their diploma/master within 31/10/2017 are as well eligible for the application.

Interested candidates should submit the application before deadline (19^th July at 1.00 p.m. Italian time) following instruction available at the links:

http://dottorato.unipi.it/index.php/it/concorsi-d-ammissione-a-a-2017-2 018.html

http://dottorato.unipi.it/index.php/it/concorsi-d-ammissione-a-a-2017-2 018/item/317.html

Instruction in English will be soon available, but in the meanwhile for any problem or information request please feel free to write us.

In the application, candidates will have to upload:

- a detailed and signed Curriculum Vitae,

- copy of University certificates with marks (foreign candidate MUST submit all certificates attesting their university qualification also translated in English),

- copy of a valid identity document (e.g. identity card or Passport),

- Any other material they consider useful for their evaluation such as: reference letters, publications, copy of the thesis, name and contact information of possible referees, a motivational letter, a letter in which they accept to spend one year abroad for research purpose in case it is required by supervisors, etc.

Applicants will have to pay a fee of 60 Euro (from abroad it can be paid online with credit card, paypal or bank transfer).

Based on the evaluation of uploaded documents, admission to oral examination will be decided and notified within the 1st of September 2017

Oral examination is scheduled on the 6^th of September 2017, starting at 9.00 a.m.

Oral examination can be performed also via Skype. Applicants willing to use this facility will have to send a specific document ("Allegato D") signed by a public officer (e.g. University supervisor), who must be present and guarantee for the correctness of the skype call that will have to be performed from a public office (e.g. University).

Positions starting date: 01/11/2017

Details about PhD positions:

- One position with fellowship (about 1040 euro/month net for 3 years) is open to any candidate

- One position with fellowship (about 1040 euro/month net for 3 years) is reserved to candidates who defended their Diploma/Master outside Italy. For this reason we are especially looking for FOREIGN applicants

- One position is without fellowship but we hope there will be the chance to find financial support with special programs or setting up collaborations with foreign laboratories. Please consider that PhD students without fellowship do have special support to get free housing in Pisa

PhD students will work in team with other Italian and foreign senior researchers, PhD and postdoc students. Our Unit has a long tradition of studies on morphology, ultrastructure, molecular phylogeny, and genomics of ciliated protist and their bacterial symbionts, as demonstrated by numerous papers published by our research group. For

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## UPPA France FishEcolEvolutionSubAntarctic

We are pleased to announce that our university (University Pau & Pays Adour, Anglet, France) invites candidates to apply for PhD grants. Our lab (Research Unit Behavioral Ecology and Fish Population Biology, INRA) should be given a PhD position depending on applying candidates and we therefore seek outstanding candidate interested in ecology and evolution of invasive fish in sub Antarctic Islands. Research topics are flexible, but would fall within current lab interests, with specific consideration for long-term evolution of anadromy in the introduced brown trout (Salmo trutta) and its impact on invasion dynamics in Kerguelen Island. In addition to analyzing sclerochronological structures (i.e. fish scales and otolith) from our historical collection (back to the 1970'), the PhD students will interpret movement pattern based on LA-ICPMS microchemical/isotopic data and could develop demographic modeling. Candidates should display a strong motivation for both practical and theoretical biology, with interest in methodological development. In this context, skills in modelling and coding are desirable, although candidate will be trained during its PhD.

The PhD position will be supported through the E2Sâconsortium (

https://e2sâ.fr/) gathering UPPAââ. Information about this program can be find here (http://t.co/IIIYITVwI6). Please note tight schedule since interested students should send application before June 10th, 2017 (see associated file for details).

For additional information regarding the subject, applicants are encouraged to contact Matthias Vignon (matthias.vignon_at_inra.fr). Further information about our Lab can be found online at: http://www6.bordeaux-aquitaine.inra.fr/st_pee_eng/UMR-Ecobiop https://twitter.com/ecobiop – Signature Couleur ** Matthias VIGNON UMR ECOBIOP INRA-UPPA "Ecologie Comportementale et Biologie des Populations de Poissons" (1)Aquapôle INRA Quartier Ibarron 64310 Saint Pée sur Nivelle France (2)UPPA, UFR Sciences & Techniques de la Côte Basque 1 Allée du parc Montaury 64600 Anglet France

E-mail : matthias.vignon_at_univ-pau.fr matthias.vignon_at_inra.fr

Matthias Vignon <matthias.vignon@inra.fr>

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## UReading MedicinalPlants ApplyBy31stJuly

UReading.MedicinalPlants.ApplyBy31stJuly

Applications are invited for a motivated PhD candidate to join a NERC-funded Centre for Doctoral Training (CDT), the Quantitative and Modelling Skills in Ecology and Evolution CDT. A project on medicinal plant barcoding is one of 16 projects currently advertised by this CDT - ultimately five of these 16 will be funded to start in October 2017.

The project is co-supervised by Dr Caroline Howard of the Medicine and Healthcare products Regulatory

Agency (MHRA) and Professor Julie Hawkins (University of Reading). The Medicine and Healthcare products Regulatory Agency (MHRA) is leading internationally in devising more effective processes for regulation of herbal medicines: the British Pharmacopeia (BP) was the first to include DNA barcode markers for commercial users. This project will focus on Drimia (squill). Squill has a long history of medicinal use and is included in commercial herbal medicines. Correct identification and quantification of species present in commerce is important, since Drimia is toxic in large amounts and toxicity may vary between species and varieties.

Any questions about the CDT, please contact Ibi Wallbank, Departmental Manager, at qmee.cdt@imperial.ac.uk.

Instructions on how to apply and information on eligibility please visit our website.

Informal Enquiries about the medicinal plant barcoding project: contact Prof Julie Hawkins, j.a.hawkins@reading.ac.uk.

Julie Hawkins <j.a.hawkins@reading.ac.uk>

## USouthernMississippi FishPopulationGenetics

A graduate assistant position (M.S. or Ph.D) is available in our laboratory to work on population genetics/genomics of marine and coastal fishes exploited in the Gulf of Mexico region. Specific research interests include spatial genetic variation and population structure of wild stocks and the development of genomic approaches to domestication and breeding programs in aquaculture species. Current lab projects rely on the exploitation of next generation sequencing methods in particular the double digest RAD sequencing protocol.

The successful applicant will be provided a 12-month full-time Research Assistantship with a tuition waiver. Candidates should possess a Bachelor's degree in a relevant field (e.g. Biology, Ecology & evolutionary biology, Fisheries science, GPA > 3.5) when applying for this position. Bioinformatics skills and experience with molecular techniques are assets. The position is available starting in spring 2018 with the possibility to work as a research assistant during the fall 2017 semester.

Interested individuals should send a CV, GRE scores if available, and unofficial transcripts to:

Eric Saillant, Ph.D Associate Professor The University of Southern Mississippi School of Ocean Science and Technology Thad Cochran Marine Aquaculture Center 103 McIlwain Drive Ocean Springs, MS, 39564 Tel. (1) 228-818-8007 Fax (1) 228-872-4204 E-mail: eric.saillant@usm.edu

Eric Saillant <Eric.Saillant@usm.edu>

## UZurich BacterialEvol

PhD thesis in experimental evolution to study bacterial multicellularity

A Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to evolve the soil-dwelling bacterium Bacillus subtilis, which is known for its multicellular colony organization (Vlamakis et al. Nat Rev Microbiol 2013). We are specifically interested in asking how environmental change may influence the evolution of colony formation by evolving laboratorial populations. The members of the Andreas Wagner Laboratory have diverse backgrounds and research projects, but are unified by their interests in evolution and life's fundamental organizational principles. Ongoing work in the lab ranges from experimental evolution of enzymes to computational analyses of genetic networks (e.g., Bratulic et al. PNAS 2015; Payne and Wagner, Science 2014). A sample of the laboratory's research can be found at http://www.ieu.uzh.ch/wagner/ . The successful candidate will have a strong background in microbiological techniques. Experience with molecular cloning, high-throughput DNA sequencing, and computational analysis of DNA sequences will be a plus. Applicants without a demonstrated interest and research history in evolutionary biology, and without a Masters Degree or equivalent cannot be considered further. We are looking for an individual who is highly self-motivated and can work independently

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and three academic references. Please include the word “EXPEVOLPHD17” in the subject line. Applications will be considered until

June 25, 2017. The position is available from the fall of 2017.

“annette.schmid@ieu.uzh.ch”
<annette.schmid@ieu.uzh.ch>

## UZurich ComputationalBiol

PhD thesis in computational biology

A Ph.D. studentship in computational biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study the molecular origins of evolutionary adaptations and innovations in microbial populations and communities. Lab members have diverse backgrounds and research projects, but are unified by their interests in evolution and life’s fundamental organizational principles. Ongoing projects cover a broad range of topics, including the role of gene expression noise in adaptive evolution, the role of genetic drift in evolution on adaptive landscapes, and the origin of new phenotypes through recombination (e.g., Aguilar-RodrÃguez et al., Nature Ecology and Evolution 2017, Hosseini et al., Proc. Roy. Soc. B 2016). A sample of the laboratory’s research can be found at http://www.ieu.uzh.ch/wagner/ . The successful candidate will have strong mathematical or computational skills, and a background in bioinformatics, computational biology, biochemistry, biophysics, or related subjects. Fluency in a major programming language, such as python is required. Familiarity with computational models to analyze complex metabolic systems, such as Flux Balance Analysis, and a solid background in biology will be a plus. Applications without a demonstrated interest and research history in computational biology will not be considered further. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and three academic references. Please include the word “COMPPHD17” in the subject line. Applications will be considered until June 25, 2017. The position is available from the fall of 2017.

Annette Schmid Administrative Assistant of Prof. A. Wagner University of Zurich Institute of Evolutionary Biology and Environmental Studies Wagner lab, Y27-J52 Winterthurerstrasse 190 CH-8057 Zurich Switzerland Mail to: annette.schmid@ieu.uzh.ch Phone +41 (0)44 635 61 42 Fax +41 (0)44 635 61 44 at the office on Monday and Thursday

“annette.schmid@ieu.uzh.ch”
<annette.schmid@ieu.uzh.ch>

## Vienna CichlidEvolution

We are searching for motivated students who would like to do their master thesis on Lake Tanganyika cichlids. In our current project we aim to investigate the ecological, developmental and endocrinological parameters that might permit the expression of cooperative behaviour in a non-cooperative species, using two closely related species: Neolamprologus pulcher (Cooperative breeder) and Neolamprologus caudopunctatus (Biparental breeder).

Master thesis could address several questions:

1) Developmental acquisition of social competence

2) Endocrinological manipulation of cooperative behaviour

3) Ecological enhancers of cooperative behaviour

We are looking forward to hosting master students who are interested in scientific questions and fish biology and are able to work independently as well as within a team. Our daily communication is mainly in English; good English skills are therefore desired. Our institute, the Konrad Lorenz Institute of Ethology, is part of the University of Veterinary Medicine Vienna and is located at the Wilhelminenberg in the 16^th district.

If you are interested or have any further questions please don????t hesitate to contact Filipa.cunha-saraiva@vetmeduni.ac.at or +43 01 25077-7419.

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[cid:image004.jpg@01D2E13D.53476C10]

Filipa Cunha-Saraiva, MSc > <(((0>

PhD candidate/Researcher

Konrad Lorenz Institute of Ethology

Department of integrative Biologie and Evolution

Veterinarmedizinische Universitat Wien (Vetmeduni Vienna)

Savoyenstra??e 1a, 1160 Wien T +43 1 25077-7419

http://www.vetmeduni.ac.at/en/konrad-lorenz-institute-of-ethology/about -us/our-team/students/cunha-saraiva-filipa/ filipa.cunha-saraiva@vetmeduni.ac.at

250 Jahre Emailsignatur (englisch)

Cunha Saraiva Filipa <Filipa.Cunha-Saraiva@vetmeduni.ac.at>

# Jobs

## AcademiaSinica Taiwan 2 EvolBiology

Tenure-Track Position in Evolutionary Biology

The Biodiversity Research Center, Academia Sinica (BRCAS, http://biodiv.sinica.edu.tw/), Taipei, Taiwan, invites applications for a tenure track position in Evolutionary 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), 3â5 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".

Tenure-Track Position in Microbial Diversity

The Biodiversity Research Center, Academia Sinica (BRCAS; 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), 3â5 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.

cmhung <cmhung@gate.sinica.edu.tw>

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## Boulder Colorado DirectorNextGenSequencingFacility

FYI - we have an opening for a new director of our core next gen sequencing facility. Please forward this announcement to anyone skilled in this field and potentially interested in this position in Boulder, Colorado.

Thanks, Erin Tripp

From: Nolan Coburn Kane <nolan.kane@colorado.edu>
Subject: fyi Date: May 30, 2017 at 4:52:27 PM MDT
To: Erin Tripp <erin.tripp@colorado.edu>

The Director of the BioFrontiers Next Generation Sequencing Facilityjob description https://cu.taleo.net/careersection/2/jobdetail.ftl?job=3D09607&lang=3Den&sns_id=mailto#.WR8tXzGS3BA.mailto University of Colorado

erin.tripp@colorado.edu

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## CambridgeU HerbariumCurator

The Cambridge University Herbarium is seeking a full-time Curator.

The successful candidate will be responsible for maintaining, organising and developing the Herbarium, its collections, services and profile. The Herbarium holds a scientifically and historically important collection of 1.1 million specimens of vascular plants, bryophytes, algae and fungi, together with an 8,000 photographic slide collection, 6,000+ book collection and other archives.

Fixed-term: The funds for this post are available for 3 years in the first instance.

For further information contact Professor Beverley Glover (bjg26@cam.ac.uk).

For more information and to apply go to:

http://www.jobs.cam.ac.uk/job/13776/
"bjg26@hermes.cam.ac.uk" <bjg26@hermes.cam.ac.uk>

## CSIRO Canberra PlantPollinatorDiversity

* An outstanding opportunity to provide support on future science research * Support world-class research in to genomics for environmental science * Join CSIRO - Australia's premier science & technology research organisation

The successful applicant will work closely with a team of research scientists from the Australian National Herbarium and the Australian National Insect Collection. You will perform molecular laboratory procedures to obtain sequence data from pollen samples using Next-Generation sequencing (NGS) techniques, as well as be involved in collection and preparation of insect specimens for identification and preservation.

More specifically you will work in an Environomics project called "Metagenomics of plant-pollinator networks" which aims to: 1) Uncover the diversity and structure of plant-pollinator communities in Australia and their changes in the last decades and 2) Identify key pollinator species for crop pollination and ecosystem functioning using genomics tools.

Location: Black Mountain, Canberra ACT Salary: $78K - $88K plus up to 15.4% superannuation Tenure: 2 year term appointment Reference: 41184

*To be eligible for this position you must be willing and able to do field-work and handle insects/plant material.

At the Commonwealth Scientific and Industrial Research Organisation (CSIRO), we do the extraordinary every day. We innovate for tomorrow and help improve today - for our customers, all Australians and the world. We imagine. We collaborate. We innovate.

How to Apply: Please provide enough information relevant to the selection criteria for this position to enable the assessment panel to determine your suitability, and upload one document containing your CV/resume and cover letter. All applications must be lodged on our website at www.csiro.au/careers . Before applying please view the full position details, selection criteria and how to apply on the CSIRO website at www.csiro.au/careers .Searching for Research Projects Officer - Plant evolution Systematics & Ecology.

Applications Close: 11:59pm AEST Monday 3 July 2017

Please do not hesitate to contact me if you require further information.

Regards

CSIRO | Jane-Anne Marshall

Senior Recruitment Consultant

CSIRO Human Resources

CSIRO Private Bag 10, Clayton VIC 3168

P: 03 9545 7968 E: Jane-Anne.Marshall@csiro.au

"Jane-Anne.Marshall@csiro.au" <Jane-Anne.Marshall@csiro.au>

## IndianaU LabDirector BehavioralEvolutionPhysiology

Job: IndianaU.LabDirector.BehavioralPhysiology&Evolution

The Center for the Integrative Study of Animal Behavior (CISAB) is seeking a Research Associate to serve as the director of its Mechanisms of Behavior Core Laboratory. The laboratory serves scientists studying genetic, neuroendocrine, and evolutionary factors shaping behavior, from departments including Biology (Evolution, Ecology, and Behavior), Psychological and Brain Sciences, Medical Sciences and Anthropology. The successful candidate will be expected to understand, explain, and conduct a range of molecular, genetic and endocrine techniques (e.g., nucleic acid extraction and quantification, PCR, sequencing, steroid and protein hormone assays, western blots, histology), train students and other researchers in these procedures, maintain laboratory equipment, and supervise the general operations of the laboratory (safety, supplies, personnel, regulatory compliance, budgeting and billing).

A Master's degree in biology or a related life sciences discipline and prior experience in qPCR and research mentorship is required, and prior experience in at least some of the other needed techniques is expected. Prior experience using molecular techniques in non-traditional model organisms would be a plus. The successful candidate must be able to work with a diverse group of people, enjoy scientific mentoring, and adapt to the shifting landscape of the research, incorporating new techniques as they become available. More information about the lab can be found at animalbehavior.indiana.edu/lab-resources/our-lab.html. A three-year commitment is expected. A competitive salary plus benefits provided. August 1, 2017 start date possible. To apply, submit a letter of application & CV that lists the names and contact information for three references to https://indiana.peopleadmin.com/postings/4031 or Attn: Jeremy Bennett, 1001 E. Third Street, Bloomington, IN 47405-3700. Applications will be considered until the position is filled, but for best consideration, apply by July 1, 2017.

Indiana University is an Equal Employment and Affirmative Action employer and a provider of ADA services. All qualified applicants will receive consideration for employment without regard to age, ethnicity, color, race, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

– Kimberly Rosvall, Ph.D. Assistant Professor Indiana University http://www.indiana.edu/~krosvlab/ kimrosvall@gmail.com

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## KewGardens UK PlantFungalTreesOfLife

Scientific Project Manager - PAFTOL (Plant and Fungal Trees of Life)

The Royal Botanic Gardens, Kew are seeking a talented and creative individual to help deliver a highly ambitious scientific research initiative, The Plant and Fungal Trees of Life project, which aims to create a major piece of global science infrastructure that is central to RBG Kew's Science Strategy 2015-2020.

This is a unique opportunity to be part of a team addressing a grand challenge in the life sciences. At this time, we are seeking to recruit a Scientific Project Manager to play a leading role in the co-ordination of our dynamic and interdisciplinary team. Are you up to the task? If so, read on to find out more and visit https://careers.kew.org/vacancy/scientific-project-manager-paftol-plant-and-fungal-trees-of-life-318530.html to apply.

Hours of work: Full time (we will consider part time working for the right candidate) Contract Type: Fixed Term, 30 Months Salary 36,000 - 39,000 per annum, depending on skills and experience Location: Kew Gardens, TW9 3AE Richmond, Surrey, United Kingdom Closing: Date 21/07/2017 Interview dates: Monday 7 August 2017 (tbc)

More details:

Kew is the world's leading botanic gardens, at the forefront of plant and fungal science, a UNESCO World Heritage Site and a major visitor attraction. We want a world where plants and fungi are understood, valued and conserved - because our lives depend on them. We use the power of our science and the rich diversity of our gardens and collections to provide knowledge, inspiration and understanding of why plants and fungi matter to everyone.

The project: There are few grander challenges in science than the tree of life - uncovering the complete evolutionary history linking all life on Earth. As part of RBG Kew's Science Strategy 2015-2020, we have initiated a five-year multimillion-pound initiative, the Plant and Fungal Trees of Life project (or PAFTOL, for short), to complete the tree of life for all genera of plants and fungi, drawing on our outstanding collections, our broad collaborative networks and the latest high-throughput DNA sequencing technologies.

This ambitious project will create a unifying framework for comparative plant and fungal research and takes us a step closer to the ultimate goal of building the tree of life for all known species. We will generate high impact findings publishable in top science journals, but we want the results to reach beyond the science community. To achieve this we will build innovative big-data and visualization tools accessible to a scientist or a school child. PAFTOL has secured generous funding from the Calleva and Sackler Foundations, and the work is now underway. This is a truly exciting time to join Kew and become an integral part of a high-profile, cutting edge global endeavour.

The team: At Kew, you'll be joining a truly multidisciplinary team comprising experts from across a range of scientific fields. Having recently recruited into research and technical positions, we are now seeking critical capacity in project management, to ensure that the project is delivered efficiently and effectively. You'll work alongside a highly supportive team of Kew staff, including senior scientists, who have actively developed the PAFTOL concept.

The role: This role is critical to the successful delivery of the project. You will be responsible for the overall co-ordination of the project and its team, and the wider dissemination of the project's results within the scientific community and the general public. You will be an active member of a high-profile, multi-disciplinary team led by the Head of Comparative Plant and Fungal Biology, with responsibility for all aspects of project management and finance, as well as engagement and communications across a wide range of stakeholders.

You: You could be an experienced project manager with a passion for science, or a scientist pursuing an career in science co-ordination and communications. Whatever your background, you'll have an agile mind, a clear and positive approach to problem-solving, and an appetite for working with people to get fantastic results.

How to apply: Please visit https://careers.kew.org/vacancy/scientific-project-manager-paftol-plant-and-fungal-trees-of-life-318530.html to complete an application via the Kew jobs portal, indicating clearly the position that you are applying for in your application form. In addition, please upload 1) a covering letter describing your motivations and qualifications for the role, and 2) your CV detailing your professional experience.

We offer a fantastic range of benefits including a generous annual leave entitlement for new starters, family friendly policies, a choice of

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## KULeuven Belgium ComputationEvolutionaryVirology

The Laboratory of Clinical and Epidemiological Virology (Rega Institute - KU Leuven, Belgium; https://rega.kuleuven.be/cev/ecv/) is looking for a motivated PhD student to perform research in a multidisciplinary team. This constitutes an exciting opportunity to work on computational and statistical methods in molecular evolution with applications in infectious diseases.

Research group

The Evolutionary and Computational Virology Laboratory at the Division of Clinical and Epidemiological Virology (Rega Institute, KU Leuven) focuses on the evolutionary processes that shape viral genetic diversity. This encompasses large-scale epidemic processes, such as population growth and spatial dispersal (a popular topic in phylogeographic and phylodynamics research), as well as small-scale transmission histories and within-host evolutionary processes, including adaptation and recombination. It is our objective to gain better insights into these evolutionary and population genetic processes and to clarify how they relate to epidemic and disease dynamics. To this aim we plan to focus on statistical and computational developments to analyze the increasing amount of data brought about by massive sequencing studies, mainly in a framework of Bayesian phylogenetic inference, for which our research group holds a strong track record. We also aim to explore the applicability of novel models and statistical inference tools, developed as part of our research, in different fields of research.

Project

This project focuses on new developments in a popular Bayesian phylogenetic inference framework (BEAST: https://github.com/beast-dev/beast-mcmc) and its applications to important evolutionary problems, with a particular focus on infectious diseases.

The project involves the development of an integrated web system and database that allows users to register, upload and retrieve sequence data to and from the database. Each user will be able to determine the sharing policy for the data he/she has provided. Such a system should be easily distributed so that other research groups can deploy it on their own server(s) and put it to use without technical interventions. Further, this system will interface with the BEAST software package to analyze the sequence data in an efficient manner. The candidate is expected to design and implement such a system and determine an appropriate strategy to properly distribute the developed system as an easily installed/deployed software package.

Additionally, multiple parallelization ideas will be implemented in the BEAST software package. BEAST is mostly written in Java, with its high-performance computational library, known as BEAGLE, being implemented in C/C++. The goal is to develop and implement efficient parallelization strategies from both a computational and a statistical perspective. The computational aspect entails the implementation of popular routines typically used in computer architecture, whereas the statistical aspect entails the development and adaptation of novel transition kernels in a Bayesian phylogenetic inference framework.

Profile

The candidate for this PhD position should have a strong quantitative background, and preferably holds a master's degree in computer science / informatics (or equivalent through experience), with an interest in statistics/mathematics and (bio)informatics. The candidate hence needs to be experienced in an object-oriented programming language such as Java or C/C++. The candidate should be sufficiently proficient in English, motivated to work in a team and publish his/her findings, and willing to travel.

Offer

The candidate will be able to perform research in a dynamic and multidisciplinary team (computer scientists, data analysts and evolutionary biologists), housed in the brand new facilities of the Rega institute at the University hospital campus, and guided by prolific supervisors. KU Leuven is one of the top universities in Europe and leads the Reuters ranking of Europe's most innovative universities for the second year in a row.

The targeted starting date will be October 1st 2017 and the candidate should obtain his/her master's degree by that time. All applicants are expected to submit a motivation letter, overview of their study results and two references (with their contact details).

Additional information, as well as the application procedure, can be found here: https://icts.kuleuven.be/apps/-jobsite/vacatures/54182826 Please use the university's job portal when applying for this position. For more information, contact Guy Baele (guy.baele@kuleuven.be) or Philippe Lemey (philippe.lemey@kuleuven.be).

The closing date for completed applications is the 31st of July 2017. Interviews will be held shortly thereafter.

guy.baele@kuleuven.be

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## LakeForestCol Chicago LabTech EcoEvoDevo

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

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

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

Candidates must have a bachelor's degree in a biology-related field, undergraduate research experience and excellent organizational and time management skills. Candidates should also have experience with Drosophila genetics and fly pushing. Familiarity with basic molecular biology techniques is preferred but not essential.

Principal Responsibilities:

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

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

Assist in supervising undergraduate researchers in various laboratory projects.

Provide laboratory-specific training for researchers.

Order laboratory supplies and manage laboratory resources.

To apply:

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

Review of applicants will begin immediately and continue until position is filled. Ideal start data is 8/1/17.

Lake Forest College embraces diversity and encourages applications from women and members of other historically underrepresented groups.

Alexander W. Shingleton Associate Professor

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

Ph: 847-735-6049 web: shingletonlab.org

shingleton@mx.lakeforest.edu

## NHM LosAngeles DirectorOfCollections

Opening for Director of Collections, Natural History Museum of Los Angeles County

The Natural History Museum of Los Angeles County (NHM) will soon be searching for a Director of Collections position, a new position that will provide vision and leadership for the development, growth, direction, and management of the Museum's vast and diverse natural and cultural collections.

NHM is the largest natural history museum in the western United States and home to one of the world's most extensive and valuable collections of natural and cultural history. These collections are world-class in size, quality, and research importance, and they sustain award-winning research, education, and exhibit programs. Included in the collections are more than 35 million specimens and objects, some as old as 4.5 billion years. These collections encompass those at the main Natural History Museum in Exposition Park, the world-famous La Brea Tar Pits and Museum in the mid-Wilshire area of Los Angeles, and the historic William S. Hart Museum in Newhall, as well as collections maintained at several off-site facilities.

The search will be conducted by an independent search firm and will officially begin in the next fiscal year (after July 1, 2017). However, I will be available to speak with any interested persons and especially to potential applicants during the upcoming SPNHC meetings in Denver.

Please contact me before or during the meeting, at jmartin@nhm.org, to schedule a time to talk informally about this opportunity. I look forward to meeting with you there.

Jody Martin

Joel W. (Jody) Martin, Ph.D. Associate Vice President, Research & Collections Curator of Crustacea Research & Collections Branch Natural History Museum of Los Angeles County 900 Exposition Boulevard Los Angeles, CA 90007 Phone: 213-763-3440, FAX: 213-746-2999; E-mail: jmartin@nhm.org

Tyler Hayden <thayden@nhm.org>

## QueenMaryU EvolutionaryBiology

We're looking for a Lecturer in Organismal Biology to join us in the School of Biological and Chemical Sciences, QMUL. People with relevant experience in Evolutionary Biology are very welcome to apply.

Full details below.

Mario dos Reis

Lecturer @QMUL mariodosreis.wordpress.com

Apply: https://webapps2.is.qmul.ac.uk/jobs/job.action?jobID=2397 Lecturer or Senior Lecturer in Organismal Biology, Ref: QMUL11708

Queen Mary is one of the largest colleges in the University of London, and one of the UK's leading research-intensive institutions. The College joined the Russell Group in 2012, was ranked 9th in the 2014 Research Excellence Framework, and has made a strategic commitment to world-class research and teaching across all its disciplines.

Within Queen Mary, the School of Biological and Chemical Sciences is a large and expanding academic unit, which provides a supportive and friendly environment and encourages interdisciplinary research. The Department of Organismal Biology is one of the School's four departments, and has particular strengths in evolutionary and developmental biology, molecular ecology and aquatic biology, underpinned by considerable success with funding (e.g. NERC, EU, and Royal Society) and publishing in leading journals.

Applications are invited for a new academic position at the level of either Lecturer or Senior Lecturer. We seek an outstanding and ambitious candidate with interests in a relevant area of organismal biology, and particularly welcome applicants whose research complements our existing strengths. Successful candidates will have an internationally-recognised research profile, with demonstrable success in gaining research funding and a strong track record of publishing high quality papers. A competitive remuneration package and start-up funds are negotiable. Applicants must have the ability to teach in relevant areas.

The School is committed to Athena SWAN principles and the promotion of equality and diversity. The School currently holds a Silver Athena SWAN Award. Applications from women are particularly encouraged.

We will also be happy to consider applications from individuals with their own fellowship funding who wish to explore proleptic positions in the School.

The post is full time and permanent starting in September 2017 or as soon as possible thereafter. The salary will be in the range of 40,182 to 59,104 per annum and will be in accordance with experience and qualifications. Benefits include 30 days' annual leave, childcare vouchers scheme, defined benefit pension scheme and interest-free season ticket loan.

Candidates must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme.

For informal enquiries, please contact the Head of the Department of Organismal Biology, Prof Stephen Rossiter (e-mail: s.j.rossiter@qmul.ac.uk).

For further information about the School, please visit the School's website on: http://www.sbcs.qmul.ac.uk . Application enquiries should be directed to recruitment@qmul.ac.uk.

Applicants must include their CV, which should include a two page summary of their proposed research at Queen Mary London.

The closing date for completed applications is 27 June 2017. Interviews will held shortly thereafter.

m.dosreisbarros@qmul.ac.uk

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## QueenMaryULondon AquaticEvolEcology

QueenMaryULondon.AquaticEvolEcology

Applications are invited for a new academic position at the level of either Lecturer or Senior Lecturer (Associate Professor) in Aquatic Ecology, in the School of Biological and Chemical Sciences. We seek an outstanding and ambitious candidate, and particularly welcome applicants whose research complements our existing strengths in evolutionary and conservation genetics, aquatic food web and ecosystem dynamics, and biogeochemical aquatic nutrient cycling.

Successful candidates will have an internationally-recognised research profile, with demonstrable success in gaining research funding and a strong track record of publishing high quality papers as a significant author. Applicants must also have the ability to teach in relevant areas at undergraduate and MSc level. Queen Mary is one of the largest colleges in the University of London, and one of the UK's leading research-intensive institutions. The College joined the Russell Group in 2012, was ranked 9th in the National 2014 Research Excellence Framework, and has made a strategic commitment to world-class research and teaching across all its disciplines. Within Queen Mary, the School of Biological and Chemical Sciences is a large and expanding academic unit, which provides a supportive and friendly environment and encourages interdisciplinary research. The School is strongly committed to promoting diversity, including gender equality. We are also happy to consider applications from individuals with their own fellowship funding who wish to explore proleptic positions in the School.

The post is full time and permanent starting in September 2017 or as soon as possible thereafter. A competitive remuneration package and start-up funds are negotiable. The salary will be in the range of pounds 40,182 to pounds 59,104 per annum and will be in accordance with experience and qualifications. Benefits include 30 days' annual leave, childcare vouchers scheme, defined benefit pension scheme and interest-free season ticket loan. Candidates must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme. The deadline for applications is the 15 June 2017, and applicants shortlisted for interview will be notified soon after. We thank other applicants for their interest but regret that we are unable to contact all applicants individually.

For informal enquiries, please contact the Head of the Department of Organismal Biology, Prof Stephen Rossiter (e-mail: s.j.rossiter@qmul.ac.uk), preferably with a CV and list of recent papers. For more information see http://www.sbcs.qmul.ac.uk/about-us/vacancies/ SJ Rossiter <s.j.rossiter@qmul.ac.uk>

## QueenMaryULondon OrganismalBiology

QueenMaryULondon.Lecturer.OrganismalBiology

Applications are invited for a new academic position at the level of either Lecturer or Senior Lecturer (Associate Professor) in the School of Biological and Chemical Sciences. We seek an outstanding and ambitious candidate with interests in a relevant area of organismal biology, and particularly welcome applicants whose research complements our existing strengths in evolutionary and developmental biology, molecular ecology and aquatic biology.

Successful candidates will have an internationally-recognised research profile, with demonstrable success in gaining research funding and a strong track record of publishing high quality papers as a significant author. Applicants must also have the ability to teach in relevant areas at undergraduate and MSc level.

Queen Mary is one of the largest colleges in the University of London, and one of the UK's leading research-intensive institutions. The College joined the Russell Group in 2012, was ranked 9th in the 2014 Research Excellence Framework, and has made a strategic commitment to world-class research and teaching across all its disciplines. Within Queen Mary, the School of Biological and Chemical Sciences is a large and expanding academic unit, which provides a supportive and friendly environment and encourages interdisciplinary research. The School is strongly committed to promoting diversity, including gender equality. We are also happy to consider applications from individuals with their own fellowship funding who wish to explore proleptic positions in the School.

The post is full time and permanent starting in September 2017 or as soon as possible thereafter. A competitive remuneration package and start-up funds are negotiable. The salary will be in the range of pounds 40,182 to pounds 59,104 per annum and will be in accordance with experience and qualifications. Benefits include 30 days' annual leave, childcare vouchers scheme, defined benefit pension scheme and interest-free season ticket loan. Candidates must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme.

The deadline for applications is the 27 June 2017, and applicants shortlisted for interview will be notified soon after. We thank other applicants for their interest but regret that we are unable to contact all applicants individually.

For informal enquiries, please contact the Head of the Department of Organismal Biology, Prof Stephen Rossiter (e-mail: s.j.rossiter@qmul.ac.uk), preferably with a CV and list of recent papers. For more information see http://www.sbcs.qmul.ac.uk/about-us/vacancies/ SJ Rossiter <s.j.rossiter@qmul.ac.uk>

## SanJoseStateU EvolutionaryEcol

Evolutionary Ecology Job Opening ID (JOID): 24148 Rank: Assistant Professor (Tenure track)

Qualifications: The Department of Biological Sciences at San José State University invites applications for a tenure-track position in Evolutionary Ecology. Applicants must have a Ph.D. or equivalent degree and postdoctoral experience in evolutionary ecology or related field. Candidates should have a proven record of excellence or evidence of promise for excellence in teaching and research. We seek a vertebrate biologist who uses molecular methods to investigate questions in evolution and development, population genetics, or molecular ecology. Candidates should have proven record of research experience and scholarly output in studies of evolutionary processes using field and/or laboratory-based research.

Responsibilities: The successful candidate will be expected to take a leadership role in evolutionary biology within the Ecology and Evolution program area. Teaching duties will include segments within the Introductory Biology series for freshmen, and specialty courses at the upper division and/or graduate-levels. These courses may include but are not limited to Evolution, Human Evolution, Vertebrate Evolution, Evolutionary Development, Population Genetics, and/or Molecular Ecology. The candidate is expected to establish a successful research lab utilizing molecular techniques to augment field and/or laboratory-based studies of vertebrate evolution. Innovation in teaching is strongly encouraged and research involving masters and undergraduate students is expected. Applicants' materials should demonstrate awareness of and sensitivity to educational goals of a multicultural population as might have been gained in cross-cultural study, training, teaching, and other comparable experience.

Starting Date: August 17, 2018

Application Procedure: For full consideration, send a letter of application, curriculum vitae, statement of teaching interests/philosophy, research plans, and at least three original letters of reference with contact information by September 30, 2017 to apply.interfolio.com/42749.

Please direct questions to: Dr. Jeffrey Honda (jeffrey.honda@sjsu.edu) Chair, Department of Biological Sciences San José State University One Washington Square San José, CA 95192-0100

– *Dr. Susan LAMBRECHT * | Professor of Biology | Department of Biological Sciences San Jose State University | San Jose, CA 95192-0100 (408) 924-4838 | susan.lambrecht@sjsu.edu http://www.biology.sjsu.edu/facultystaff/lambrecht/ Susan Lambrecht <susan.lambrecht@sjsu.edu>

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## TempleU DataAnalyst Deadine Jun15

Genomics and Evolutionary Data Analyst

Multiple positions are available for individuals with skills to assist in the application of standard research practices and bioinformatics techniques in genomics and evolution. Responsibilities include analysis of various types of sequence and related data, including high throughput data for empirical research. We require proficiency in (a) statistical or computational tools for molecular evolutionary analysis using genome scale sequence datasets AND (b) conducting data analysis, including the building of pipelines for data retrieval and analysis. Knowledge of principles of molecular evolution, population genetics, biomedical data, or next generation sequencing will be considered a plus. Successful candidates will solve variable problems, make complex decisions under general policies and specialized standards, and consider suggestions of project team members. Ultimately, they will serve as a technical resource and work in highly skilled team. Required qualifications include a Master's degree or Bachelor's degree with at least two years of experience in relevant data analysis and/or computer programming. Postdoctoral candidates will also be considered. Interested applicants should send a CV and cover letter detailing related experience to igem@temple.edu

Application will be reviewed on June 15, 2017 and July 30, 2017, and every month after that until the positions are filled. For any scientific or other questions, please write to s.kumar@temple.edu

Sudhir Kumar

www.kumarlab.net igem.temple.edu

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## TempleU Phylogenomics DeadlineJun15

Research Faculty Positions (iGEM@Temple)

A multi-year research faculty position (non-tenure-track) is available in the Institute for Genomics and Evolutionary Medicine (iGEM) at Temple University in Philadelphia, USA. We are interested in early and mid-career scientists who integrate concepts, methods, and tools from evolutionary biology to address significant questions in Phylogenomics. Successful candidates will have a primary focus on one or more of the following: large scale analytics of sequences, big data phylogenetics, and development of methods and computational tools. They will be core faculty of iGEM @ Temple. They will work closely with and benefit from our expertise in molecular evolution, population genetics, phylogenomics, phylomedicine, and computational biology.

Applicants should submit their detailed curriculum vitae and a summary of current and future research interests by an e-mail to igem@temple.edu (send a single PDF file). Successful candidates will be provided salary support for an initial period and they will work closely with one or more of the current or future tenured faculty in iGEM (http://igem.temple.edu/people/core). They will be expected to develop a strong, extramurally funded, and collaborative research program. [Applicants interested in postdoctoral fellowships are also encouraged to apply.] For all questions, please contact Sudhir Kumar by email (s.kumar@temple.edu). Application will be reviewed on June 15, 2017 and every month after that until the positions are filled.

Temple University located is in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is home to a large biotech industry and has many outstanding academic and research institutions.

Sudhir Kumar

s.kumar@temple.edu

Director, iGEM@Temple

Institute for Genomics and

Evolutionary Medicine

Carnell Professor, Biology

Temple University

1925 N. 12th Street

Philadelphia, PA 19122

"s.kumar@temple.edu" <s.kumar@temple.edu>

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## UBuffalo 2yr TeachingEvolution

Position Title Clinical Assistant Professor for Evolution, Ecology, & Behavior

Posting Number F1700108

Employer State

Appointment Term Term

Position Type UUP Faculty

Posting Detail Information

Position Summary

The initial 10 month appointment begins on August 24, 2017, and is renewable for two additional years. The successful candidate will teach courses and provide advisement and administrative duties in support of the degree programs in Evolution, Ecology & Behavior; Environmental Geosciences; and Environmental Studies.

The successful candidate will take primary responsibility for teaching an undergraduate ecology course, an undergraduate laboratory course in ecological research methods and specialized courses in the areas of ecology and the environment. The instructor will also assist in the advisement of undergraduate students interested in degrees in the broad areas of ecology and environmental sciences. Other responsibilities may include, developing online curricula, supervising teaching assistants, advising graduate students, participating in on-going curricula development, and representing the department in recruitment, fundraising, and community outreach efforts.

The teaching load will be four courses per semester, some of which may be duplicate sections of some courses, or equivalent advisement/administrative responsibilities. Additional teaching and salary opportunities may be available during winter and summer sessions.

Minimum Qualifications

Ph.D. in a field related to ecology or environmental sciences/studies, conferred by the start of the appointment. Some experience in undergraduate teaching is required. Excellent written and oral communication skills as well as computer skills including facility with Microsoft Office (Word, Excel, Powerpoint) are needed.

Preferred Qualifications

University teaching experience is preferred.

Physical Demands

Light lifting; supervising outdoor laboratory exercises in local ecosystems, including walking on uneven terrain in a variety of weather conditions.

FTE 1.00

Campus North Campus

Special Instructions to Applicants

All applications must be submitted via UB Jobs (https://www.ubjobs.buffalo.edu/postings/9660) and should include a cover letter, CV, teaching statement, and contact information for three professional references.

Additional Information

Pursuant to Executive Order 161, no State entity, as defined by the Executive Order, is permitted to ask, or mandate, in any form, that an applicant for employment provide his or her current compensation, or any prior compensation history, until such time as the applicant is extended a conditional offer of employment with compensation. If such information has been requested from you before such time, please contact the Governor's Office of Employee Relations at (518) 474-6988 or via email at info@goer.ny.gov.

Contact Information

Contact's Name Howard Lasker

Contact's Title Professor

Contact's Email hlasker@buffalo.edu

Contact's Phone 716-645-4870

Posting Dates

Posted 06/02/2017

Deadline for Applicants Open Until Filled

Dr. Katharina Dittmar Associate Professor University @ Buffalo, SUNY Department of Biological Sciences 109 Cooke Hall Buffalo, NY, 14260 Tel: 716 645 4912 kd52@buffalo.edu http://evolutionecologybehavior.buffalo.edu http://katharina-dittmar.squarespace.com/ Katharina Dittmar de la Cruz <kd52@buffalo.edu>

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## UCalifornia Berkeley PaleontologyEvoDevo

Tenured faculty position in the area of Paleontology and Evolutionary Developmental Biology University of California, Berkeley The Department of Integrative Biology (IB) and the Department of Molecular and Cell Biology (MCB) at the University of California, Berkeley are soliciting applications for a 100% (50 % IB, 50% MCB) time new senior level faculty member actively working at the interface between the fields of paleontology and evolutionary developmental biology; this position is open at the tenured level. Potential start date is January 1, 2018 or July 1, 2018.

Through leadership and expertise in the field of paleontology, and the fields of organismal, evolutionary, molecular, cellular, and developmental biology, Berkeley faculty explore questions in adaptation, speciation, ecology, and the genetic and genomic events that have generated organismal diversity. We seek candidates who work at the interface between paleontology and evolutionary developmental biology to leverage the strengths of these fields to address any of a number of questions in evolutionary biology. Areas include (but are not limited to) the evolution of important transitions such as the generation of body plans during the Cambrian, the transition from water to land, the evolution of flight, and the appearance of developmental novelties.

We envision that the position will create synergies for collaborative initiatives in research, teaching and fundraising. The successful candidate will build bridges across disciplines at UC Berkeley (including collaborations with the Departments of Earth and Planetary Sciences, Plant and Microbial Biology and Environmental Science, Policy and Management). S/he will bridge the museum and molecular focused faculty in IB with the molecular and cellular faculty in MCB.

Paleontology and Evolutionary Developmental Biology are fields that have great appeal to the public, and an interdisciplinary research scope will provide ample opportunities to highlight the strength of both Departments to the public through outreach programs that could also form the basis for successful fundraising in the future.

Preferred qualifications include demonstrated excellence in research, extensive field or lab experience, evidence of outstanding scholarship within a relevant discipline, a dedication to excellence in teaching at the undergraduate and graduate level, and a commitment to working in an inclusive and interdisciplinary environment. A Ph.D. and/or M.D. or equivalent degree in biology, geology, or a related field is required at the time of application.

Serious consideration will be given to the candidate's potential for success in mentoring Ph.D. students and teaching at both the undergraduate and graduate levels. We seek someone who combines significant strength in an interdisciplinary program that crosses the Departmental boundaries, which will enhance not only our research standing, but our ability to educate undergraduates and graduate students at the cutting edge of interdisciplinary science. Professional service, including issues of access to and diversity in higher education and the academic profession will also be considered.

Application Procedure: Applicants who are currently tenured at an institute of higher education/ are an independent investigator must complete an online application via the following link: https://aprecruit.berkeley.edu/apply/JPF01343 . If your candidacy progresses, you will be asked to provide contact information for 3-5 referees. We will only contact your referees if you are a finalist for the position, and we will seek your permission before doing so. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e., dossier service or career center), to the UC Berkeley statement of confidentiality (http://apo.berkeley.edu/evalltr.html) prior to submitting their letters All applications should include: - Curriculum Vitae - Your most recently updated C.V.

- A brief summary of current and future research objectives, teaching interests, and a statement addressing past and/or potential contributions to diversity through research, teaching, and/or service.

The final deadline for applications is July 19, 2017. To receive full consideration, please submit a completed application by this date.

Please direct questions to ib_ap_assist@berkeley.edu.

IB and MCB are 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 .

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

## UDuisburg-Essen Germany EvolutionaryPhycology

At the University of Duisburg-Essen, the Faculty of Biology invites applications for a

Professorship for Phycology (W2 level)

with the tentative job start in March 2018.

We seek internationally-renowned scientists with an outstanding track record of own scientific achievements in the field "Biology of Microalgae" to represent this subject in university research and teaching. Applicants shall use modern approaches in the molecular analysis of microalgae, e.g. using high-throughput methods. Preferably, candidates integrate transcriptomic and genomic methods in their research. Ideally, candidates use the organismic breadth available in algal collections and have experience in the isolation and cultivation of microalgae. We expect publications in peer-reviewed journals as well as experiences in the acquisition of third-party funding. Furthermore, university-teaching skills are a prerequisite.

The candidates shall strengthen the research focus on Aquatic Biodiversity and Ecology of the Center for Water and Environmental research (ZWU, https://www.uni-due.de/zwu/start.php) and the Faculty of Biology (https://www.uni-due.de/biology/index.php). We welcome active collaboration in local research networks. Furthermore, we expect the successful candidate to maintain a competitive third-party funded program or project.

Active involvement in university teaching (botanical and microbiological classes) as part of the B.A./B.Sc. and M.A./M.Sc. studies in Biology are expected. Furthermore, engagement in the international M.Sc. studies in "Biodiversity", "Transnational Ecosystem-based Water Management" or "Environmental Toxicology" is welcomed. Teaching languages are German and English. Non-German applicants are expected to acquire German language skills for teaching within two years. Active participation in the organisation of the studies, student advisory service and academic self-organisation is obligatory.

Publications in international peer-reviewed journals and experience with the acquisition and management of own third-party projects, in particular DFG-funded projects are expected.

The University of Duisburg-Essen prioritizes quality in teaching. Therefore, a prospective teaching concept that considers the profile of the Faculty of Biology is requested. The appointment requirements for this position comply with Article 36 of the law on higher education in North-Rhine-Westphalia (Hochschulgesetz NRW).

The University of Duisburg-Essen aims to increase the diversity of its members (please see https://www.uni-due.de/diversity). It is seeking to increase the number of women on its scientific staff and therefore strongly encourages suitably qualified women to apply. In case of equal qualification, women will be given preference in accordance with state equal opportunity legislation. Applications from suitable disabled persons and equivalent applicants according to Article 2, Paragraph 3 of the social code (SGB IX) are also welcome.

Applications including a curriculum vitae, publication list, scientific track record, statement of future research, teaching experience, third-party funding and copies of certificates shall be sent within 6 weeks from the announcement preferably via e-mail (dekanat@biologie.uni-due.de) to the Dean of the Faculty of Biology, Prof. Dr. Jens Boenigk, Universitaetsstr. 2, 45141 Essen, Germany.

For questions concerning this announcement, contact the head of the nomination committee, Prof. Dr. Florian Leese (florian.leese@uni-due.de).

Further information about the university and this position can be found at the following internet address: http://uni-due.de/biologie/fakultaet/stellen.php . http://www.uni-due.de Announcement: 26.5.2017 https://www.uni-due.de/imperia/md/content/stellenmarkt/stellenangebote_an_universitaeten/professoren-juniorprofessoren_an_der_ude/2017/0522_ude_prof.pdf "Leese, Florian" <florian.leese@uni-due.de>

## UFlorida TeachingBiology

The Department of Biology at the University of Florida, College of Liberal Arts and Sciences invites applications for a position at the rank of lecturer to begin August 2017. This is a 12-month, time-limited, renewable, non-tenure-track position. The lecturer will serve as both an instructor for the UF Online Biology Major, including development of two courses in the first year and delivery of two courses per semester in all three years; and as a coordinator between UF Online, the Department of Biology, and the trans-college Biology Majors Executive Committee to ensure the excellence of the UF Online Biology major.

The successful candidate should possess a Ph.D. in Biology or other life sciences field, or in STEM education. Experience with instruction at the undergraduate level is required and experience with online education is highly desirable. Excellence in teaching is expected. For more information and instructions on how to apply, please go to: http://explore.jobs.ufl.edu/cw/en-us/job/502664/lecturer For full consideration, please submit an application by 29 June 2017, although the position will remain open until filled.

Thank you! Marta

Marta L. Wayne, Ph. D. Professor and Chair P.O. Box 118525 Department of Biology University of Florida Gainesville, FL 32611-8525 (courier: 876 Newell Drive) vox: 352-392-9925 fax: 352-392-3704 http://people.biology.ufl.edu/mlwayne/ "Wayne,Marta L" <mlwayne@ufl.edu>

## Umea Sweden BioinformaticsSupport

1 temporary position providing advanced bioinformatics support, located at the National Bioinformatics Infrastructure Sweden at SciLifeLab, UmeÃ¥, Sweden.

SciLifeLab (www.scilifelab.se) in Sweden serves as a national infrastructure to support advanced high-throughput life science research. The National Bioinformatics Infrastructure Sweden at SciLifeLab (www.nbis.se) is a national infrastructure in rapid development, now looking for 1 staff member to join the Bioinformatics Long-term Support team (WABI), placed in UmeÃ¥. The Bioinformatics Long-term Support team provides advanced bioinformatics analyses to some of the most scientifically exciting projects across Sweden, and with more than 20 full-time senior bioinformaticians, the team is one of the strongest units for analysis of large-scale genomics and integrative omics in Sweden.

We are looking forward to your application at the latest June 22, 2017 https://umu.mynetworkglobal.com/en/what:job/jobID:152637/ Björn Nystedt, bjorn.nystedt@scilifelab.se Pär Engström, par.engstrom@scilifelab.se Joint Heads of SciLifeLab Bioinformatics Long-term Support (WABI)

http://www.nbis.se/support/longtermsupport.html http://www.scilifelab.se/platforms/bioinformatics/ Bjorn Nystedt, PhD Manager, SciLifeLab Bioinformatics Long-term Support (WABI) www.scilifelab.se/facilities/wabi/ BMC E10:3206, entrance C11 Husargatan 3, SE-752 37 Uppsala

Phone: 018 - 471 4413 E-mail: bjorn.nystedt@scilifelab.se

bjorn.nystedt@scilifelab.se

## UReading 2 Bioinformatics

Dear EvolDir members,

Two jobs are available at the School of Biological Sciences, University of Reading, UK - for further details please see the links below.

Lecturer in Bioinformatics for Genomics: https://jobs.reading.ac.uk/displayjob.aspx?jobid=1019 The University of Reading is building on its highly successful research profile within the School of Biological Sciences through the appointment of a new post at the Lecturer level in Bioinformatics for Genomics. The appointee will be an experienced bioinformatician with a PhD in Bioinformatics, Computational Biology, Genetics, Computer Science or a related field. Evidence of leadership and the ability to attract external funding will be advantageous. The appointee will be expected to support the research themes within the University and to develop their own independent research portfolio.

Bioinformatician (Research Fellow): https://jobs.reading.ac.uk/displayjob.aspx?jobid=1018 We are seeking to appoint a skilled and motivated bioinformatician to strengthen our bioinformatics support across the Schools at the University of Reading. The postholder will work to enhance the effectiveness of multidisciplinary research at Reading, strengthening our synergistic working environment, and will improve the sustainability of bioinformatics expertise within the University. The bioinformatician will provide University wide support, to increase the speed and quality of research outputs, to improve the success of grant applications, and to train those PhD students and post-docs appointed as a result of these grants.

Informal enquiries are welcome - contact Dr Liam McGuffin l.j.mcguffin@reading.ac.uk or Prof Rob Jackson r.w.jackson@reading.ac.uk

Louise Johnson <l.j.johnson@reading.ac.uk>

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## UToronto 2 EEB Professorships

ECOLOGY AND EVOLUTION - Two Assistant Professorships

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for two tenure-stream appointments in ecology and evolution. These appointments will be at the rank of Assistant Professor, with an expected start date of July 1, 2018.

We seek candidates who conduct conceptually driven research in ecology and evolution, especially those with research programs in disease and/or theory. We seek applications from candidates whose research program complements the research programs of the highly collaborative faculty currently in the department.

The successful applicants must have a PhD in a related field by July 1, 2018 or soon thereafter, with a record of sustained publications in top-ranked, field-relevant journals. The appointees will be expected to build an active, externally funded and internationally recognized research program. The successful candidates will also demonstrate excellence in teaching and contributions to the education and training of undergraduate and graduate students. Evidence of demonstrated excellence in research and teaching should be documented through the applicant's CV, publications, research and teaching statements, strong letters of reference from referees of high standing and where appropriate, course evaluations.

The University of Toronto is a leading academic institution with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change Science, Dalla Lana School of Public Health, the School of the Environment, the University network of leading academic research hospitals (www.uhn.ca, sunnybrook.ca/) and research groups with provincial and federal government agencies. The University owns a nearby field station dedicated to ecological research (the Koffler Scientific Reserve; www.ksr.utoronto.ca). Toronto is a vibrant and cosmopolitan city, one of the most desirable in the world in which to work and live.

Salary to be commensurate with qualifications and experience.

All qualified candidates are invited to apply online. Applications must include a CV and statements of research and teaching interests combined into a single PDF file, plus three representative publications. Applicants should arrange to have three confidential letters of recommendation (signed and on letterhead) sent directly to: Professor Donald Jackson, Chair of Search Committee, Department of Ecology and Evolutionary Biology, 25 Willcocks Street, University of Toronto, Toronto, Ontario, M5S 3B2 Canada. Letters of reference may be e-mailed to chairsec.eeb@utoronto.ca. Deadline for receipt of applications, including reference letters, is September 13, 2017.

For further information on the Department of Ecology and Evolutionary Biology, please visit our website at www.eeb.utoronto.ca. Questions regarding this position can be directed to Liz Rentzelos at chairsec.eeb@utoronto.ca or (416-946-3340).

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. As part of your application, you will be asked to complete a brief Diversity Survey. This survey is voluntary. Any information directly related to you is confidential and cannot be accessed by search committees or human resources staff. Results will be aggregated for institutional planning purposes. For more information, please see http://uoft.me/UP. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

< http://mahlerlab.com/ >

Luke Mahler <luke.mahler@utoronto.ca>

## UZurich FieldAssist BirdsLapland

Expenses paid field assistant positions to study the foraging ecology of Siberian Jays in Swedish Lapland

For the upcoming field season (21 August-31 October 2017) we are looking for a highly motivated expenses paid field volunteer to join our field project (main responsible Dr. Michael Griesser, University of Zurich, Switzerland) investigating life-history evolution in Siberian jays. The study site is located near Arvidsjaur, Swedish Lapland.

Our current project investigates the influence of habitat quality on the foraging and food storing behaviour of Siberian jays. The work of the field volunteers will be to help with field experiments, behavioural observations, catching birds, and data management. This work will give insight into exciting experimental fieldwork and will be carried out partly in managed forests and partly in scenic pristine boreal habitats. We will work 5-6 days per week in the field depending on the workload of the experiments. Observe that temperatures in the end of the season can be as low as -10C. The work is physically strenuous at times. The team will vary in size depending on the weeks, but at least two other people will be present during the whole field season.

Qualifications: (1) BSc/MSc in Biology, Ecology, Evolution or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing (5) bird ringing and mist-netting experience (6) Driving license (7) Fluent in English

We will cover for the accommodation, travel expenses from and to the study site (in total up to 300 Euros), as well as the living expenses.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be send to Michael Griesser michael.griesser@uzh.ch, preferably in a single PDF.

Applications received until 14 July 2016 will be given full consideration.

Michael Griesser <michael.griesser@uzh.ch>

# Other

## Apply Phylotastic Hackathon Aug8-11

The Phylotastic project (http://www.phylotastic.org) aims to make expert knowledge of species phylogeny more accessible for purposes of research, education, and public outreach. We invite interested scientists, programmers and educators to apply for a 4-day hackathon centered on leveraging resources of the project, including its graphical web portal, its suite of web services, and its toolbox code.

Full information on the scope and aims of the hackathon is available at http://bit.ly/2qMyMSc . We offer full travel support to accepted participants. Whether you are a researcher, a curator, an educator, or something else, we encourage you to apply for participation. To apply, use the online form at http://bit.ly/2qAXuDk to provide brief descriptions of your ideas, your skills and your domain knowledge. Members of underrepresented groups are especially encouraged to apply. Applications are due June 16, 2017.

We encourage pre-application questions, which may be directed to Arlin Stoltzfus (arlin@umd.edu), Enrico Pontelli (epontell@cs.nmsu.edu), Brian O'Meara (bomeara@utk.edu) or Dmitry Mozzherin (dmozzherin@gmail.com).

Arlin Stoltzfus (arlin@umd.edu) Research Biologist, NIST; Fellow, IBBR; Adj. Assoc. Prof., UMCP IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org Arlin Stoltzfus <arlin@ibbr.umd.edu>

## LundU 1mnthSummerScholarship FlySpeciation

Summer scholarship for ambitious student at Lund University, Sweden

I have a one month summer scholarship (July 1st -31st) for a project on host plant driven speciation in Tephritis conura available for an ambitious and independent student with a drivers license. The tax free scholarship amounts to 10500 SEK (ca. 1100 Euro) and we can arrange for cheap accomodation. Field work consists of sampling of thistle buds infested by larvae in Southern Sweden, and potentially the Stockholm area, Denmark and/or southern Finland. Approximately 40 hours working weeks are expected. The student will get valuable insights in to experiment design and research methods.

Please contact Anna.Runemark@biol.lu.se for questions or applications, and please provide contact details for two references when you apply.

Anna Runemark <anna.runemark@biol.lu.se>

## Morocco 4PhD Internships PollinatorEvolution

ICARDA Graduate Research Internships - Call for Applications

4 PhD Internships on "Wild Pollinators in Morocco"

Location of the Graduate Research Internship: ICARDA- Rabat, Morocco Closing date: 20 June 2017

Main purpose : The four selected PhD students (Moroccan nationals) will be based in Rabat, Morocco and will have the opportunity to write their thesis under the additional supervision of Prof. Pierre Rasmont and Prof. Denis Michez, University of Mons, Belgium, as part of ICARDA/IUCN/INRA's project "Conservation of pollinator diversity for enhanced climate change resilience" within the Biodiversity and Integrated Gene Management Program. This project shall comprehensively introduce the Farming with Alternative Pollinators (FAP) approach in the MENA-region. Wild pollinators provide most of the pollination services. They play a major role in crop pollination and in adaptation to climate change. Nevertheless, their diversity is in decline in all continents. FAP is a new approach to trigger farmers' motivation to enhance habitats for pollinators. The approach includes FAP-fields with enhanced habitats and control fields (monoculture) and compares insect diversity and total net income to develop an incentive for farmers. The project will also develop the first inventory of crop pollinators in North Africa. The four students will contribute to this work and can prepare their thesis within the project.

We are looking for * 1 Phd student on: Wild pollinators in mountainous agro-ecosystems * 1 Phd student on: Wild pollinators in oasis * 1 Phd student for: Long tongue pollinators * 1 Phd student for: Short tongue pollinators

The students can write their thesis within the spectrum of their main responsibilities: * Regular collection and identification of pollinator species in FAP and control fields in Morocco * Measure abundance of pollinators * Describe the habitat requirements of some main crop pollinators * Develop nesting support out of local material for main crop pollinators * Evaluate impact of nesting support * Contribute to trainings and field days for farmers and extension staff and to the development of manuals

Education, qualifications and experience * MSc in entomology, agronomy or biology, preferably with focus on pollination; * Excellent written and oral communication skills in English * Fluent French would be an advantage * Knowledge of data management and statistical analysis with popular computer software * Willingness to travel also to remote areas

Terms of the award * The graduate students will receive financial support for a maximum of 36 months, equivalent to 1,000 Euro per month that will be paid in Moroccan Dirham in order to cover joining and returning transportation to ICARDA Rabat office, subsistence allowance, insurance, accommodation and daily transportation in Morocco * They will be trained in Rabat and will receive also three intensive trainings at the University of Mons, Belgium. * The initial contract will be for 3 years, of which the first year will be probationary period.

How to apply Please send your CV, Motivation letter, copy of your University PhD registration and a letter from your University supervisor indicating her/his approval for you to conduct an internship period of three years at ICARDA under one of the research topics indicated to - Dr. Stefanie Christmann, ICARDA Expert on Farming with Alternative Pollinators, Email: S.Christmann@cgiar.org and copy to - Mr. Charles Kleinermann, Head - Capacity Development Unit- ICARDA Email: c.kleinermann@cgiar.org

About ICARDA The International Center for Agricultural Research in the Dry Areas (ICARDA) is an international autonomous, non-profit, research organization temporarily based in Beirut, Lebanon supported by the Consultative Group on International Agricultural Research (CGIAR). ICARDA is committed to the improvement of livelihoods of the resource-poor in dry areas by enhancing food security and alleviating poverty through agricultural research, and the equitable use of natural resources. For more details: www.icarda.org WWW.ICARDA.ORG

Denis MICHEZ <Denis.MICHEZ@umons.ac.be>

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## Phyloseminar BarbaraHolland Jun22 DateCorrection

Correction: previous email had incorrect date.

Next on phyloseminar.org:

Developing a statistically powerful measure for quartet tree inference using phylogenetic and Markov invariants Barbara Holland University of Tasmania Thursday, June 22, 2017, 2:00 PM PDT

Recently there has been renewed interest in phylogenetic inference methods based on phylogenetic invariants, alongside the related Markov invariants. Broadly speaking, both these approaches give rise to polynomial functions of sequence site patterns that, in expectation value, either vanish for particular evolutionary trees (in the case of phylogenetic invariants) or have well understood transformation properties (in the case of Markov invariants).

While both approaches have been valued for their intrinsic mathematical interest, it is not clear how they relate to each other, and to what extent they can be used as practical tools for inference of phylogenetic trees. By focusing on the special case of binary sequence data and quartets of taxa, we are able to view these two different polynomial-based approaches within a common framework.

We present three desirable statistical properties that we argue any invariant-based phylogenetic method should satisfy: (1) sensible behaviour under reordering of input sequences; (2) stability as the taxa evolve independently according to a Markov process; and (3) explicit dependence on the assumption of a continuous-time process. Motivated by these statistical properties, we develop and explore several new phylogenetic inference methods. In particular, we develop a statistically bias-corrected version of the Markov invariants approach which satisfies all three properties. We also extend previous work by showing that the phylogenetic invariants can be implemented in such a way as to satisfy property (3). A simulation study shows that, in comparison to other methods, our new proposed approach based on bias-corrected Markov invariants is extremely powerful for phylogenetic inference.

Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ ematsen@gmail.com

## Phyloseminar BarbaraHolland June21

Next on phyloseminar.org:

Developing a statistically powerful measure for quartet tree inference using phylogenetic and Markov invariants Barbara Holland University of Tasmania Wednesday, June 21, 2017, 2:00 PM PDT

Recently there has been renewed interest in phylogenetic inference methods based on phylogenetic invariants, alongside the related Markov invariants. Broadly speaking, both these approaches give rise to polynomial functions of sequence site patterns that, in expectation value, either vanish for particular evolutionary trees (in the case of phylogenetic invariants) or have well understood transformation properties (in the case of Markov invariants).

While both approaches have been valued for their intrinsic mathematical interest, it is not clear how they relate to each other, and to what extent they can be used as practical tools for inference of phylogenetic trees. By focusing on the special case of binary sequence data and quartets of taxa, we are able to view these two different polynomial-based approaches within a common framework.

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Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ ematsen@gmail.com

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## Request ForSamples Oxalis acetosella

Hello,

For a range-wide phylogeographical study, we need samples of the rhizomatous flowering flower plant Oxalis acetosella. This species, commun in most of Europe and parts of Asia, can be found in moist woods, moorland and shady habitat. Regarding the sampling protocol, this is simple. We only need one individual sampled per population. A population is here defined as any isolated individual or cluster of individuals which are distant of 10m from the next isolated or cluster of individuals. To sample a population, just collect the 3 to 9 youngest leaves of a single rosette (individual) of Oxalis acetosella within the population. Collect only safe leaves (no hole or sign of herbivory, no chlorosis or virus attack). Put the fresh leaves in an envelope (standar small paper envelope) with GPS coordinates of that population written on the envelope or at least the name of the locality but lat/long coordinates is the best. So, one enveloppe per population. If you could then collect several populations (15 would be ideal, so 15 envelopes total) from the same forest patch but which are not too close from each others (cf. populations >10m away), this would be optimal. The idea is to collect several (when available) populations from a given forest patch so that the sample is representative of the sampled forest patch.

When you are done, put all collected populations from the sampled forest patch (cf. all envelopes with coordinates written on it) in another bigger envelope and send it to this address:

Prof. Annie Guiller

Edysan FRE 3498 CNRS - UPJV

Laboratoire BIPE, BÃ'timent des Minimes

33 Rue Saint-Leu, 80000 Amiens

FRANCE

Thank you for your help.

Annie

– Annie GUILLER Edysan FRE 3498 CNRS - UPJV 33 rue St Leu 80000 Amiens France Tel. : 33 (0)3 22 82 75 56

annie <annie.guiller@u-picardie.fr>

## Software DAMBE update

Dear Colleagues,

I have updated the PhyPA function (Phylogenetics from pairwise alignment):

1. Now it can really work with homologous sequences as long as the titin sequences (~100,000) accurately, and it does not require a lot of memory because it uses a fast/accurate anchored alignment illustrated with two sequences below:

S1 NNNNNNNNNNNNNNNNAACGTTACTTNNNNNNNNNNNNGCGGATTTTNNNNNNNNNNNNNNNNNNNNN
S2 NNNNNNNNNNNNNNNNAACGTTACTTNNNNNNNNNNNNGCGGATTTTNNNNNNNNNNNNNNNNNNNNN

DAMBE will first find the non-overlapping highly homologous segments that I call sequence anchors (there are two such anchors above), so alignment needs to be done only for segments before, after and between the anchors. It takes little computational time to find the sequence anchors, which is obvious for anyone who have used BLAST or FASTA suites of programs.

2. The function is now available in the Mac and Linux version of DAMBE.

A new version has been uploaded to http://dambe.bio.uottawa.ca/DAMBE/dambe.aspx. Please try it and you will be impressed.

PS. I have also included a number of functions to automate the supermatrix approach. That is, for a set of species, you have compiled a number of file each containing a set of homologous sequences, e.g., Gene1.fas. Gene2.fas, etc. Each file may contain a subset of the species, e.g., Gene1.fas may contain 20 Gene1 sequences from 20 species, Gene2.fas may contain 15 Gene2 sequences from 15 species, and so on. You want to alignment them by MAFFT or MUSCLE (You need to download MAFFT and MUSCLE and save them on your computer so that DAMBE can use them) and then concatenate them into a single file in the form of

Sp1 ACGTACGTACGTACGTACGT Sp2 ACGTACGTACGTACGTACGT Sp3 ACGTACGTACGTACGTACGTACGTACGTACGTACGTACGT... Sp4 ACGTACGTACGTACGTACGTACGTACGTACGTACGTACGT... Sp5 ———
———ACGTACGTACGTACGTACGT... Sp6
————————ACGTACGTACGTACGTACGT... Sp7
————————ACGTACGTACGTACGTACGT... Sp8
————————ACGTACGTACGTACGTACGT...

(You need a equal-spaced font sush as courier font to see sequences above properly. It results from the first file containing four sequences, the second file containing six, with Sp3 and Sp4 present in both files)

All these can be done in a few clicks.

There is also a function for evaluating MAFFT and MUSCLE alignment based on the sum of all pairwise alignment scores (SP). Once you have aligned N sequence files with MAFFT or MUSCLE, you may wish to have something like this:

File MAFFT_SP MUSCLE_SP Gene1.fas 1323445 1323400 Gene2.fas 1323445 1323400 ...

This helps you to decide which alignment file (MAFFT-aligned or MUSCLE-aligned) you should use in assembling the final supermatrix. With the most accurate options for both, MAFFT performs a bit better than MUSCLE based on this criterion. For 100 files aligned by either MAFFT or MUSCLE, you may find about 40 MAFFT-aligned files with high PS than the corresponding MUSCLE-aligned files, about 10 MUSCLE-aligned files with high PS than MAFFT-aligned files, and the rest being equal. This function is under the 'Alignment' menu.

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

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## Software DAMBE update

Dear All,

I have implemented bootstrapping with the PhyPA method for those who have requested. A new version of DAMBE has been uploaded. Please download and try it. Keep in mind that PhyPA is really for highly diverged sequences. For lowly diverged sequences from which a reliable multiple sequence alignment can be obtained, maximum likelihood methods are better.

For those who have not heard of PhyPA or DAMBE: PhyPA is phylogenetics with pairwise alignment, and DAMBE is a comprehensive software for data analysis in molecular biology and evolution.

Xia X. 2016. PhyPA: phylogenetic method with pairwise sequence alignment outperforms likelihood methods in phylogenetics involving highly diverged sequences. Molecular Phylogenetics and Evolution 102:331-343

Xia X. 2017. DAMBE6: New tools for microbial genomics, phylogenetics and molecular evolution. J Hered 108(4):431-437

Xia, X. 2013. DAMBE5: A comprehensive software package for data analysis in molecular biology and evolution. Molecular Biology and Evolution 30:1720-1728

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

## Software funding

I have an open-source web based app that is useful in the pop gen community. Is anyone aware of any small grants or funding sources to help (or that I can apply to) to support me in hosting the said app. The cost is around 440USD per year. I can provide more details if required.

Thanks,

Roy

Roy Mathew Francis Evolutionary Biology Centre Uppsala University Sweden

Roy Francis <roy.m.francis@outlook.com>

## SSB Election

Ballot for President-Elect and Council – Try 2

We had only 89 votes in the SSB presidential and council election. We also had reports from long term, involved members (including two past presidents) that they had not seen the ballot. The Executive Vice President and President decided to extend voting for this election for this reason. Voting will now continue until Sunday, June 25, at noon US Pacific time. Results will be announced at the members' business meeting following Anne Yoder's SSB Presidential Address. If you already voted, please do not vote twice. If you haven't voted, please vote once! Original ballot info follows (modified only by deleting the previous due date). Please use the link below to cast your votes.

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We must vote for president-elect and SSB council. All members are eligible to vote. Short biographies and other information about each candidate (listed alphabetically by last name) are included below. You can vote at https://docs.google.com/forms/d/e/1FAIpQLSfpt3i0FN3DDDVwcwyYZzDAMOfL hygBB386Im-yo7cxc_8WVA/viewform?usp=sf_link. Dean Adams, Executive Vice President Candidates for President-Elect (vote for 1)

Cecile Ane Ph.D. (2000) Professor, Departments of Statistics and Botany University of Wisconsin - Madison www.stat.wisc.edu/~ane/ Research interests: Statistical methods and theory for molecular evolution and for trait evolution. One particular area is phylogenomics: to explain the variability of gene genealogies, possibly due to incomplete lineage sorting, non-vertical inheritance, duplication/loss, and systematic errors. Another area of interest is on models for trait evolution, to develop adapted model selection methods and fast computing tools.

SSB activities: SSB Council Member (2011-2013), Associate Editor for Systematic Biology (2007-2014), panel discussant for SSB Standalone meeting (2015), SSB symposium organizer (2012). Other: Associate Editor for Evolution (2016-2018) and Genome Biology and Evolution (2012-2015), instructor at NESCent workshops (2013-2014), co-maintainer of software packages like BUCKy, phylolm, and PhyloNetworks.

Bryan Carstens Ph.D. (2004) Associate Professor, Department of Evolution, Ecology, and Organismal Biology The Ohio State University http://carstenslab.org.ohio-state.edu/ Research interests: Our work is focused on the methodology used in phylogeographic and species level phylogenetic investigations, and is conducted on organisms ranging from salamanders to bats to carnivorous plants.

Dr. Carstens has been active in SSB starting as a council member, and later serving as a Program Officer and Executive Vice President. Bryan has served SSB as a judge for the Mayr talks, has helped to organize symposia, and contributed to pre-meeting workshops at Snowbird, Raleigh, Guaruja, and Baton Rouge. As President of SSB, Bryan will prioritize efforts to expand our membership and improve communication across all sections of SSB.

Candidates for Council (Vote for up to 5)

Rayna C. Bell Ph.D. (2014) Curator of Amphibians and Reptiles National Museum of Natural History www.raynacbell.com Dr. Bell received her Ph.D. in Ecology and Evolutionary Biology from Cornell University, and was awarded a University of California Chancellor's Postdoctoral Fellowship in the Museum of Vertebrate Zoology at the University of California, Berkeley. Rayna's research focuses on the ecology and evolution of amphibians and reptiles with an emphasis on island biogeography, hybrid zones, and coloration phenotypes. As a Ph.D. student, Rayna received Graduate Student Research and Ernst Mayr awards from the Society of Systematic Biology. Rayna helped establish the Dr. Margarita Metallinou Postdoctoral Travel Award for the Society for the Study of Amphibians and Reptiles, and chairs the selection committee.

Robb Brumfield Ph.D. (1999) Director, Museum of Natural Science Professor, Dept. of Biological Sciences Louisiana State University https://sites01.lsu.edu/faculty/brumfieldlab/ Research interests: collections-based evolutionary biology, molecular systematics, comparative phylogeography, population genetics, hybrid zones, biogeography, and taxonomy of birds. SSB activities: Associate Editor of Systematic Biology (2009 - 2017), Reviewer for Systematic Biology (1999 - present), Program Director for NSF (DEB: Phylogenetic Systematics, 2012-2013), Reviewer and

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

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## USunshineCoast Vol KoalaConservation

Volunteer Position - Koala research using detection dogs

I am seeking a dedicated field assistant for the 2017 field season (start of August to end of October) in the Frere Lab at the University of the Sunshine Coast, Queensland, Australia. This is a fantastic opportunity to get involved in innovative research and gain new skills. This research is conducted as part of the Detection Dogs for Conservation Program (https://www.usc.edu.au/DDC), which uses specially trained detection dogs to study and protect koalas.

The field assistant will be helping me organise and conduct surveys of koala habitat (i.e. bushland vegetation) with a detection dog specially trained on the odour of koala scats. We will be searching for koalas and their scats and recording habitat characteristics in the Moreton Bay, Sunshine Coast, Noosa, Gympie and Fraser Coast Council regions of south-east Queensland.

This research forms part of a PhD project studying the distribution, abundance and health status of koalas in rehabilitated vegetation and is part of a long-term study of koala behaviour, ecology and genetics.

Timeframe: 3 months (start of August to end of October 2017)

Location: The Moreton Bay, Sunshine Coast, Noosa, Gympie and Fraser Coast Council regions of south-east Queensland.

About: Office-based duties include contacting private landholders, community groups and government bodies to organise surveys of their properties; and data entry and processing. In the field, assistance will be required to operate field equipment whilst the handler instructs the dog to search the bases of trees for koala scats. The assistant will help to record data in data sheets and data loggers; collect, label and organise koala scat samples; take photos; and record features of observed koalas. Other tasks include laboratory sample preparation and assisting with dog training and testing, as required.

Weather permitting, days in the field can be consecutive, long and tiring in variable environmental conditions. Some of the fieldwork will involve overnight stays at various locations in south-east Queensland. For these trips, suitable accommodation will be arranged at no expense to the assistant. This is an unpaid, volunteer position and the successful candidate will need to make his/her own way to Brisbane or the Sunshine Coast. However, food and accommodation will be covered once in the Sunshine Coast.

The volunteer will be covered by University insurance.

Responsibilities:

* Helping organise field work * Recording site locations on a GPS * Taking photos * Recording features of observed koalas * Timing the koala habitat surveys with a stopwatch * Recording data in data sheets and data loggers * Collecting, labelling and organising koala scats * Assisting in genetic sample preparation and processing * Data entry and processing * Assisting with dog training and testing, as required

Qualifications: The ideal volunteer will be a recent graduate with a science background and a genuine interest in threatened species monitoring and conservation. This position is well-suited to recent graduates of environmental science, environmental management, ecology, zoology, genetics or similar fields looking to gain additional analytical and field experience.

He/she must:

* Be 18 years or older * Have a positive attitude * Love to learn * Pay attention to detail and be thorough * Listen and follow instructions * Possess basic computer skills * Be flexible and patient * Have great organisational skills * Be comfortable performing menial, repetitive tasks * Have a high work ethic * Be fluent in English * Be both willing and comfortable with engaging with the community * Be willing to make the full 3-month commitment * Have prior field research experience * Be prepared to work long, consecutive days, including weekends * Be comfortable working in the Australian bush (hot days, snakes, ticks) * Maintain a good mood when tired, hot, cold, wet, hungry, bitten by mosquitoes, etc.

We live and work in close quarters so mature and respectful candidates are required.

If interested, please email Natalie.Dowling@research.usc.edu.au with the subject line RESEARCH ASSISTANT by Friday 7th July 2017. Please include in the email:

1. Letter of interest 2. CV 3. Email contacts for 2 references

Looking forward to hearing from you.

Cheers, Natalie Dowling PhD Candidate University of the Sunshine Coast Sippy Downs, Australia www.celinefrerelab.com Natalie Dowling <Natalie.Dowling@research.usc.edu.au>

# PostDocs

## AustralianNationalUni PlantPhenotypicPlasticity

Multi-trait plasticity in response to a changing climate: PostDoc position

A position for a post-doctoral fellow is available in the Division of Evolution and Ecology at the Australian National University, Canberra, in the groups of Loeske Kruuk and Adrienne Nicotra, to study multi-trait phenotypic plasticity of an alpine plant in response to warming temperatures.

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. However studies of plasticity frequently rely on simplifying assumptions, and an understanding of the genomic and epigenomic mechanisms underlying plasticity is only just emerging. Using large-scale temperature-manipulation experiments an Australian alpine herb, the waxy bluebell (Wahlenbergia ceracea), the project will combine genomic and multivariate statistical analyses to determine whether multi-trait phenotypic plasticity is adaptive, whether it can evolve, and what are the (epi)genomic mechanisms driving it. The ultimate aim is both to explore fundamental ecological and evolutionary questions and to provide insights into the impact of environmental change on alpine flora. The project constitute an exciting opportunity for highly-motivated postdoctoral and PhD researchers with experience and interest in evolutionary ecology, quantitative genetic and genomic analyses, and/or plant thermal biology.

The project is funded by an Australia Research Council Discovery Project, and epigenomic analyses will be conducted in collaboration with AProf Christina Richards at the University of South Florida.

Applicants should possess (or be nearing completion of) a PhD in a relevant area of evolutionary ecology or genetics. They should have strong skills in complex statistical analyses and ideally familiarity with mixed model analyses; experience of research on phenotypic plasticity, plant physiology and/or epigenetics are also preferable. Excellent communication and writing skills and a strong track record of publication in academic journals are essential. The position is available for 30 months, ideally starting in February 2018. The starting salary is AUD $86,646 p.a. (+17% superannuation).

Further information is available at: http://biology.anu.edu.au/research/projects/multi-trait-plasticity-response-changing-climate-postdoc-and-phd-positions - or contact us directly at Loeske.Kruuk@anu.edu.au or Adrienne.Nicotra@anu.edu.au. Applications close: 16 July 2017 11:55:00 PM Australian Eastern Standard Time.

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

## BoiseStateU MolecularInnovationsRNA

The Hayden Lab at Boise State University is seeking a postdoctoral researcher interested in molecular mechanisms of RNA functional evolution. The lab uses laboratory selection of RNA and high-throughput sequencing to study the distribution of functions in sequence space and the evolution of novel functions. These experiments have implications for the understanding of evolutionary innovations in general, have implications for life's origins, and also have applications in synthetic biology. The lab aims to use synthetic biology approaches to study evolution, and to use evolution to expand the synthetic biology toolbox. The preferred candidate will have a PhD and experience with molecular biology, RNA sequencing, and next-generation sequence data analysis. Experience with programming is preferred (R, python, matlab, perl, etc.). Funding is available for up to three years. The applicant will have an opportunity to interact with graduate students and faculty in our multidisciplinary Biomolecular Sciences graduate program that spans Molecular Biology, Biochemistry and Biophysics at Boise State.

To apply, please email a merged pdf to erichayden@boisestate.edu with the following: 1) Cover letter describing your interest in this research, 2) CV with references and 3) the name and email address of three references. Review of applications will begin on July 5, and will remain open until filled.

– Eric J. Hayden Assistant Professor Biological Sciences Mail Stop: 1515 Boise State University Boise, Idaho, USA 83725

Eric Hayden <erichayden@boisestate.edu>

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## CalAcademySciences CommunityPhylogenomics

3-year Postdoctoral Research Fellow, Community Phylogenomics at California Academy of Sciences, San Francisco, CA 94118

Position Summary: The three-year NSF-funded (DEB-1655076) Postdoctoral Fellow will investigate community structure and diversity patterns, as well as potential drivers of community assembly and species endemism, in ants in Madagascar. The postdoc will assemble a phylogenomic dataset of ultraconserved elements (UCEs) for 1300 species of Malagasy ants and combine this data with over 100,000 curated specimen records with climatic niche data to model species distributions for all Malagasy ants. The postdoc will lead analyses to characterize the phylogenetic patterns of ant community structure and diversity in Madagascar based on these phylogenomic and community datasets. This a collaborative project between Brian Fisher, California Academy of Sciences, and Bonnie Blaimer at North Carolina State University in Raleigh, NC [previously Smithsonian]. This study bridges genomic techniques with ant biogeography and ecology across multiple scales, from local communities to the whole Malagasy region.

There are numerous opportunities to interact with other faculty and postdocs in the departments of both institutions. The project will also include trips to Madagascar where training for students will occur. The postdoc is expected to publish in leading international journals and to present his/her results at international and national conferences.

Essential Duties and Responsibilities: The postdoc will be involved in all aspects of this NSF-funded project, including genomics laboratory work and analyses at NC State with Bonnie Blaimer, and teaching in Madagascar. The postdoc is required to maintain up-to-date records of all experiments and data collected. Critical thinking and independence are a necessity as is lead participation in data analyses. Manuscript writing and publication are expected and required. The postdoc will interact with graduate and undergraduate students and other personnel in the Fisher lab, and also in Bonnie Blaimer's lab. Two months of travel including a trip to Madagascar each year.

Education and/or Experience: Qualified applicants must have successfully obtained their PhD degree in molecular systematics, evolutionary biology, ecology or related fields. The position requires excellent verbal and written communication skills (English) and a strong background and publication record. Experience with unix/command line and the R environment is required. Proficiency in programming (perl or python) and niche modeling is preferred, but a willingness to learn is acceptable. A background in ants is desirable, but not necessary.

Knowledge, Skills and Abilities: Perl or Python - Proficiency in programming (perl or python) and niche modeling is preferred, but willingness to learn is acceptable. R - the R environment is required for modeling and analyzing species distributions, diversity, and ant community structure. Unix - Experience with unix/command line.

Application Instructions: Please apply online: http://calacademy.snaphire.com/jobdetails?ajid=3DybQU8 and include the following attachments: cover letter highlighting candidate's motivation to apply; skills and science research background and expertise which support the application; detailed CV including a list of publications and other achievements; and names and contact details of three referees.

Duration of Position: The successful candidate will be offered a position for 12 months initially, with the potential for renewal for up to 24 more months, starting preferably before 1 January 2018.

Questions: Contact Brian L. Fisher <bfisher@calacademy.org> (fisherlab.org) or Bonnie Blaimer <bonnieblaimer@ gmail.com>

Brian Fisher Curator of Entomology and Patterson Scholar 55 Music Concourse Drive California Academy of Sciences San Francisco, CA 94118, USA www.fisherlab.org Insects and People < http://ipsio.org > Madagascar Biodiversity Center < http://madagascarbio.org > www.antweb.org ResearchGate < https://www.researchgate.net/profile/Brian_Fisher7 >

"Brian L. Fisher" <bfisher@calacademy.org>

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## ClemsonU FishMacroevolution

We are looking for a postdoctoral researcher to work on an NSF funded project on the ecological and environmental drivers of body shape evolution across teleost fishes. It is a collaborative project between Samantha Price, at Clemson University, and Peter Wainwright, at the University of California, Davis; the postdoc will be based at Clemson. Research involves the generation and analysis of ecomorphological databases of morphometric measurements and geometric morphometric descriptions of fish shape taken from museum specimens, as well as environmental and ecological data collated from existing sources. These data are analyzed using phylogenetic comparative methods in a high performance-computing framework. The postdoc will assist in data collection and analysis, as well as supervising undergraduate researchers and will be expected to write and publish scientific papers.

Research in the Price lab is broadly focused on phylogenetic approaches to macroevolution and biodiversity, with the aim of identifying repeating themes and general principles governing the evolution of vertebrate diversity. We study both living and fossil animals and use data and techniques from across evolutionary and organismal biology, palaeobiology and data science.

It is a one-year appointment renewable for one or more additional years conditional upon performance. Applicants should have completed a Ph.D. or expect to do so prior to starting in the position. Starting date negotiable but strongly prefer Jan 2018.

Review of applications will begin on Aug 7th 2017 and the position will remain open until filled.

A successful applicant will have:

- A doctoral degree in a relevant subject.

- One or more of the following skill sets: geometric morphometrics, phylogenetic comparative analyses, functional morphology, fish diversity and natural history.

- Experience collecting, collating and analyzing large morphometric and ecological datasets and working in museum collections.

- A solid track record of scientific publications and international conference presentations.

Interested candidates should email (1) an application letter summarising research interests, goals and qualifications as well as experience mentoring undergraduate research, (2) a CV and (3) contact information for at least two references to Samantha Price saprice@ucdavis.edu. Please don't hesitate to contact me if you wish to discuss the position prior to applying. Review of applications will begin on Aug 7th 2017 but the position will remain open until filled.

Samantha Price, Ph.D. Dept. Evolution & Ecology UC Davis Davis, CA 95616 USA Website: www.evovert.com Starting Fall 2017: Dept. Biological Sciences Clemson University South Carolina 29634, USA

"saprice@ucdavis.edu" <saprice@ucdavis.edu>

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## ColoradoStateU MolecularEvolution

The Sloan Lab at Colorado State University is seeking inquiries from postdoctoral researchers with experience in molecular biology and evolution to lead projects supported by new grants from NIH (5 yrs) and NSF (4 yrs). The focus of our research is on the evolution of plant organelle genomes and their coevolution with the nucleus. In particular, we are interested in mutational mechanisms, selective pressures, and the causes/consequences of extreme changes in rates of evolution in mitochondrial and plastid DNA. More information about our past research projects and publications is available at our lab website: https://sites.google.com/site/danielbsloan/ We anticipate opportunities for highly motivated postdoctoral researchers who are excited about addressing evolutionary questions at the molecular level and want to contribute to a positive and collaborative intellectual environment.

Relevant skills and areas of expertise for these different projects would include:

- Genetic modification (transformation) of the plastid genome and plant tissue culture

- Mutation detection and analysis of deep sequencing data

- Library construction for next-generation sequencing

- Evolutionary genomics and phylogenetics

Our lab is in the Department of Biology at Colorado State University, which is housed in a state-of-the-art research facility that was just completed in 2017. The department includes numerous labs in the fields of both plant molecular biology and evolutionary biology, so there are ample opportunities for collaboration outside the lab group. The university is in Fort Collins, Colorado, which routinely ranks among the top locations in the country in terms of overall quality of life.

To get more information and discuss opportunities, inquiries can be e-mailed to Dan Sloan (dbsloan@rams.colostate.edu) and should include a CV and a very brief statement of research/career goals. Our lab will be attending the upcoming SMBE meetings, so researchers who will be at the conference are also encouraged to e-mail Dan to set up a time to meet in Austin. Review of inquiries will begin immediately.

dbsloan@rams.colostate.edu

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## CornellU EvolutionaryBiochemistry

Academic Job Description

Section of Plant Biology, SIPS, Cornell University

Postdoctoral Associate in Evolutionary Biochemistry

Position Function

This advertisement seeks to fill a postdoctoral position in the Moghe Lab in the Plant Biology Section at Cornell University. The lab, which will start from August 2017, will host a cross-disciplinary biochemical genomics program investigating evolution of specialized metabolism in diverse plant lineages. This position requires a researcher with expertise in molecular biology and experimental biochemistry. The researcher will primarily work on discovering functions of poorly understood metabolic enzymes in cultivated tomato and related species using gene knockouts, mass spectrometry, RNA-seq, enzyme assays and comparative genomic approaches. The overall research goal is to create a robust foundation for computationally predicting functions of unknown enzymes across the plant phylogeny using evolutionary genomics, network reconstruction and machine learning approaches. The researcher will also be expected to contribute to additional projects in the lab that include characterizing the evolutionary origins of novel specialized metabolite classes from select non-model species. More information can be found on the Moghe Lab website: https://www.moghelab.org. This is a one year term appointment, with possible extension depending on funding and performance.

The researcher will have opportunities to present at national/international conferences, attend workshops, participate in collaborative projects and enhance their teaching credentials through occasional guest lectures. Given the multi-disciplinary nature of the lab, the researcher will also have opportunities to learn different bioinformatic approaches such as Python/R coding, working in a Unix environment and techniques for RNA-seq, chemo-informatics and comparative genomics research, making them highly competitive for future academic or industry careers.

Anticipated Division of Time

75% : Experimental research as described above

15% : Manuscript preparation, presentations

10% : Mentoring and professional development

Requirements

PhD in Plant Biology, Biochemistry, Genetics or other related field.

Required skills:

* Experience in handling and manipulating model or non-model plant species * Standard molecular biology techniques (Gels, PCR, bacterial transformation etc.) * Gene cloning using different vectors * Generation of knockout/knockdown/over-expression lines * Excellent written and verbal communication skills * Evidence of performing high-quality research as part of a team

Preferred skills: * Mass spectrometry and/or NMR * Enzyme purification, assay and kinetics * RNA-seq data analyses * Comparative genomic analysis

Supervision Exercised

The researcher will be expected to mentor undergraduate and/or early graduate students.

How to Apply

Interested applicants should email their CV, statement of research interests and copies of two publications as a single zip file to Dr. Moghe (gdm67@cornell.edu). Applicants should also arrange for three reference letters to be sent directly to the above email address.

About the Institution

The postdoctoral researcher will join a vibrant, internationally-renowned and highly collaborative research community in Cornell's School of Integrative Plant Science (SIPS). For more information about SIPS, visit http://sips.cals.cornell.edu/ . Cornell University is a member of the Ivy League. The main campus of Cornell University, which overlooks 40-mile-long Cayuga Lake, is located in the Finger Lakes region of Upstate New York, a scenic environment of spectacular lakes, waterfalls, gorges, rolling hills, farmland, vineyards, and state parks. It is an area with outstanding recreational and summer and winter sports opportunities for individuals and families. The Cornell campus itself is one of the most beautiful in the country. The Ithaca community is culturally diverse with excellent theater, music, sports, and other activities befitting a major university town, yet also has the warmth and friendliness of a small community. The area is known for its many bookstores and restaurants, an extensive walking trail system, arboretum, Laboratory of Ornithology, marina, Farmers Market, a hands-on Science Center, and art and science museums. For more information and links to individual attractions, visit http://www.visitithaca.com/ . Cornell University is an innovative Ivy League university and a great place to work. Cornell's inclusive community of scholars, students and staff impart an uncommon sense of larger purpose and contribute creative ideas to further the university's mission of teaching, discovery and engagement.

Gaurav Moghe Postdoctoral Researcher Dr. Robert Last Lab

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## Dartmouth MicrobialEvolution

A postdoctoral researcher position is available in the lab of Olga Zhaxybayeva (a.k.a. the lab of OZ) in the Biological Sciences Department of Dartmouth College in Hanover, NH to study evolution of gene transfer agents and microbial adaptations to temperature and salinity. The research approaches include comparative omics analyses, mathematical modeling, population genetics and phylogenetics.

Qualified applicant must have a Ph.D. in bioinformatics, applied mathematics, computer science, statistics, biology, microbiology, or a related field with strong interest in molecular evolution and at least some programming experience.

The successful candidate will join a vibrant research and educational environment of Dartmouth College, will have the opportunities to establish his/her own independent projects and participate in professional development programs offered via Dartmouth's Postdoctoral Association. More information about Zhaxybayeva's lab is available at http://www.dartmouth.edu/~ecglab/ . Review of applications will begin immediately and continue until the position is filled. Start date is negotiable. Interested applicants should send a single PDF file containing CV, one-page statement of research interests and contact information of three referees to Olga Zhaxybayeva at ECGLabJobs@gmail.com.

Dartmouth offers competitive salary and benefits along with the opportunity to live in a picturesque rural region that offers year-round recreational activities and is located near the culturally vibrant cities of Boston, Montreal, and New York.

Dartmouth College is an equal opportunity/affirmative action employer with a strong commitment to diversity and inclusion. We prohibit discrimination on the basis of race, color, religion, sex, age, national origin, sexual orientation, gender identity or expression, disability, veteran status, marital status, or any other legally protected status. Applications by members of all underrepresented groups are encouraged.

– Olga Zhaxybayeva, Ph.D. The Simons Foundation Investigator and Assistant Professor Department of Biological Sciences Dartmouth College 333 LSC 78 College Street Hanover, NH 03755 USA

Office: (603) 646-8616 Lab: (603) 646-9397 Email: olgazh@dartmouth.edu Web: http://www.dartmouth.edu/~ecglab/-http://dartmouth.edu/faculty-directory/olga-zhaxybayeva "Olga.Zhaxybayeva@dartmouth.edu" <Olga.Zhaxybayeva@dartmouth.edu>

## EotvosU Budapest 2 EvolutionaryGenomics

ERC.2.EvolutionaryGenomics

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 2021 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 coexisting 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

## FordhamU SelectionInRice

Postdoctoral Associate, Selection on Patterns of Gene Expression in Response to Stress in Rice

A postdoctoral position will be available in the lab of Steve Franks in the Department of Biology at Fordham University in New York City. The position will involve performing selection analysis on phenotypes and gene expression patterns in populations of rice experimentally subjected to salt and drought stress, as part of a larger project examining systems genomics and adaptation. The project is in collaboration with Michael Purugganan and Richard Bonneau, at New York University (NYU), and with the International Rice Research Institute. The position will be based at the Rose Hill campus of Fordham, in the Bronx, with work also conducted at the NYU campus in Greenwich Village. The postdoc will also conduct research projects on related topics, and will have access to the institutions affiliated with Fordham, including the New York Botanical Gardens, Bronx Zoo, American Museum of Natural History, and the Louis Calder Field Station. For more information on the lab, see sfrankslab.wordpress.com.

The candidate should have a Ph.D. in Ecology, Evolution, Genetics or a related field, and knowledge of these subject areas. The candidate should be proficient in conducting phenotypic selection analysis and should be able to use statistical programs such as R. Skills in quantitative genetics, bioinformatics, and lab work related to genomics is also desired, and prior experience working with plants would also be helpful. The postdoc will be expected to participate in the research projects, help to mentor graduate and undergraduate students, and contribute to scientific publications. The postdoc must be eligible to work in the United States, and will undertake a background check and drug screening. Compensation includes a competitive package of salary and benefits.

The target start date for the position is on or after September 1, 2017. The initial appointment will be for one year, which can potentially be extended for an additional year.

To apply, please send a C.V., statement of research interests and goals, and contact information for 3 references to Steve Franks at franks@fordham.edu. The application materials should be received by August 1, 2017.

Fordham University is an academic institution that in matters of employment complies with federal, state, and local employment laws and does not discriminate on the basis of race, color, creed, religion, age, gender, sex, national origin, marital status, sexual orientation, sexual preference, citizenship, alienage, veteran status, disability, genetic information, status as a victim of domestic violence or any other basis prohibited by law.

Steven J Franks

Professor

Department of Biology

Fordham University

Bronx, NY 10458

< http://sfrankslab.wordpress.com/ >

Steve Franks <franks.steve@gmail.com>

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## GuangxiU 4 Phylogenomics

Four postdoctoral fellowships available immediately in Plant Phylogenomics, Ecological Genomics and Adaptive Evolution

Four Postdoctoral Fellowships are available immediately at the Plant Ecophysiology and Evolution Group of Guangxi University (Nanning, China). We are seeking highly motivated and productive postdoctoral fellows to engage in 2-year projects in the following fields:

- Plant Phylogenomics (2 funded fellowships available) - Ecological Genomics and Adaptive Evolution (2 funded fellowships available)

Plant Ecophysiology and Evolution Group at Guangxi University (Nanning, China) http://www.plant-ecophysiology-evolution.com/ http://www.plant-ecophysiology-evolution.com/person/joeri-sergej-strijk/ http://www.plant-ecophysiology-evolution.com/person/alison-kim-shan-wee/ 1 Plant Phylogenomics Two fellowships are available in the Biodiversity Genomics team, led by Associate Prof Joeri S. Strijk. We focus our research efforts on understanding the origin, rise and persistence of tropical plant biodiversity by combining the latest NextGen sequencing techniques and advances in genomics with molecular systematics, taxonomy, ecology and historical biogeographical reconstruction. Our study area covers the greater tropical Australasian zone and extends to include the flora of the Madagascar and Indian Ocean Island Biodiversity Hotspot. Members of the team address a wide range of research topics, ranging from understanding the effects of palaeogeographic changes in landmass configuration on patterns of plant genome evolution and divergence, studying community assembly and in-situ plant diversification patterns on oceanic islands, to using genomic data to clarify the links between gene divergence, diversification and distribution, and employing the latest NGS techniques to resolve longstanding botanical and evolutionary questions typical for amorphic, speciose and widespread tropical tree families.

-REQUIREMENTS: Prospective candidates should have a PhD with a strong background in plant genomics and/or systematics, bioinformatics, molecular dating and/or biogeographical reconstruction, and should have a proven track record of successful publication in peer-reviewed journals. Additional experience in botanical collecting and fieldwork, taxonomy and herbarium experience are considered a major advantage when applying. The candidate will join a dynamic and international team that uses the latest advances in genomics to push the boundaries of our knowledge on plant biodiversity and plant divergence. Within the team's programs, a number of topics are available for discussion following a successful application.

2 Ecological Genomics and Adaptive Evolution Two fellowships are available under supervision by Associate Prof Wee Kim Shan. In our unit we pursue a system-level understanding of adaptation and evolution in non-model plants, combining experimental ecophysiology and cutting-edge sequencing technology.

-REQUIREMENTS: Prospective candidates should have a PhD with a strong background in plant ecophysiology, plant biology and genetics, and a proven track record of successful publication in peer-reviewed journals. Experience in field collection (in the tropics), plant breeding and handling next generation sequencing data (especially transcriptomes) is highly preferable. The candidate will be part of an international team studying stress response, phenotypic plasticity and natural variation of selected plant lineages in Asia. A number of topics are available for discussion following a successful application.

***Fellowship details*** Opportunities for the development of individual research projects as well as collaborative work exist within the Plant Ecophysiology and Evolution Group.

The postdoctoral tenure will be two years and renewable for one more year upon evaluation. The fellowship covers an annual salary, a furnished apartment on campus and medical insurance. A small research fund (30,000 Yuan RMB) is provided by the university and the host supervisor will cover the rest of the initial research expenses. Prospective candidates are required to take part in external funding applications to support the joint research work. In addition, the selected candidate will be eligible to apply for a National Postdoctoral Scholarship through Guangxi University.

***General information Guangxi University*** The Plant Ecophysiology and Evolution Group is part of the College of Forestry, under the State Key Laboratory of Conservation and Utilization of Subtropical Agro-bioresources, and the newly proposed Guangxi Key Laboratory of Forest Ecology and Conservation, which houses a wide range of laboratories and research teams. We are centrally located on the large

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## Ireland ViralBioinformatics

The lab of Prof. Dr. Colin Hill has a 2.5 years postdoctoral position available within the APC Microbiome Institute working in the area of bioinformatics of the gut phageome.

*Position Summary*

The APC Microbiome Institute is a trans-disciplinary research centre, with clinicians, clinician-scientists and basic scientists from diverse backgrounds working in teams, sharing ideas and resources. Although focused upon the gastrointestinal bacterial community (the microbiota), the scale and scope of the work has become one of the fastest moving areas of biology. The microbiota is not only a target for treatment and prevention of disease, it is a repository for functional food ingredients and even new drugs and is a source of novel biomarkers of disease risk. The scientific organisation of the APC consists of a matrix of 'spokes' or themes of intellectual pursuit.

This position is within APC's Gut Phageomics Laboratory, consisting of up to 20 researchers investigating the role of the gut phageome in health and disease. The Research Fellow will work within APC's 'Spoke 5' which is collaborating with a major multi-national pharmaceutical company to explore the role of bacteriophages in shaping the human gut microbiome. He/she will lead the bioinformatics team with the group and should have a proficiency in analyzing Illumina sequnence data, familiarity with the working with such data in the linux terminal environment as well as statistical analysis of microbiome count data in the R programming language. Experience with Bioconductor and/or Biopython would also be beneficial.

*Qualifications/experience*: The candidate should hold a PhD with preferably 4-5 years' experience, ideally with a background in microbiome data analysis, and a proven ability to conduct independent research to very high level.

*Post duration:* 2.5 years

*Salary:* euro 52,716- euro 57,442 p.a. (IUA Scale)

*Project:* Gut Phageomics

*ROLE SUMMARY*

The Researcher Fellow title should be awarded to individuals who have personally secured their own independent external research funding inclusive of their salary following an open, transparent and competitive selection process by the research funding body or who have been appointed by the HEI following an open competition. The Research Fellow would still be associated with a Principal Investigator who would act as mentor and facilitate access to research infrastructure.

The role also allows the Research Fellow the professional development opportunity to demonstrate the capacity for independent and self-directed research and scholarship and the management of a research team. The role allows the Research Fellow to assemble a portfolio of independent achievement and render themselves competitive for tenured academic positions or senior scientific roles in industry.

*KEY ACCOUNTABILITIES*

- To manage and conduct a specific programme of research and scholarship. - To independently identify research objectives and potential funding sources and to prepare and write bids for funding proposals. - To have a strong track record in securing external funding, including own salary. - To disseminate the outcomes of the research, including peer-reviewed academic publications of international standing. - To take a leading role in the further development of the research programme and in seeking and pursuing appropriate external funding. - To participate fully in the wider research and scholarly activities of the Research Centre, School and College. - The Research Fellow may also have some teaching and mentoring duties. - To supervise post graduate research students as co-supervisor. - To mentor and assist students and early-stage researchers in the research group, School and College. - To take responsibility for, manage and conduct administrative and management tasks associated with the research programme. - To engage in appropriate training and professional development opportunities as required by the Principal Investigator, School or College. - The employee will be expected to carry out any additional duties as may reasonably be required within the general scope and level of the post.

*CRITERIA*

- A PhD qualification, significant relevant research experience and secured independent research funding. - The capacity to work independently on research projects. - The ability to assess and evaluate concepts/theories in order to develop original solutions and particular knowledge of, and expertise in research methodologies. - Hold a track record of high quality peer reviewed publications. - Experienced in post graduate supervision. - Project management experience. - Ability to provide leadership to small research teams. - Ability to secure independent external research funding - Ability to contribute to broader organisational and management processes.

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## JagiellonianU AmphibianEvolutionaryGenomics

Postdoc position in Amphibian Evolutionary Genomics (3 years)

A postdoctoral position in amphibian evolutionary genomics is available in the group of WiesÂ$^3$aw 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.

Wieslaw 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: http://www.molecol.eko.uj.edu.pl/en_GB/-zespol/pracownicy/wieslaw-babik Wieslaw Babik <w.babik76@gmail.com>

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## KielU BioinformaticsGenomics

Postdoc in bioinformatics/genomics (Kiel University, Germany)

We are looking for professional and competent support to start as early as possible.

The institute of Clinical Molecular Biology (IKMB) together with Kiel Life Sciences (KLS) is looking for a bioinformatician with a PhD in bioinformatics, molecular biology, genetics or related discipline to join our genomics core facility. A key focus of the position will be the support of denovo genome projects conducted in collaboration with external partners within the German Network for Bioinformatics Infrastructure, de.NBI. Previous experience with the assembly and annotation of eukaryotic genomes is therefore desirable. The candidate will furthermore have experience/interest in the implementation of large-scale infrastructure, pipeline development, analysis of next-generation sequencing data and have strong command of the English language, both written and orally.

The IKMB is embedded in multiple high-profile research efforts, including a recently established DFG Collaborative Research Center (CRC 1182) and a German DFG "Excellence Cluster", and thus offers a highly stimulating and interactive working environment. Through the de.NBI, the candidate will have the opportunity to interact with national and international colleagues working on genome projects and related software/infrastructure and further improve her/his professional profile in these areas.

What we offer:

This is a fixed-term position for two years, with the possibility of extension. Weekly working time is 100% of a full-time position (currently 38,50 hours per week). Working part-time is possible. Salary will be, depending on qualifications, according to the German salary scale E14 TV-L. The UKSH has been certified as a family-friendly institution and is committed to further improve the compatibility of work and family life. The University Medical Center Schleswig-Holstein is an equal opportunity employer. People with disabilities will be given preference in case of equal qualifications.

Additional Information:

For more details on the position, please contact Dr. Marc Hoppner of the IKMB at m.hoeppner@ikmb.uni-kiel.de. Questions on administrative aspects can be addressed to Jana Gisdepski via e-mail: karriere@uksh.de.

We are looking forward to your application. Please submit your application within the next 4 weeks, indicating your earliest possible starting date as well as the reference number 20170528.

Please apply via our online portal: www.uksh.de/-Bewerbung.html?nr 170528

– Marc P. Hoeppner, phil.lic. PhD Head of Computational Genomics

Institute of Clinical Molecular Biology Christian-Albrechts-University of Kiel

University Hospital Schleswig Holstein - Campus Kiel
Rosalind-Franklin-StraÃÅe 12 - 24105 Kiel, Germany

Fon: +49 (0) 431 / 500 - 15156 m.hoeppner@ikmb.uni-kiel.de - www.ikmb.uni-kiel.de "Marc P. Hoeppner" <m.hoeppner@ikmb.uni-kiel.de>

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## Krasnoyarsk Russia ForestGenomicsBioinformatics

Call for a postdoc in genomics and bioinformatics!

15.06.2017

A postdoctoral position (for 1 year with potential extension for 2 more years) is available at the Siberian Federal University (SibFU) in the Laboratory of Forest Genomics in Krasnoyarsk (Russia) focusing on studying genomes of Siberian conifer species and their major phytopathogens.

Job description

- Teaching: lecturing in a Master's program "Genomics and Bioinformatics";

- Research: work on the main project of the laboratory ≪Genomics of the key boreal forest conifer species and their major phytopathogens in the Russian Federation≫ supervised by Prof. K.V. Krutovsky;

- Coaching and/or mentoring: Bachelor and Master Degree students.

Posdoc fellow positions requirements: * To qualify for the postdoc position, the applicant must have a PhD or similar degree in Biology, Computer Science, Mathematics, Informatics or Biophysics; * Experience with the NGS techniques: genome and transcriptome assembly and annotation, RNA-seq, phylogenetic analysis, candidates with strong skills in bioinformatics and computer programming are also considered; * Fluent English, at least B2 (ALTE); * At least 3 WoS / Scopus publications in the last 3 years (2014-2016).

Salary

The salary of the appointed researcher will be 120 000 RUR per month (equivalent of ˜2000 euro).

Official application deadline:

June 30, 2017

What we offer:

- The results obtained in our laboratory are unique, only a few laboratories in the world conduct research on the complete genomes of conifers, thus, there is a good opportunity to get original results and publish them in high-quality journals;

- There are two sequencing machines - Illumina HiSeq 2000 and MiSeq in our Laboratory, equipment for manipulating with nucleic acids, a cluster for high-performance computing, a server for processing genomic data with 3 TB of RAM;

- The master's program on Genomics and Bioinformatics was established in 2016 at the related department of the SibFU, where you can practice teaching and giving lectures;

- Comfortable and inexpensive housing in the residence hall at the SibFU campus;

- Reimbursement of travel expenses for relocation (one-way flight tickets).

Please, contact:

Putintseva Yuliya, Research Associate at the Laboratory of the SibFU Center for Genomic Research, tel.: +7 913 527 79 96, e-mail: yaputintseva@mail.ru

Natalia Oreshkova, Research Associate at the Laboratory of the SibFU Center for Genomic Research, tel.: +7 (391) 249-46-25, e-mail: oreshkova@ksc.krasn.ru

Anastasia Garmash, Manager of International Recruitment Office, tel.: +7 (391) 206-25-13, e-mail: agarmash@sfu-kras.ru for further information.

Application Procedure

The following documents must be attached to the application:

- Academic curriculum vitae in English;

- Passport copy;

- Copies of the academic degree and academic title;

- Statement of Intent to participate in the Postdoc Fellowship program;

- Motivation letter;

- The list of publications in international peer-reviewed journals;

- A brief description of research merits and action plan in English;

- Contact information of two persons whom may be asked to give a statement of the candidate;

- Consent to personal data processing.

To see more details and submit your application, please, click here.

Thank you.

Prof. Dr. Konstantin (Kostya) V. Krutovsky Department of Forest Genetics and Forest Tree Breeding Georg August University of Gottingen Busgenweg 2, D-37077 Gottingen, Germany E-mail: kkrutov@gwdg.de http://www.uni-goettingen.de/en/414626.html http://essm.tamu.edu/people/faculty/adjunct-faculty/krutovsky-konstantin http://genome.sfu-kras.ru/en/krutovsky +49-(551)-393-35-37 (off.) +49-(551)-39-83-67 (fax)

"Krutovsky, Konstantin" <konstantin.krutovsky@forst.uni-goettingen.de>

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## MaxPlanckInst Jena 2 AncientMetagenomics Dairy

Two Postdocs at Max Planck Institute for the Science of Human History

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Postdoc ' Metagenomics and Bioinformatics Max Planck Institute for the Science of Human History

Position Title: Postdoc in Metagenomics & Bioinformatics Employer: Max Planck Institute for the Science of Human History Location: Jena, Germany Classification: TVoD E13 Salary: EUR 50,900-53,600 annually Work Type: Full time Duration: 2 years, extendable Closing Date: Initial application review 30 June 2017. Position open until filled.

Dr. Christina Warinner is seeking a postdoc in Metagenomics & Bioinformatics to join her Microbiome Sciences research group at the MPI-SHH. Research will focus on both contemporary and ancient microbiota. For questions, please contact Christina Warinner (warinner@shh.mpg.de) and cc Anke Trinkler (trinkler@shh.mpg.de).

*** Please note that excellent candidates with a strong bioinformatics background in biology, microbiology, or computer science are encouraged to apply. Prior experience analyzing HTS microbial data from the human microbiome and/or other complex microbial environments is strongly desired.***

For further details please see below, and/or: http://www.shh.mpg.de/jobs The Department of Archaeogenetics at the Max Planck Institute for the Science of Human History (MPI-SHH) is offering a two-year postdoc position in Metagenomics and Bioinformatics, with the possibility of extension. The position requires a PhD degree and proficiency in bioinformatics and/or computational approaches, with experience working with metagenomic data. Experience with programming and shell scripting languages Python, Perl, and/or R is required. Prior experience analyzing HTS microbial data from the human microbiome and/or other complex microbial environments is strongly desired.

The primary research focus of this postdoctoral position is the investigation of human oral and gut microbiome ecology and evolution through time, with the opportunity to analyze data from contemporary non-human primates and diverse contemporary societies, as well as extraordinary samples (dental calculus and paleofeces) spanning human evolution and broad periods of human history and prehistory. In addition to metagenomics data, concurrent projects in the Microbiome Sciences Group on metaproteomics and metabolomics provide rich complementary data sets for integrative analysis. Particular areas of interest are microbiome biodiversity, community structure analysis, functional analysis, genome assembly, and strain diversity characterization. Additional responsibilities include supervision of graduate students, support of ongoing research projects, and leadership of independent research projects. Opportunities are also available to teach in the International Max Planck Research School (IMPRS).

The position will be supervised by Prof. Dr. Christina Warinner. Your qualifications Essential: - Have or are about to obtain a PhD degree in bioinformatics, computer science, biology, microbiology, biochemistry or related subject - Proficiency in programming and shell scripting languages (Python, Perl, and/or R) - Experience analyzing large HTS metagenomic datasets - Experience in microbial genomics, including genome reconstruction and annotation

Advantageous: - Programming experience with C++ and/or Java - Experience analysing microbiome data - Experience in human, animal, and/or plant genomics and/or proteomics

Additional points: - Interest in genetic data generated from prehistoric and historic samples - Have an strong academic and research record - Are enthusiastic and hard-working - Have proficient English skills

We offer: - The opportunity to be involved in transformative research projects that provide opportunities for cross-disciplinary collaboration - Cutting-edge facilities, instruments, and computational support - An excellent research environment - An English language working environment

The overarching goal of the Max Planck Institute for the Science of Human History is to explore the history of humans using state-of-the-art analytical methods. Scientists from different disciplines, such as genetics, linguistics, archaeology, anthropology and history are working together to answer fundamental questions about the biological and cultural evolution of man from the Paleolithic until today, and they jointly develop innovative methods, in particular in the areas of genome sequencing, language documentation, bioinformatics and phylogeography.

We offer an interesting and responsible job in a competitive, dynamic and stimulating international research environment. Remuneration will follow the public service pay scale TVoD level E13 for full-time employment (100%), corresponding to an annual gross salary of 50,900-53,600 EUR, depending on qualifications and experience. In addition, social benefits are paid according to the regulations of the Civil Service.

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## Melbourne InfluenzaEvolution

The WHO Collaborating Centre for Reference and Research on Influenza is looking for a postdoctoral virologist, with a primary focus on the use of in vivo experimental models to investigate a novel influenza antiviral drug. The successful researcher will have good classical virology skills (cell culture, growth of influenza viruses, and experience in various functional assays), molecular biology skills (PCR, sequencing, cloning, site directed mutagenesis and reverse genetics) and extensive experience conducting in vivo mouse or ferret influenza studies. Experience working with influenza antivirals and performing next generation sequencing is desirable.

The position requires a scientist with a PhD in virology or microbiology with post-doctoral laboratory experience, preferably with a strong background in influenza virus research. The successful researcher must be able to contribute effectively as a team member, but have the independence to plan, organise and conduct experiments with minimal supervision.

Further details are available via the following link:

https://melbournehealth.mercury.com.au/-ViewPosition.aspx?id=1povSeFNPT4=&jbc=ere
If you require further information please email A/Prof. Aeron Hurt (aeron.hurt@influenzacentre.org)

"Hurt, Aeron" <Aeron.Hurt@influenzacentre.org>

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## Montpellier MicrobialAdaptation

18 months Postdoct position in mathematical evolutionary biology in Montpellier: modelling adaptation and demography in microbes (using PDEs and stochastic processes).

Project description: A postdoctoral position (co-funded by Labex CEMEB, NUMEV and AGRO) is available at the University of Montpellier, France. The postdoctoral fellow will develop analytical models of adaptation dynamics coupled with non-equilibrium demographic dynamics ('evolutionary rescue' ER), in asexual microbial populations facing a harsh environmental challenge. These dynamics have wide applications in health and agronomy: antibiotic resistance, cancer emergence and relapse after treatment, host shifts in pathogens etc. The goal of the project is to develop a theoretical framework that accounts for a complex genetic basis of adaptation to stress, and for various scenarios of environmental change. The main activity of the postdoctoral fellow will be theory development but he/she will interact with people ranging from mathematicians to empiricists. If interested, he/she may participate to the design or analysis of experiments, ongoing in the host lab, on the probability and dynamics of antibiotic resistance emergence across doses and drug combinations in the bacterium E.coli .

Tools and skills: The postdoctoral fellow will use phenotype-fitness landscapes (Fisher's geometric model) to describe adaptation to environmental change (abrupt or not). He/she will analyze the resulting multi-type stochastic birth-death model for the demographic dynamics. The resulting dynamical system will be simplified by taking relevant statistical limits, using Partial Differential Equations (PDE) governing the joint distribution of birth and death rates in the population, over time, following a method recently developed in ( Martin and Roques 2016 , Gil et al. 2017 ).

The candidate should have experience in at least one of the three following fields: analytical modelling in population biology (ecology, evolution), PDE analysis or stochastic processes.

Research and life environment: The researcher will be working under the joint supervision of Drs. Guillaume Martin (evolutionary theory/experimental evolution), Matthieu Alfaro (analysis of PDEs) and Bertrand Cloez (stochastic processes), and in collaboration with O. Ronce (evolutionary ecology) and L. Roques (analysis of PDEs). The three host labs are within close distance of each other in the Montpellier University area. They also provide extensive computational facilities for individual-based simulations. Montpellier provides a very dynamic environment to develop multidisciplinary research in mathematics and biology. It is also an international center of ecological and evolutionary research (next ESEB-ASSE joint conference will be held in Montpellier in 2018). Additionally, it is a lively and culturally rich city on the Mediterranean coast, and has beautiful surroundings.

Salary, duration and eligibility : Net salary is approximately 2100 euro /months plus 100 euro /months supplement per year of postdoctoral experience. The duration of the postdoc is 18 months, possibly prolonged to 24 months and the contract must start no later than 1 st January 2018, and be signed no later than 25 th August 2017. The candidate must have a PhD from any structure outside the three Montpellier Labex CEMEB, NUMEV or AGRO. The candidate must have no more than six years of postdoctoral experience. For candidates with more than two years postdoctoral experience, they must have spent no more than one year in France over the past three years. One page applications with a cover letter and CV (publications may include submitted Arxiv or Bioarxiv drafts) should be sent as a single pdf-file to Guillaume Martin ( guillaume.martin@umontpellier.fr ), Matthieu Alfaro ( matthieu.alfaro@umontpellier.fr ) and Bertrand Cloez ( bertrand.cloez@inra.fr ). Review of applications will run until 24 th July 2017 and final decision will be given by 28 th July 2017.

webpages :

Guillaume Martin :

http://www.isem.univ-montp2.fr/recherche/equipes/-metapopulations/personnel/martin-guillaume/

Matthieu Alfaro :

http://ens.math.univ-montp2.fr/˜alfaro/

Bertrand Cloez:

https://sites.google.com/view/bertrandcloez

References :

- Martin, G. and L. Roques. 2016. The Nonstationary Dynamics of Fitness Distributions: Asexual Model with Epistasis and Standing Variation. Genetics 204 :1541.

- Gil, M.-E., F. Hamel, G. Martin, and L. Roques. 2017. Mathematical properties of a class of integro-differential models from population genetics. SIAM J. Appl. Math. in press .

Guillaume Martin <guillaume.martin@umontpellier.fr>

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## Montpellier PhylogeographyRainForestPlants

2-yr postdoc on "Phylogeography and evolutionary dynamics of African rain forest plants"

Research Area and Project Description: This postdoc is part of the project "Central AFrican Rain fOrests: past DYNamics and future resilience" (AFRODYN), funded by the French ANR. AFRODYN aims to understand the evolutionary dynamics of central African rain forests using a multispecies approach and an unprecedented DNA sequence dataset for African plant species. The overall objectives of AFRODYN are to 1) test different hypotheses of Central African rain forests dynamics in the past within and between species using a statistical comparative phylogeographic approach and 2) infer the potential resilience of this ecosystem to future climate change. Specifically, the post doc will be in charge of analyzing a large dataset of ˜800 exons (ca. 200 kpb) captured for over 600 individuals of six different plant species (palms and Annonaceae) sampled across central Africa. This dataset is partly already available and no lab work is required. Finally, the postdoc is expected to contribute ideas and concepts to the project and lead at least two high-quality papers in this research area, contribute to the project's public outreach, as well as collaborate with other team members, including students and sharing skills.

Qualifications and Specific Competences: Applicants must have a PhD degree in evolution, phylogenetics, tropical biodiversity or equivalent, or have submitted their PhD thesis for assessment before the application deadline. Proven experience with 1) phylogeographic (or phylogenetic) analyses and molecular dating and 2) analyses of next generation data (NGS) are required; with experience in Approximate Bayesian Computation (ABC) a strong advantage. Experience with species distribution modeling is a plus but not required. Strong skills in bioinformatics and being familiar with Linux and R languages are expected. The successful candidate is expected to have good collaborative skills, proven abilities to publish, and have good skills in English. International applicants who do not have English as their first language must prove strong English language writing skills and fluency. Finally, the post doc will be expected to present results at international conferences.

Supervisors and collaborators: Project PI Dr. Thomas L.P. Couvreur will be the main supervisor. The postdoc will join a multidisciplinary team with strong skills in population genetics, modeling, and phylogenetic reconstruction (DYNADIV) led by Dr. Yves Vigouroux.

Place of Employment and Work: The place of employment and work is “Institut de Recherche pour le Développement” (IRD), UMR DIADE, DYNADIV team, 911 Avenue Agropolis, Montpellier France. Montpellier is a pleasant Mediterranean town with a vibrant and internationally recognized research community.

Application dead-line: July 28th 2017. Starting date: October 1st 2017, but negotiable.

Application procedure: A short list of applicants will be selected by a 5-member committee shortly after the dead line for applications. An interview will be planned for short listed applicants, mainly via skype or google talk, tentatively planned for the week of the 28th of August 2017. Once the recruitment process is completed a final letter of rejection is sent to the deselected short listed applicants, including the main considerations emphasized during the selection process. The application must be in English and include a motivation letter, a 2-page max curriculum vitae (including number of citations and H-index from Google Scholar), degree certificate, full list of publications (including in press or submitted), names and email of two recommenders (no recommendation letter should be sent in the application; recommenders will potentially be contacted directly afterwards). All interested candidates are encouraged to apply, regardless of their personal background.

Contact: All questions, about the project or the employment conditions, can be directly addressed to Thomas Couvreur, thomas.couvreur (at) ird.fr

Thomas L.P. Couvreur, PhD

UMR DIADE, équipe #DYNADIV

IRD Montpellier

911 avenue d’Agropolis

BP 64501

34394 Montpellier Cedex 5

Tel: 00 33 (0)4 67 41 64 74

Follow me on twitter: @tlpcouvreur or #DYNADIV

http://couvreurlab.weebly.com/ http://annonaceae.myspecies.info/ http://palms.myspecies.info/ Associate Editor PhytoKeys and Biodiversity Data Jounal

http://www.pensoft.net/journals/phytokeys/ http://www.biodiversitydatajournal.com/ Thomas Couvreur <thomas.couvreur@ird.fr>

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## Morocco PollinatorBiodiversity

ICARDA Post Doc Fellow - Call for Applications

Location of the Research: ICARDA- Rabat, Morocco Closing date: 20 June 2017

Reports to: Prof. Pierre Rasmont (https://www.researchgate.net/profile/Pierre_Rasmont) and Prof. Denis Michez (https://www.researchgate.net/profile/Denis_Michez), IUCN Bumblebee Research Group/UMONS (science) and to ICARDA, FAP-project coordinator (administratively)

Main purpose of the position : The Post-Doctoral Scientist will be part of a project on “Conservation of pollinator diversity for enhanced climate change resilience” within ICARDA Biodiversity and Integrated Gene Management Program. This project shall integrate Farming with Alternative Pollinators (FAP) approach in the MENA-region. The position is based at ICARDA’s North Africa platform in Rabat, Morocco.

Main responsibilities * Train and co-supervise 4 PhD-students (and eventually Master-students visiting the project) together with University of Mons (Belgium) on pollinator collection, identification and habitat enhancement (incl. nesting support out of local materials) * Guide the PhD-students concerning analysis and description or habitat requirements of some important crop pollinator species * Supervise regular collection, preparation and identification of pollinator specimens in FAP and control fields in Morocco * Supervise the measure of pollinators abundance and impact of nesting support * Contribute to the national assessment on regions with pollinator deficits, analysis of reasons and recommendations for respective regions * Contribute to trainings of local actors and development of FAP-manuals for 4 agro-ecosystems * Contribute to the inventory of crop pollinators of North Africa * Co-lead the publications of research findings in ISI-peer reviewed scientific journals with high Impact Factors, together with the scientific team (ICARDA, University of Mons, INRA) * Manage the new pinned collection of pollinators and reference collection * Collaborate with the ICARDA/INRA-entomologist working on predators and pests * Perform any other duties as required by Head Genetic Resources, BIGM program Director and ICARDA management * Willingness to travel to remote areas within Morocco

Education, qualifications and experience PhD in agricultural sciences with a focus on pollinator taxonomy or pollination ecology * Ability to work efficiently in a highly interdisciplinary team * Ability to train and guide students * Ability to collaborate with a broad range of farmers, including illiterate farmers * Excellent interpersonal skills to work effectively in a multidisciplinary and multi-cultural work environment * Demonstrated ability to plan, conduct and interpret research results through publications in ISI peer-reviewed scientific journals * Excellent written and oral communication skills in English * Knowledge of French * Knowledge of data management and statistical analysis with popular computer software * National driving license. * Desirable : Working experience in North Africa

Terms of appointment, salary and benefits

This is an is an internationally recruited position for which ICARDA offers an attractive compensation package including a competitive salary, housing allowance, medical insurance and leave provisions. All benefits are denominated and paid in US Dollars. The successful candidate will be appointed on an initial contract of two years. Confirmation of the contract is subject to a probationary period of one year. Subsequent employment is determined based on the performance, continued need for the position and availability of funds.

How to apply Please apply online at www.icarda.org/iea/ by 20 June 2017

About ICARDA The International Center for Agricultural Research in the Dry Areas (ICARDA) is an international autonomous, non-profit, research organization supported by the Consultative Group on International Agricultural Research (CGIAR). ICARDA mission is to reduce poverty, enhance food, water and nutritional security, as well as environmental health in the face of global challenges including climate change. We do this through innovative science, strategic partnerships, linking research to development and capacity development that take into account gender equality and the role of youth in transforming the dry areas. ICARDA works in partnership with governments, universities, civil society, national agricultural research organization, other CGIAR research Centers, and the private sector. With its temporary Headquarters in Beirut, Lebanon, ICARDA operates in regional and country offices across Africa, Asia and the Middle East. For more details: www.icarda.org

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## Munich OriginEukaryoticSex

The Parmenides Foundation offers a stipend up to 3000 EUR per month up to 3 years for theoretical investigations into the dynamics of the origin of eukaryotic sex. Candidates are expected to have demonstrated excellence in population genetics and statistical physics. Send CV and publication list to Carsten Freitaeger, email carsten.freitaeger@parmenides-foundation.org by the 29th of June.

Thank you! Carsten

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

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

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## Nantes France HumanPopulationGenetics

Population Genetics in French population

Position :Post-doctoral Position, Type of employment : Fixed term contract, Duration 12 months renewable, Work Place l'institut du thorax, Nantes, France, To begin January 2018 (to be discussed), Our Reference RR/IR/20

Project Context

L'institut du thorax is a structure at the forefront of translational research against cardiac, vascular, metabolic and respiratory diseases. In the context of our research program on genetic of rare genetic variants and their effect on disease, we develop project large projects on population genetics. ; l'institut du thorax has a successful track record on genetics of cardiovascular diseases [1] [2] and, more recently, in population genetics [3]. ; The goal of the project is to study genetic structure and demographic history of a French population using cutting edge statistical methods.

The post-doctoral fellow will join the FROGH (French Regional Origin Genetics for Health) project and will analyze whole genome sequences and SNP chips of hundreds of individuals. Analysis of complete genomes should unravel the demographic and adaptive processes that have shaped the genome of a French population. The proposed strategies span from descriptive analyses of genetic structure to sophisticated strategies, which involve simulation of population of genomes under various demographic models.

The data has been generated in the FranceGenRef project (Investissement d'Avenir), which aim is to set up a reference panel for genetic studies in the French population. The successful candidate will therefore work in collaboration with a large panel of members of both the FranceGenRef Consortium and members of the ANR in a highly collaborative context.

This work will be carried out under the joint supervision of Dr. Christian Dina, geneticist at l' institut du thorax in Nantes and Dr. Michael Blum, statistician at the lab TIMC-IMAG in Grenoble. The postdoctoral fellow will mainly work at l'institut du Thorax, in Nantes. He/She will join the research team "Cardiovascular Genetics" led by Dr. JJ Schott, which includes geneticists, bioinformaticians and biostatisticians. The team is composed of 28 members, of which 5 are working in biostatistics and bioinformatics. This team is also working in close collaboration with the bioinformatics core (GenoBiRD).

Qualifications, Knowledge and Experience:

Essential:

PhD in Population Genetics or a related field.

Experience in bioinformatics, genomics and statistical genetics

Competency in programming.

Evidence of research productivity: publication, international conference presentations.

Desirable:

Experience of Linux, scripting and use of a High Performance Computing Linux cluster.

Skills, Abilities and Competencies:

- Strong computational skills, including statistical programming (ideally R) and a programming language such as Python, Perl or C++.

- High level of proficiency in English, sufficient to undertake research and teaching to communicate effectively with staff and students.

- Ability to work independently and also as part of a research team.

- Excellent written and oral communication skills.

Contract:

A full-time position for 2 years (12 months renewable). Salary will be similar to postdoc positions offered by the INSERM (Institut National de la Sante et de la Recherche Medicale). Starting date January 2018 but alternative dates can be discussed.

Application:

Candidates are asked to supply a CV and a covering letter to support the application. Contact details for referees would be a strong asset. Applications should be sent to christian.dina@univ-nantes.fr. Review applications will begin on August 15^th, 2017 and continue until the position is filled. Applications received by August 1^st will be given priority consideration.

Application

Applications should include a letter of interest, a complete CV (including publication list), and email addresses of three academic references. The application should be submitted to chrisitian.dina@univ-nantes.fr before August 15^th 2017.

1 Bezzina, C.R. et al. (2013) Common variants at SCN5A-SCN10A and HEY2 are associated with Brugada syndrome, a rare disease with high risk of sudden cardiac death. Nat. Genet. 45, 1044-1049

2 Dina, C. et al. (2015) Genetic association analyses highlight biological pathways underlying mitral valve prolapse. Nat. Genet. 47, 1206-1211

3 Karakachoff, M. et al. (2014) Fine-scale human genetic structure in Western France. Eur. J. Hum. Genet. DOI: 10.1038/ejhg.2014.175

Christian Dina I.R. CNRS Epidemiologie Genetique - Genetic Epidemiology l'institut du thorax Unite Inserm UMR 1087 / CNRS UMR 6291 IRT-UN, 8 Quai Moncousu BP 70721 44007 Nantes cedex 1

Tel: +33 (0)2.28.08.01.54 Fax: +33 (0)2 28 08 01 30 http://www.umr1087.univ-nantes.fr/ E-Mail : Christian.Dina@univ-nantes.fr

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## OhioStateU PopulationGenetics

We seek an interdisciplinary post-doctoral research associate experienced in population and/or landscape genomics and genetics of adaptation using modern sequencing and bioinformatic approaches. This position will primarily research the population and landscape genomics and demographics of the Antarctic midge, Belgica antarctica. The post-doctoral research associate will design and implement a genomics strategy to understand the linkage between physiological adaptation and genomic diversity from populations dispersed among different isolated Antarctic islands. The research associate will also be expected to lend expertise and training for other research projects including sequence analysis and divergent selection among soybean pathogen strains and adaptation in the soybean aphid. Demonstrated experience in population or landscape genomic analysis as well as competency in a computer programming language (e.g. R, python, linux) is required. Please see https://www.jobsatosu.com/postings/79317. This position is for 1 year, with an option for multiple years, and is based in Wooster, OH at the Ohio Agricultural Research Development Center.

Please send a C.V. (including contact information for 3 references) and a 1 page statement of interest to Dr. Andy Michel (michel.70@osu.edu), Dr. David Denlinger (denlinger.1@osu.edu) and Dr. Anne Dorrance (dorrance.1@osu.edu). Review of applications begins June 26, with an expected starting date of late summer or autumn 2017.

“Michel, Andrew” <michel.70@osu.edu>

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## Omaha 2 NGS Conservation

SUMMARY

Omaha’s Henry Doorly Zoo & Aquarium Department of Conservation Genetics based in Omaha, Nebraska, is seeking two post-doctoral researchers with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

RESPONSIBILITIES AND DUTIES include the following. Other duties may be assigned.

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows.

The researchers will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar.

Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. Data on a variety from a variety of species has already been generated, thus candidates will be able to quickly start analysis and manuscript preparation.

Travel to Madagascar to support the field programs of Omaha Zoo and the Madagascar Biodiversity Partnership is required for a minimum of five week intervals twice a year.

WORKSKILLS: Strong people skills, detailed oriented, willingness to learn and contribute, follow directions, meets deadlines

Basic Qualifications:

Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group’s focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidates will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds, and have outstanding written and verbal communication skills. The successful applicants must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicants will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Madagascar the researchers will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires candidates with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. Candidates must also be able to jump between a variety of projects, based on needs of the research group.

Time Frame

These positions will be part of an on-going team of rotating postdoc fellows. One of the positions is expected to begin as soon as possible, while the second is expected to start in January 2018. Initial appointment will be for two years, with possibility to extend to three years.

Application

Please submit your CV with the contact information for 3 professional references, a letter describing your interests and goals, and copies of a few publications. Please apply at: http://www.omahazoo.com/careers/ Learn more at: https://madagascarpartnership.org/ Must be legally entitled to work in the USA. Visa sponsorship is not available.

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From: Genetics Department Sent: Monday, June 19, 2017 3:18:21 PM To: Golding@McMaster.CA Subject: EvolDir -for announcement section

Job Title: Postdoctoral Fellow - Madagascar Biodiversity Genomics

Date Position Opens: June 19, 2017

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## Omaha Nebraska MadagascarFauna

Job Title: Postdoctoral Fellow - Madagascar Biodiversity Genomics

Date Position Opens: June 19, 2017

Date Position Closes: July 17, 2017

FLSA Status: Non-exempt

Hours: Full-time

SUMMARY

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics (OHDZA-CG) based in Omaha, Nebraska, is seeking a post-doctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

RESPONSIBILITIES AND DUTIES include the following. Other duties may be assigned.

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows.

This individual will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar.

Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts.

Travel to Madagascar to support the field programs of OHDZA-CG is required for a minimum of five week intervals twice a year.

WORKSKILLS: Strong people skills, Detailed oriented, willingness to learn and contribute, follow directions, meets deadlines

Basic Qualifications

Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds with outstanding written and verbal communication skills. The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicant will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Madagascar the applicant will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires a candidate with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. The candidate must also be able to jump between a variety of projects, based on needs of the research group.

Must be legally entitled to work in the USA. Visa sponsorship is not available.

Application:

Applicants should send curriculum vitae, a statement of research interests and career goals, a few publications. Please apply at: https://workforcenow.adp.com/jobs/apply/posting.html?client=omahazoo Genetics Department <genetics@omahazoo.com>

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## RiceU PhylogenomicsMethodology

Postdoctoral Position in Phylogenomics Methodology Development

A postdoctoral position is available in Luay Nakhleh's group in the Computer Science Department at Rice University.

The successful candidate will lead efforts to develop new models and methods for phylogenomic analyses (inference of gene and genome evolutionary histories while accounting for processes such as incomplete lineage sorting, gene duplication and loss, and reticulation). The candidate is expected to work closely with the PI and with graduate students in the group. The candidate will be given much flexibility in the research direction as long as the work is related to phylogenomics and, preferably, the continued development of the PhyloNet software package (http://bioinfocs.rice.edu/phylonet).

A PhD in Computer Science, Statistics, Genetics, Bioinformatics, or a similar discipline is required. Programming and analytical skills are essential, and so are communication skills. Knowledge of phylogenetics and/or population genetics methodologies (e.g., phylogenetic inference, the coalescent, etc.) are also required. Recognizing that a great majority of the commonly used phylogenetic software tools were written by biologists, interested biologists with very good programming and analytical skills are highly encouraged to apply.

Interested applicants should email a CV and cover letter outlining qualifications to Luay Nakhleh (nakhleh@rice.edu).

Luay Nakhleh <nakhleh@rice.edu>

## SpelmanC Atlanta MicrobialEvolution

Postdoc Position in: Microbial Evolution, Behavior and Genomics

Location: Atlanta, Georgia, USA

Funding Source: CURE Postdoctoral Fellowships [Spelman College is piloting a postdoctoral fellowship program that combines a traditional principal-investigator directed postdoctoral research experiences with mentored teaching experiences.]

A postdoc position (upto 2 years) is available to conduct experimental and computational research on small eukaryotic amoeboid microbes relating to their evolution and sexual life cycle behavior. Candidates should have an inter-disciplinary training or familiarity with molecular (e.g. next generation sequencing) and computational (bioinformatics, phylogenetics) skills.

Potential research topics include (i) genomics and evolution of phenotypic traits in cryptic species, (ii) evolution of sexual-like behavior and development in amoeboids, (iii). origin, evolution and biodiversity of amoeboids using large-scale analysis. (iv). evolution of amoeboid movement and cytoskeleton architecture. Additional projects under similar topics can be also considered based on individual experience and interest. For additional information contact: ytekle@spelman.edu

This position offers competitive salary and benefit. Candidates should complete Ph.D. training before starting this position. This position is open to US citizens and lawful permanent residents only. Screening of applicants will begin immediately and continue until the position is filled.

Spelman College is a private four-year liberal arts college located in Atlanta, GA, and ranked one of the top 100 liberal arts colleges by the US News.

Please email a copy of curriculum vitae, a short statement of research interest, names and contact information of at least three individuals familiar with your research to Dr. Yonas Tekle through ytekle@spelman.edu

350 Spelman Ln SW, Box 1183,

Department of Biology, Spelman College, Atlanta, GA 30314-4399

LOCATIONS

Yonas Isaak Tekle <yonastekle@gmail.com>

## SyracuseU MolEvolSexualSelection

Description: A postdoctoral position is available in the laboratories of Drs. Steve Dorus and Scott Pitnick in the Center for Reproductive Evolution (cre.syr.edu) at Syracuse University. The broad goal of this NSF-funded, collaborative research project (with Dr. Mariana Wolfner, Cornell University) is to determine how molecular interactions between sperm and the female reproductive tract evolve across closely related species and their contribution to reproductive isolation. Sperm undergo numerous modifications as they move through the male and female reproductive tracts, although the nature of these interactions and their importance for fertilization success is not well understood. This project will characterize these changes at the molecular level, within closely-related species of fruit fly, as well as following hybrid inseminations, to understand their evolutionary history and influence on sperm survival and fertilization success.

Qualifications: PhD in Genetics, Genomics, Evolution or a related field is required, and the candidate should have a demonstrated history of research excellence. Preference will be given to candidates with a strong background in molecular evolution, genomics and/or proteomics of reproductive systems. Experience conducting research with Drosophila or other insects would be beneficial, but is not required.

Details: The start date for this position is flexible but could be as early as 9/1/17. Funding is available for up to three years (conditional on satisfactory performance). All enquiries should be sent to Steve Dorus (sdorus@syr.edu) and Scott Pitnick (sspitnic@syr.edu).

Applications: Interested individuals should submit a cover letter, CV, a short statement of research interests, and the contact information of 3 or 4 references to https://www.sujobopps.com/postings/70054. Priority consideration will be given to applications received by July 31st, 2017.

Center for Reproductive Evolution: The CRE is a highly collaborative, multi-laboratory collective dedicated to advancing our understanding of reproductive trait evolution. Occupying a shared suite of laboratories within SU's Life Sciences Complex, CRE researchers work together on diverse taxa using highly integrative approaches to explore molecular, physiological, morphological and behavioral mechanisms of male-female interactions to understand adaptive processes underlying the origin and maintenance of biodiversity.

Steve Dorus Scott Pitnick

Center for Reproductive Evolution Syracuse University 107 College Place Syracuse, NY 13244 CRE website: http://cre.syr.edu sdorus@syr.edu

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## Toulouse France ChemicalMicrobialEvolution

1-year postdoc "The role of bacteria in the production of social scent in birds"

Animal bodies house trillions of bacteria, which can influence host behavior in ways that have far-reaching implications for host ecology and evolution. Recent studies have revealed surprising roles for bacteria in shaping behaviors across many animal taxa. But questions remain and recent perspective papers have thus emphasized the need of studying the interaction between non-pathogenic bacteria and host behavior. In particular, bacteria can influence host behavior indirectly by affecting chemical cues that animals use to communicate. The fermentation hypothesis for animal olfactory signaling posits that bacteria metabolize glandular secretions and produce volatile, organic compounds, that are used in communication by the host. However, despite the potential importance of microbes in the olfactory communication of their host, very few studies have focused on the microbiota of animal scent integuments.

The main objective of the project is to inquire whether bacteria in scent integument may be responsible for the production of social odors in birds. However, the research objective is not set and may depend on the research interests of the successful candidate. Among others, it may involve i) testing the covariation between olfactory cues and bacterial communities in scent integuments, ii) combining chemical analyses with in-vitro cultures of the specific bacterial strains found in the scent integuments to determine to what extent bacteria produce the compounds used by birds to communicate with their conspecifics, or iii) testing the role of immune genes (known to affect bird odor) on bird microbiota.

A sound knowledge of chemical ecology and associated techniques (GC-MS) is essential. Previous experience in bacterial culture is not a pre-requisite, but some experience in laboratory work (DNA extraction, PCR, etc.) is particularly desirable. Some experience with next-generation sequencing data would be an asset.

This 1-year position is expected to start in September 2017. It will be based in Toulouse at "Laboratoire Evolution & Diversité Biologique" (CNRS). http://www.edb.ups-tlse.fr/ To apply, please send CV and statement of interest to Sarah Leclaire (sarah.leclaire@univ-tlse3.fr).

Sarah Leclaire <sarah.leclaire@univ-tlse3.fr>

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## UCaliforniaLosAngeles EvolutionAntibioticResistance

A two-year post-doctoral position is available (start date flexible, can start as early as July, 2017) in the labs of Dr. Pamela Yeh and Dr. Van Savage in the Department of Ecology and Evolutionary Biology at UCLA. Yeh works on evolution of antibiotic resistance and development of novel strategies to combat multi-drug resistant pathogens. Savage combines mathematical models with analysis of large datasets to uncover insights into biological systems. The overall goal is to better understand, both empirically and theoretically, higher-order interactions in biological systems and/or experimental evolution of antibiotic resistance. In this context, higher-order interactions means beyond pairwise interactions that involve three or more objects. The project has the potential to involve experiments, theory development, numerical simulations, and data analysis. Yeh and Savage will both mentor the postdoc in designing and conducting research projects, writing papers, giving talks, and applying for jobs.

UCLA is a major research university with the Faculty of Arts and Sciences, Medical School, and Engineering School all on the same campus, allowing access to myriad researchers and resources that could be useful to this project. UCLA is consistently in the top 5 in terms of federal research funding awarded to universities. Los Angeles is a vibrant, diverse city with outdoor activities available nearby, including beaches and mountains. L.A. also has a wide array of arts and culture, including world-class museums, theater, music, and of course, movies.

Candidates are expected to be independent, highly motivated problem solvers who communicate well and enjoy working in a collaborative environment. The ideal candidate would have a background in evolution, microbiology, or mathematical modeling. Experience with programming languages such as Matlab, R, Mathematica, C, and

Python would be helpful. Applicants with only a subset of these skills are encouraged to apply. Applications and any questions should be sent to pamelayeh@ucla.edu. The application should include a Curriculum Vitae that details education, past research, and publications. Applicants should also submit a cover letter that describes their interest in the project and the names of three references. Review of applications will begin immediately and continue until the position is filled.

UCLA is an AA/EOE that is strongly committed to diversity and excellence among its researchers.

Pamela Yeh <pamelajeanyeh@gmail.com>

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## UCalifornia SantaCruz AvianAdaptation

*Postdoctoral Position: Conservation Genomics*

The Bird Genoscape Project is seeking a *Postdoctoral Fellow in Conservation Genomics*. The successful candidate will use genomic methods to identify patterns of migratory connectivity and explore the impact of climate change on several species of North American migratory birds. We seek a creative and highly motivated individual to work closely with our multi-disciplinary team of technical staff, graduate students, senior researchers, post-docs and faculty on the development and implementation of bioinformatics pipelines for the analysis of genome-wide sequencing data. In addition, the candidate may have the opportunity to lead/assist in field work in North America and the tropics, as need and funding necessitates.

Required qualifications:

§Ph.D. by the time of start date in evolutionary biology, genomics, population genetics, integrative biology or some equivalent.

§Excellent communication (verbal and written) and organizational skills.

§Strong expertise in genomics and its applications to evolutionary and conservation questions.

§Experience generating, analyzing, and/or integrating large datasets - whole genome sequencing, RAD sequencing, or transcriptome sequencing.

Preferred qualifications:

§Experience leading and conducting avian research, including mist-netting, banding and taking genetic samples.

§Strong quantitative, statistical, and computational skills. Fluency in Python or Perl, and R.

§Spanish language speaking skills

The successful candidate will work under the Bird Genoscape Co-Directors, Drs. Kristen Ruegg and Thomas B. Smith, and can be based at either the Center for Tropical Research at the University of California, Los Angeles, the University of California, Santa Cruz, or, in some circumstances, remotely. More information about the Bird Genoscape Project can be found here: http://-www.birdgenoscape.org/ The initial appointment will be for one year, with the possibility of extension for an additional year, contingent on performance and funding. The salary will be commensurate with experience. Preferred start date is September 2017.

*To apply:* E-mail a single PDF including a cover letter, a CV, and the names and contact information of three references to Dr. Kristen Ruegg ( kruegg@ucsc.edu), with the subject line as "Postdoctoral application <your name>". Review of applications will begin July 15 and continue until a suitable candidate is identified. Informal inquiries prior to application are welcome.

kruegg@ucsc.edu

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## UColoradoDenver AdaptationGenomics

The Ragland lab at the University of Colorado, Denver is searching for a postdoctoral fellow to conduct research on the genomic architecture of adaptive, complex phenotypes, and on the evolution of gene regulatory networks. This is a flexible position that will contribute to ongoing, NSF-funded research on 1) seasonal adaptation in the Rhagoletis pomonella species complex and associated parasitoid communities, a model for ecological and cascading speciation via seasonal isolation, 2) the role of developmental pleiotropy and regulatory network structure in constraining thermal adaptation in Drosophilid species, and 3) leveraging genetic markers to predict phenology and voltinism in forest pest species. For more information see https://raglandlab.wordpress.com . In addition to current research priorities, the selected candidate will have ample opportunity to develop new studies and research directions in these and possibly other systems. Many projects in the lab are collaborative, and there will be opportunities to interact with collaborators at the University of Notre Dame, University of Florida, and BOKU Vienna.

In general, I would like to recruit an enthusiastic postdoc who can interface well with other lab members with diverse interests in ecology, evolution, physiology, and genetics, and who will be willing to tap into resources on both of our downtown and medical campuses. More specifically, the successful candidate will have a Ph.D in Biology, Computer Science, or a closely related field with a strong background in evolutionary biology or comparative physiology. A background in the application of statistical models (e.g., glm, mixed models, multivariate analysis) is required, as is experience with Linux command line environments and scripting languages (R, python, perl). Wet lab experience with nucleic acids and the preparation of Next Generation sequencing libraries is preferred. Candidates should also demonstrate evidence of successful communication of results through published manuscripts, conference presentations, or related activities.

The University of Colorado, Denver, hosts a vibrant community of life science researchers on both the downtown Auraria campus and the Anschutz medical campus, including an active postdoctoral association (http://www.ucdenver.edu/faculty-staff/postdoctoral/-ucdpostdoctoralassociation/Pages/default.aspx). The Department of Integrative Biology spans cell, molecular, ecological, and evolutionary research, with strengths in ecological physiology, molecular genetics, and developmental biology. Denver is a fantastic and progressive city with endless possibilities for outdoor activities, well-developed public transportation and cycling infrastructure, and excellent museums, theaters, restaurants, and breweries.

Please submit a cover letter including research interests and addressing the desired qualifications, curriculum vitae, and contact information, including e-mail addresses of at least three references by email to Greg Ragland (gregory.ragland@ucdenver.edu). Screening of applications begins July 1, 2017 and will continue until a suitable candidate is found.

“Ragland, Gregory” <GREGORY.RAGLAND@UCDENVER.EDU>

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## UConnecticut GenesInHaloarchaealPopulations

Postdoctoral fellowship to study rare alleles and genes in haloarchaeal populations. University of Connecticut, Storrs, Connecticut, USA. Mentor: J. Peter Gogarten, Co-mentor: Thane Papke;

Collaborators: Lilach Hadany, Uri Gophna.

The hired postdoctoral fellow will engage in an international and interdisciplinary project to explore the origin, persistence and function of rare genes and alleles in haloarchaeal populations and communities. The project addresses the following questions: How do those archaeal lineages diverge and adapt to new environments? What is the role of rare genes in the adaptation process? Genes of interest include self-splicing selfish genetic elements, restriction modification and CRISPR/Cas systems, and genes encoding weakly selected and niche adapting functions.

The fellow's research will (i) identify genes having limited distribution in populations from two different model genera, Haloferax and Halorubrum, using genome and meta-genome sequence data, (ii) characterize these genes through bioinformatics based approaches, to discover the evolutionary forces leading to allelic persistence and/or coexistence in populations and communities and (iii) select suitable candidates for genetic experimentation. The fellow will also have the opportunity to collaborate on other aspects of this project such as genetic engineering, growth experiments, and modeling of population dynamics.

The project is led by Dr. Johann Peter Gogarten, collaborators include Drs. Lilach Hadany (Tel Aviv University), Thane Papke (University of Connecticut), and Uri Gophna (Tel Aviv University). The fellow will work at the University of Connecticut in Storrs.

Candidates must have a PhD degree in relevant fields, such as evolution, bioinformatics and microbiology. Excellent written and verbal communication skills, the ability to work harmoniously in a collaborative research team, experience in genome assembly, comparative genomics, R, and scripting languages such as Perl or Python are required.

Applicants should send their CV, a letter of intent describing candidate's motivation, qualifications, skills, and experience relevant to this position, and contact information for three references to gogarten@uconn.edu.

The University of Connecticut is an EEO/AA employer.

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J. Peter Gogarten Board of Trustees Distinguished Professor Department of Molecular and Cell Biology & Institute for Systems Genomics 91 North Eagleville Road, Unit 3125, BPB 404 Storrs CT 06269-3125, USA

Phone: 860 486 4061 (office) 860 486 1887 (lab) 860 465 6267 (cell) FAX: 860 486 4331 Email: gogarten@uconn.edu www: http://gogarten.uconn.edu/ JohannPeter Gogarten <gogarten@uconn.edu>

## UExeter 2 CulturalEvolution

Two 3-year post-doctoral positions on the Cultural Evolution and Ecology of Institutions

Applications are invited for two 3-year post-doctoral positions to work with Dr. Thomas Currie at the Human Biological and Cultural Evolution group, Centre for Ecology & Conservation, Department of Biosciences at the Penryn Campus of the University of Exeter on his ERC-funded project, The Cultural Evolution and Ecology of Institutions.

One position will focus on mathematical models and computer simulation of the evolution of institutions and cooperation in humans, and is suitable for candidates with a background in modelling social evolution and/or evolutionary ecology. The other position will focus on the creation of datasets and statistical analysis in order to test these models, and may be suitable for those with experience of phylogenetic methods, comparative methods, and/or epidemiological models of disease transmission (particularly if they have experience working with datasets relating to human cultural diversity). Details of these positions and online application system can be found at the following links:

1) Modelling: https://tinyurl.com/yd9fdvpl 2) Data/Analysis: https://tinyurl.com/y8ncylm8 Starting date for these positions is ideally September 1^st 2017. However, a later start date may be agreed for suitable candidates.

Closing date for applications: 19^th June 2017.

Applicants are encouraged to contact Tom Currie (T.Currie@exeter.ac.uk) ahead of applications to discuss the positions.

Dr. Thomas Currie Senior Lecturer in Cultural Evolution Program Director, BA/BSc Human Sciences Centre for Ecology & Conservation College of Life & Environmental Sciences University of Exeter Penryn Campus, Cornwall TR10 9FE Website http://biosciences.exeter.ac.uk/-staff/index.php?web_id=Thomas_Currie Human Sciences degree http://www.exeter.ac.uk/undergraduate/-degrees/humansciences/humansciences/ Human Biological and Cultural Evolution Group (HuBCEG) http:/-/biosciences.exeter.ac.uk/research/groups/humanbio/ "Currie, Thomas" <T.Currie@exeter.ac.uk>

## UIdaho PopulationGenomics

An NSF-funded postdoctoral position is available in population genomics and statistical genomics at the University of Idaho.

The research program combines experimental laboratory evolution of brewer's yeast with next-generation sequencing to understand how genome-wide patterns of variation respond to controlled, replicated evolutionary conditions. We are particularly interested in the roles of standing genetic variation, divergent selection with migration, and recombination on patterns of neutral genetic variation in the chromosomal neighborhood around loci under selection. The experimental genomic data will be used to develop and validate novel analytical tools, based on Approximate Bayesian Computation (ABC), for population genomics in natural systems. The postdoc researcher will also have opportunity to apply analytical approaches to data from other empirical systems, including some with conservation applications (Tasmanian devils, threespine stickleback, and others).

We seek a highly motivated, independent researcher with a Ph.D. in biology, microbiology, evolutionary genetics, bioinformatics, statistics, or a related field. Experience in working with yeast or other laboratory microorganisms, genomic sequencing and bioinformatic analysis, and/or statistical methods is required. The postdoc will work closely with other members of the lab group on the different components of this project, and will also have the opportunity to conduct outreach and instruction in the analytical tools at workshops and short courses in population genomics.

The postdoc will join the Institute for Bioinformatics and Evolutionary Studies (IBEST), a vibrant interdisciplinary group of faculty and researchers. Mentors on this project are Dr. Paul Hohenlohe (Depts of Biological Sciences and Statistical Science), who specializes in evolutionary population genomics in a wide array of organisms, and Dr. Erkan Buzbas (Dept of Statistical Science), who specializes in statistical genomics.

The position is expected to begin as soon as possible. Initial appointment will be for one year, with possibility to extend to three years. Please submit a C.V. with contact information for 3 references, and a letter describing your interests and goals. For full consideration, please submit materials by August 1, 2017.

For further information please contact Paul Hohenlohe: hohenlohe@uidaho.edu

Hohenlohe website: http://hohenlohelab.github.io/- Buzbas website: https://www.uidaho.edu/sci/stat/-people/faculty/erkanb "Hohenlohe, Paul (hohenlohe@uidaho.edu)" <hohenlohe@uidaho.edu>

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## ULeeds GenomicsSenescence SeychellesWarbler

3-year Post-doctoral Research Fellow in Genomics of Senescence in the Seychelles warbler

Are you an ambitious researcher looking for your next challenge? Do you have an established background in evolutionary genomics, quantitative genetics or a related relevant discipline?

As individuals reach older ages their bodies deteriorate - a process known as senescence. It is clear that individuals differ greatly in the age at which they start to senesce, and how quickly they then deteriorate. However, why individuals senesce so differently remains unresolved. Understanding this question is fundamentally important from an evolutionary perspective. It also has massive ramifications for human health, animal husbandry and conservation, as reducing exposure to factors that negatively impact senescence would enable individuals to live longer healthier lives

You will work on the Natural Environment Research Council funded project 'The genomics of senescence in the Seychelles warbler' which is led by Dr Hannah Dugdale (Leeds) and Professor David Richardson (East Anglia), in collaboration with Professor Terry Burke (Sheffield) and Professor Jan Komdeur (Groningen). The project uses the outstanding Seychelles warbler dataset, a major model system in the study of evolution, cooperative breeding and senescence. Crucially, this study focuses on an isolated island population, which has allowed us to follow all individuals (over many generations) throughout their lives, collect blood samples (thus allowing individual genetic characteristics and intrinsic biomarkers to be measured) and measure concurrent environmental conditions, social experiences and individual characteristics.

You will oversee the collation of genomic data and the quantitative genetic analysis of senescence. You will quantify the overall relative impact of environmental, social, transgenerational and genetic factors, across the genome, on when and how quickly individuals deteriorate with age. There will be an opportunity to get involved in the other components of the wider Seychelles warbler project, including fieldwork.

You will have a PhD in evolutionary genomics, quantitative genetics or a closely allied discipline along with experience in generating and analysing data using bioinformatics, quantitative genetics and statistical skills in R.

Interviews are expected to take place between 18 July and 20 July 2017.

To explore the post further or for any queries you may have, please contact:

Hannah Dugdale, Lecturer in Conservation Biology

Tel: +44 (0)113 343 5598, email: h.dugdale@leeds.ac.uk

Location: University of Leeds - Main Campus Faculty/Service: Faculty of Biological Sciences School/Institute: School of Biology Category: Research Grade: Grade 7 Salary: 32,004 to 38,183 p.a. Due to funding limitations an appointment cannot be made above 32,004 p.a. Working Time: 100% Post Type: Full Time Contract Type: Fixed Term (for 3 years due to funding. Latest start date 1 September 2017) Closing Date: Monday 10 July 2017 Interview Date: Wednesday 19 July 2017 Reference: FBSBY1069 Downloads: Candidate Brief < https://jobs.leeds.ac.uk/Upload/vacancies/files/8501/-FBSBY1069%20RF%20in%20Genomics%20of%20senescence%20in%20t >

View the job details and apply online at the following link: http://jobs.leeds.ac.uk/FBSBY1069 Hannah Dugdale <H.Dugdale@leeds.ac.uk>

## UMaryland QuantitativeGenetics

We are seeking a postdoctoral fellow to join our research group as part of our U01 grant "NHLBI TOPMed Program: Integrative Omics Approaches for Analysis of TOPMed Data". We will develop novel statistical methods and cutting edge software tools for quantitive genetics analysis of large scale whole-genome sequence (currently at 60K high coverage whole genomes), methylation, metabolomics, proteomics, and transcriptome data sets. The research project team is led by Dr. Jeff O'Connell and includes Drs. Tim O'Connor, May Montasser, and James Perry with broad expertise in statistical, computational and evolutionary genetics, genetic epidemiology, and bioinformatics.

Our research team are active members of TOPMed Working Groups through the Phase I Old Order Amish Study, which provides the postdoctoral fellow unique opportunities for study of the genetic architecture of a founder population in addition to large data analysis across diverse studies.

The ideal candidate will have a PhD with strong background in statistics, statistical genetics, computational methods, bioinformatics, C/C++/Java programming and text/data processing skills and familiarity with genetic analysis software tools. The candidate will be responsible for leading independent projects that include evaluation of new statistical methods and software tools through simulation and TOPMed data, interfacing with TOPMed Working groups to deploy new tools, and writing papers.

Additional information on the university, our programs and TOPMed visit: University of Maryland School of Medicine http://www.umaryland.edu/ Program in Personalized and Genomic Medicine http://www.medschool.umaryland.edu/genetics/ Division of Endocrinology, Diabetes and Nutrition http://-www.medschool.umaryland.edu/endocrinology/ NHLBI TOPMed Program https://www.nhlbiwgs.org/ To apply please send CV and cover letter to Jeff O'Connell at joconnel@som.umaryland.edu. The position is open until filled.

Timothy D. O'Connor, PhD Assistant Professor Institute for Genome Sciences and the Department of Medicine University of Maryland School of Medicine Biopark II, Room 653 801 W. Baltimore Street Baltimore, MD 21201 Google Voice: 443-681-9995 Office: 410-706-6784 http://www.medschool.umaryland.edu/-profiles/OConnor-Timothy/ Timothy O'Connor <timothydoconnor@gmail.com>

## UMelbourne StatisticalGenomics

Post-doc - Statistical Genomics (2 positions) University of Melbourne

Position Title: Research Fellow Statistical Genomics Employer: University of Melbourne Location: Main (Parkville) Campus, Melbourne, Australia Classification: Research Fellow Level B Salary: AUD $98,775 - $117,290 per annum plus 9.5% superannuation Work Type: Full time Duration: Fixed term, 3 years Closing Date: 5pm (Melbourne time) Wednesday 14 June 2017

I am currently recruiting two senior post-doctoral research fellows in statistical genomics.

*** Please note that excellent candidates with a strong statistical background from any quantitative scientific discipline (e.g. physics, engineering, etc) are encouraged to apply. ***

For further details please see below, and/or:

http://jobs.unimelb.edu.au/caw/en/job/890905/-research-fellow-statistical-genomics-2-positions Best wishes,

Stephen

– A/Prof. Stephen Leslie Associate Professor of Statistical Genomics Centre for Systems Genomics Schools of Mathematics and Statistics, and BioSciences, The University of Melbourne Honorary Fellow, Murdoch Childrens Research Institute A: Building 184, Royal Parade, University of Melbourne, Parkville 3010, Victoria, Australia T: +61 3 8344 0441 | M: +61 407 264 734 E: stephen.leslie@unimelb.edu.au | W: http://-sysgen.unimelb.edu.au/ —–

Applications are invited for two post-doctoral researchers to join the Statistical Genomics Group in the Centre for Systems Genomics, University of Melbourne, headed by Associate Professor Stephen Leslie. The group's work focuses on methodological developments for the analysis of high throughput genetic data and the application of these methods to studies of disease and natural population variation. These methods typically combine modern computationally-intensive statistical approaches with insights from population genetics models. Specifically the group works on statistical methods for imputing immune system (and other) genes from incomplete genetic data; the application of these methods to studies of autoimmune and other diseases; methods for detecting and controlling for population stratification; and understanding the causes and consequences of genetic variation in populations. The group has strong established collaborations with the Donnelly and McVean groups at the Wellcome Trust Centre for Human Genetics in Oxford.

The positions involve working on problems at the cutting edge of human genetics, and represent an exciting opportunity for a statistical geneticist, or someone with a strong statistical background and skills wishing to move into this field. The successful applicants will focus on developing methods to type HLA, KIR and other immune system related loci from genomic data. They will further apply these methods to studies of auto-immune and other disease, with a particular focus on psoriasis. They will work directly on projects arising from the collaboration between the Leslie group and A/Prof. Wilson Liao at UCSF, investigating the role of HLA and KIR in psoriasis. The appointees will also contribute to the group's other research projects as directed by A/Prof. Leslie. They will be encouraged to develop their independent research projects where appropriate, as long as they are generally consistent with the research priorities of the Leslie group and the Centre for Systems Genomics as a whole.

We are seeking highly motivated scientists, with a PhD in statistics or a closely related area. Applications are encouraged from people who can demonstrate a strong statistical or other quantitative background and wish to move into statistical genetics research. Ideally you will have experience of genetic analyses but this is not essential. You must have considerable programming experience with a low level language (e.g. C, C++) and preferably also with the statistical software R. The successful applicants will have an aptitude for visualizing data, problem solving and careful statistical analysis. They should be able to work alone and collaboratively, and be able to digest and communicate scientific ideas effectively. The positions are available for three years.

The Research Fellows will be located in the Centre for Systems Genomics, a joint initiative of the Faculty of Science and the Faculty of Medicine, Dentistry and Health Sciences. The positions will report to A/Prof. Stephen Leslie, Associate Professor of Statistical Genomics, and the appointees will be part of the Leslie Group.

Informal enquires can be directed to Stephen Leslie (stephen.leslie@unimelb.edu.au).

The position description and information on how to apply can be obtained from:

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

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## UMinnesota PlantPollinatorInteractions

We seek to hire a motivated and conceptually driven post-doctoral associate to work in the lab and field to understand the impact of environmental nitrogen, sodium, heavy metal, and insecticide supply on plant chemistry (leaves, nectar, and pollen), physiology, and plant-insect interactions. This position is part of a larger collaborative group project studying the impacts of road traffic on roadside vegetation and pollinators.

This work will focus on, but not necessarily be limited to, investigating the role of elemental (nutrient and metal) supply rates or ratios on plant chemistry, growth, allocation to defense, and rates of herbivory, and examining the relevance of predictions from ecological stoichiometry for interpreting empirical results. The successful applicant will work within a collaborative research team of faculty and graduate students that includes empirical expertise in pollinator (bee and butterfly) biology and behavior (Emilie Snell-Rood, Marla Spivak, Dan Cariveau, Karen Oberhauser), molecular mechanisms of plant nectar and pollen production (Clay Carter), and plant-animal-environment interactions (Elizabeth Borer). We are particularly interested in applicants with a strong background in ecological stoichiometry, plant physiological ecology, or ecological responses to nutrients by plants and arthropods. Demonstration of excellent writing skills is an essential qualification for this position.

The appointment is initially for one year, but may be renewed annually. Starting date is negotiable and may begin as soon as October 1, 2017 and as late as March 1, 2018. Application review will begin August 1, 2017. Salary is $47,500.

*Essential Qualifications* Advanced degree (Ph.D. or equivalent) in ecology, plant physiological ecology, plant-insect interactions, or a closely related discipline and excellent writing skills. Successful candidates will have demonstrated empirical and analytical skills necessary to design experiments and analyze complex data, the field skills needed for leading a large-scale field experiment as well as some lab chemistry experience.

*Preferred Qualifications: *Demonstrated capacity for leadership and ability to manage multiple projects effectively. Strong communication skills and ability to work comfortably with a diverse group of researchers. Scientific creativity, reliability, and independence in research. Ability to think on their feet, identify important research questions, and manage and work with heterogeneous data.

To apply, submit a CV along with a cover letter detailing career/postdoc goals, your interest in the project, and a list of three references. Apply through http://www1.umn.edu/ohr/employment/ (Job ID# 318176). For questions, please contact Emilie Snell-Rood (emilies@umn.edu) or Elizabeth Borer (borer@umn.edu)

“emilies@umn.edu” <emilies@umn.edu>

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## UNewHampshire TreePathogenDiversity

The Garnas lab (http://colsa.unh.edu/faculty/garnas) seeks a highly motivated postdoctoral scientist to study 1) patterns and consequences of microbial diversity in the beech bark disease (BBD) pathogen complex and associated bark communities; and 2) impacts of divergent life histories among the dominant BBD associates on pathogen gene flow and population structure across the range of the disease. Within this framework, the successful candidate will be encouraged to develop his/her own ideas to advance basic and applied knowledge around fungal evolution in the context of a complex, multiplayer decline disease.

Brief background

Beech bark disease (BBD) is a widespread decline disease arising from complex interactions among a non-native scale insect and at least two putatively native pathogens that differ in key aspects of their biology and ecology. Recent work also suggests that associated microbes may play a role in disease development and/or attenuation. In addition to being highly relevant ecologically (e.g., to wildlife and to forest stand development), the BBD system represents fertile ground for scientific inquiry, with many key questions that are currently unexplored.

Details of the position and skills sought

The ideal candidate will have both experience and a proven publication record that demonstrates a keen interest and background in population genetics and/or bioinformatics as well as facility with the core concepts of eco-evolutionary dynamics. While the research will be primarily lab and bioinformatics-based, a non-trivial field component to help augment current collections across the range of the disease may be required, together with fungal isolation and culture curation. Experience working with fungi is preferred but not required.

Funding is for 2 years at with an annual salary of $48K plus benefits. Target start date is October 1, 2017 < http://airmail.calendar/2017-10-01%2012:00:00%20EDT >.

The University of New Hampshire and the Department of Natural Resources and the Environment are home to a vibrant community of productive researchers with a strong commitment to student success (see: http://www.unh.edu/unhtoday/2017/03/excellence-ecology and https://www.unh.edu/unhtoday/2017/05/unh-top-10). Located in the town of Durham, UNH is a beautiful campus surrounded by forest and natural landscapes. Only 30 minutes from the sea and less than 2 hours from the White Mountains, outdoor and other recreational activities abound, including right on campus.

Interested applicants should please send the following as a single pdf file to jeff.garnas@unh.edu:

- CV

- Statement of purpose that summarizes research goals/interests/trajectory and relevant experience

- 2-5 relevant publications, with an annotated list of the applicant’s role/contribution for each

- Contact information for three references

Position will be open until filled. Review of applications will begin on or around the first week of July.

Apologies for any cross-postings.

Jeff.Garnas@unh.edu

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## UOslo MolecularPhylogenetics

https://www.jobbnorge.no/en/available-jobs/job/139323/researcher-in-mol ecular-phylogenetics

A 2.5-year position as a research fellow in Molecular Phylogenetics is available at the Natural History Museum, University of Oslo, in association with the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences, Faculty of Mathematics and Natural Sciences,University of Oslo, Norway.

The research fellow will be part of the European Research Council Consolidator Grant project macroevolution.abc (Abiota, biota and constraints in macroevolutionary processes) lead by Associate Professor Lee Hsiang Liow (PI). The main goal of this project is to develop a new model system using bryozoans to provide answers to previously intractable questions in evolutionary biology.

The Natural History Museum and the Centre for Ecological and Evolutionary Synthesis: The position is organized under the Natural History Museum (NHM), University of Oslo, with affiliation to CEES (www.cees.uio.no), a national centre of excellence (CoE). The appointed researcher will carry out research at both the Natural History Museum at its Toyen location (http://www.nhm.uio.no/) and at the Blindern campus of the University of Oslo. In addition, the recearcher will likely travel to NHM in London sevaral times during this project period.

The candidate will work closely with the PI and her collaboratores: Hugo de Boer (NHM, Oslo), Sanne Bossenkool (CEES, Oslo) and Andrea Waeschenbach (NHM, London).

Project description: The main goal of the project is to develop a new model system using bryozoans to provide answers to previously intractable questions in evolutionary biology. These questions include whether ecological interactions that are important for colony growth and survival matter for speciation and extinction patterns observed on very long time scales, and why we can expect to wait a million years for bursts of phenotypic change.

The research fellow has the designated task of isolating material from and sequencing bryozoans using genome skimming, target enrichment and other highthroughputput sequencing approaches, as well as designing and performing bioinformatics pipelines on the resulting sequence data in order to estimate robust phylogenies and to answer macroevolutionary questions.

The ideal candidate has a broad experience with molecular lab techniques, including an extensive and up-to-date knowledge of high throughput sequencing methods, documented skills for the development of pipelines for the assembly and annotation of genomic and transcriptomic reads, knowledge of the theory and implementation of modern phylogenetic methods, including comparative approaches, and will make a major contribution to the planned research. Some knowledge of the target group, bryozoans, is desirable but not obligatory.

The Natural History Museum has an ambition of being a leading research museum. Candidates for researcher fellowships will be selected in accordance with this, and expected to be in the upper segment of their class with respect to academic credentials.

Requirements: Applicants should hold a PhD-degree (or other corresponding education equivalent to a Norwegian doctoral degree).

We seek a motivated, enthusiastic and hard-working researcher who is keen on understanding bryozoan evolution and who has the skills to complete the tasks at hand. She/he should have excellent communication and writing skills to foster understanding across fields.

Applicants must show good interpersonal skills and be willing to work in close collaboration with the project PI and other members of the project team, as well as have the ability to work independently. Applicants should have a good publication record for their career stage.

A good command of English is required.

Please also refer to the regulations pertaining to the conditions of employment: https://www.uio.no/english/-about/regulations/index.html The application must include: * Application letter including a statement of interest, briefly summarizing your scientific work and interests and describing how you fit the description of the person we seek. * CV (summarizing education, positions, and other qualifying activities). * Copies of educational certificates. * A complete list of publications and unpublished work, and up to 5 academic papers that the applicant wishes to be considered by the evaluation committee. * Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number).

Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English or a Scandinavian language.

We offer:

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

## UOtago NewZealand AnthropologicalPalaeogenomics

The Ancient Human and Evolutionary Genomics (AHEG) lab at the University of Otago is looking for a postdoctoral fellow to conduct palaeogenomic studies of the history and health of early colonising populations.

Our lab is undertaking several ancient DNA/palaeogenomic projects investigating migration, adaptation and health of early colonizing populations in island environments. We are seeking a postdoctoral fellow to join our team for a two-year fellowship (NZ $74,896 p.a.). The position will contribute to the development and progression of projects which broadly focus on the sequencing and analysis of ancient genomes of humans, their commensal plants and animals, and the microbes they carry or encounter when they settle new island environments. Specific topics include the genetic identification and impact of Phoenician settlers in the Mediterranean; the evolutionary history of tuberculosis in New Zealand; and demographic reconstructions of colonisation in pre- and post-European contact New Zealand. The ideal candidate will have experience in ancient DNA laboratory work and strong skills in the analysis of next-generation sequencing data, including population palaeogenomics. The AHEG lab group collaborates widely with colleagues in the Departments of Anthropology and Archaeology, Biochemistry, Microbiology, and Zoology and with numerous colleagues overseas, so the ability to work as part of an international, cross-disciplinary team is essential. For further details or inquiries please contact Dr Michael Knapp (michael.knapp@otago.ac.nz) or Prof Lisa Matisoo-Smith (lisa.matisoo-smith@otago.ac.nz) before 23 June 2017, or see http://www.otago.ac.nz/anatomy/research/bioanthropology/index.html . For application details please refer to the following website: http://www.otago.ac.nz/anatomy/about/vacancies/index.html The project is listed under “Palaeogenomic studies of the history and health of early colonising populations” Expressions of interest close on the 25th of June (NZ time).

The University of Otago is one of the most research-intensive Universities in New Zealand with a world-class reputation in the life sciences. It provides an environment that allows its students and staff to undertake internationally recognised research, in a diverse and vibrant environment and has been ranked as one of the 15 most beautiful campuses in the world. The postdoctoral fellow will be hosted by the Department of Anatomy, a diverse and research-oriented department with expertise ranging from genomics to biomedical sciences.

“michael.knapp@otago.ac.nz”
<michael.knapp@otago.ac.nz>

## UPennsylvania EvolutionaryGenetics

Kamberov Laboratory, Department of Genetics in the Perelman School of Medicine at the University of Pennsylvania, USA.

Post-doctoral positions are available in the field of evolutionary and developmental genetics.

Our lab’s research focuses on unraveling the developmental networks and genetic changes that underlie the divergence of humans from other species and for the diversity of present-day human populations. We are broadly interested in evolution of humans, but the core focus of the lab is on the skin and its appendages. We pursue these goals in order to not only understand the genetic origins of human specialization and variation but also seek to apply our findings to the betterment of human health. Available projects include: dissection of genetic pathways of skin appendage development and regeneration in mouse models; discovery and modeling of human adaptive variants using transgenic mice; high throughput screening for genetic elements controlling the development and uniqueness of human skin appendages.

A doctorate in biology or related field is required. Applicants with a strong background in genetics/genomics, developmental biology and molecular biology are encouraged to apply.

Interested candidates should provide: 1) your CV 2) A brief letter detailing your interest in the lab and relevant past research experience 3) The contact information for three references who can comment on your research. Application materials and any questions regarding the position should be sent to Yana Kamberov: yana2@mail.med.upenn.edu

– Yana Kamberov Assistant Professor Department of Genetics Perelman School of Medicine University of Pennsylvania Philadelphia, PA Office (215)746-4757 yana2@mail.med.upenn.edu www.kamberovlab.com "yana2@mail.med.upenn.edu" <yana2@mail.med.upenn.edu>

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## UPennsylvania MicrobeEvolution

Postdoctoral Researcher University of Pennsylvania, Department of Biology

A three-year postdoctoral position is available in the Evolution and Ecology of Disease Systems laboratory at the University of Pennsylvania to study evolution of infectious microbes. The main foci of the projects involves both bacteria and protozoan pathogens of humans and other animals including Borrelia burgdorferi (Lyme disease), Plasmodium (malaria), Leishmania (Leishmaniasis), and several microbiome associated species. The major aims of the projects concentrate on molecular evolution and population genomic analyses. All projects in the lab intellectually integrate multiple scales of biological complexity (i.e. molecular-level, organism-level, and population-level) potentially using laboratory, field, and computational studies.

The positions require highly motivated, enthusiastic, and enquiring individuals with strong backgrounds in evolutionary biology and statistical analysis. Strong molecular genetic skills are highly advantageous. The ideal candidate should have experience troubleshooting molecular protocols, working with genomic data, and have enthusiasm for evolutionary based questions. Quantitative skills are essential. This post is part of a larger project on the population genomics of microbial pathogens that includes researchers at Penn and other universities around the world.

The Department of Biology has a long-standing tradition of maintaining an integrated research and educational program across all basic biological sciences including Ecology and Evolution, Plant Sciences, Molecular and Cellular Biology, Genomics, and Neuroscience. The Department values interdisciplinary research, collaboration, and collegiality, emphasizing Life in its Natural Context. The University of Pennsylvania has a strong group of evolutionary biologists that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools. Unlikely many universities, the proximity of the medical, veterinary, and arts and science schools are centrally located on the Philadelphia campus, which promotes a cross-talk and collaboration. The University of Pennsylvania is an equal opportunity employer. Minorities, women, individuals with disabilities, and protected veterans are encouraged to apply.

The position is available as early as Fall 2017. Salary is commensurate with experience based on the NIH guidelines.

To apply, please send (1) a cover letter outlining your previous experiences that make you suited for this position as well as your research, training, and career goals, (2) CV, and (3) Contact information for 3 references via email to dbrisson@sas.upenn.edu.

Please send enquiries to dbrisson@sas.upenn.edu

Dustin Brisson, Associate Professor Director, Evolution and Ecology of Disease Systems Laboratory Department of Biology University of Pennsylvania Philadelphia PA 19104-6018 http://www.bio.upenn.edu/faculty/brisson/ https://sites.sas.upenn.edu/brisson-lab/ dbrisson@sas.upenn.edu

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## UPittsburgh AdaptiveLandscape

POSTDOC: Role of spatial structure in shaping the adaptive landscape (University of Pittsburgh)

The Wright Lab (http://wrightlabscience.com) is seeking an enthusiastic postdoctoral associate to lead a project aimed at understanding the role of spatial structure in shaping the adaptive landscape. The successful candidate will develop methods for creating spatially structured environments and observing the evolution of microbes. The project will also involve studying the spatial structuring of naturally occurring microbial communities, such as those in soil. This research provides the opportunity to test theories about how spatial structuring shapes the ecology and evolution of microbial communities.

The Wright Lab is a rapidly growing experimental evolution and comparative genomics lab at the University of Pittsburgh. We are affiliated with the Department of Biomedical Informatics, and collaborate closely with other experimental evolution and microbiology labs on campus. Our lab offers opportunities to gain experience giving presentations, lecturing, mentoring students, & writing proposals and papers. We are part of a broader effort to make the University of Pittsburgh a leader in applying evolution to the improvement of medicine. The university consistently ranks in the top 10 nationally for biomedical research funding. Pittsburgh, PA is often voted the most livable city in the US featuring eclectic neighborhoods, diverse culinary and entertainment opportunities, as well as easy access to natural areas (http://www.coolpgh.pitt.edu/).

QUALIFICATIONS: Qualifications for this position include a PhD in microbiology, evolutionary biology, or related field. Ideal candidates would have experience in experimental evolution, robotics, 3D printing, high-throughput sequencing, and/or the analysis of microbial genomic sequences. The candidate should 1) be fluent in written and spoken English, 2) be able to work independently and as a member of a team, 3) be hard-working, motivated, and eager to learn, & 4) have an interest in evolutionary theory.

TO APPLY: Please email applications (including cover letter, curriculum vitae, & names and email addresses for 3 professional references) to Dr. Erik Wright (eswright@pitt.edu). The position is available starting as early as July 2017 for 1 year, renewable up to 3 years contingent upon satisfactory performance. Salary is commensurate with experience and includes a comprehensive benefits package. Review of applications will begin immediately and continue until the position is filled.

Erik Wright Assistant Professor Department of Biomedical Informatics University of Pittsburgh Pittsburgh, PA http://www.dbmi.pitt.edu/person/erik-s-wright-phd-ms "ESWRIGHT@pitt.edu" <ESWRIGHT@pitt.edu>

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## UPorto EvolCooperativeBreeding

Post-doc position available to study audience effects in a cooperative breeder

A post-doc position in Behavioural Ecology is available from mid-September for 1.5 years to study experimentally whether cooperative behaviour is influenced by sex-specific audience effects. The project will integrate a broader research program which investigates the potential role of social and sexual selection in the evolution and maintenance of cooperation in a colonial cooperative bird from Southern Africa, the sociable weaver. The successful post-doc candidate will integrate an international research group based in Portugal, France and South Africa and will be working closely with Rita Covas (CIBIO, University of Porto, Portugal), Claire Doutrelant (CEFE-CNRS, France) and Fanny Rybak (University of Paris-Sud, France). The project is based on acoustic and behavioural field experiments and requires spending an initial period of 4-6 months in the field. Previous experience with fieldwork, behavioural work and acoustics, as well as motivation to conduct behavioural experiments in field conditions are therefore essential prerequisites. Candidates are equally required to have solid knowledge of evolutionary ecology and preferably of cooperation and social evolution. Pre-application enquiries are encouraged and should be sent to rita.covas@cibio.up.pt , claire.doutrelant@cefe.cnrs.fr and fanny.rybak@u-psud.fr . More information about the project can be found at http://www.fitzpatrick.uct.ac.za/-fitz/research/programmes/longterm/sociableweaver; https://cibio.up.pt/people/details/rcovas; https://-www.cefe.cnrs.fr/fr/recherche/ee/esp/777-c/152-claire-doutrelant; http://www.cb.u-psud.fr/Fanny.htm The application deadline is 14 July 2017. Applications must include Curriculum Vitae (CV), motivation letter, copy of academic certificates, and contact details of two references, sent to: bolsas.cibio@cibio.up.pt

Rita Covas <rita.covas@gmail.com>

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## UQueensland CoralAdaptation

We are seeking candidates with postdoctoral research interests in the long-term ecological dynamics of biological communities. The successful applicant will conduct empirical research into understanding the long-term ecological dynamics of reef coral communities using multiple large data sets at multiple temporal scales. As part of the Marine Palaeoecology Lab in the School of Biological Sciences and the ARC Centre of Excellence, the position duties are primarily related to the implementation of novel quantitative techniques applicable to time-series data that test fundamental ecological hypotheses in community ecology.

http://jobs.uq.edu.au/caw/en/job/500700/-postdoctoral-research-fellow-in-quantitative-ecology Thanks!

K-le

Dr Maria del Carmen (K-le) Gomez Cabrera Marine Palaeoecology Lab. School of Biological Sciences The University of Queensland, QLD 4072 Australia

Ph: +61 7 3365 7262 / Fax: +61 7 3365 4755

Visit marinepalaeoecology.org

Visit www.australiancoralreefsociety.org "The trouble with fiction; is that it makes too much sense. Reality never makes sense" - Aldoux Huxley

K-le Gomez-Cabrera <klegomez@uq.edu.au>

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## USheffield AvianMacroevolution

The Thomas lab at the University of Sheffield is looking for a postdoctoral researcher work on a European Research Council funded project on avian macroevolution and macroecology. The project focuses on modelling the tempo and mode of evolution of species traits, linking trait evolution to speciation, and more broadly understanding how and why evolutionary rates vary on the tree of life and shape large-scale trends in the temporal, phylogenetic and geographic distributions of biological diversity. The successful candidate will have the opportunity to work with extensive new data on bill shape and plumage colour in birds, generated from natural history collections and through the citizen science project Mark My Bird (www.markmybird.org).

This position offers an exciting opportunity to link cutting edge analytical techniques with novel and comprehensive trait data to address key macroevolutionary questions. The successful candidate will have the opportunity to develop their own ideas within the broad scope of the project, and could include a focus on data analysis, modelling evolutionary processes, or using the large datasets already collected to help develop novel analytical tools. You will work closely with a research team including the PI, postdocs, PhD students and research assistants. Further information on the Thomas lab can be found at http://macroevolution.group.shef.ac.uk/ You will have a PhD with emphasis on macroevolution/ phylogenetic approaches to evolutionary biology (or equivalent experience) and demonstrable experience in using phylogenetic comparative methods (e.g. modelling trait evolution, diversification).

The position is available for 18 months with a start date from August 7th and preferably before November 2017. The closing date for applications is June 30th.

All applications must be made through the University of Sheffield online application system. Details of the job and a link to the online application are here: https://goo.gl/sUq6Lk Enquiries should be sent to gavin.thomas@sheffield.ac.uk

Dr. Gavin Thomas Royal Society University Research Fellow Department of Animal and Plant Sciences Alfred Denny Building University of Sheffield Western Bank Sheffield, S10 2TN +44 (0)114 2220136 (Sheffield) gavin.thomas@sheffield.ac.uk http://macroevolution.group.shef.ac.uk https://www.markmybird.org Gavin Thomas <gavin.thomas@sheffield.ac.uk>

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## UToronto FellowshipOpportunties

Opportunities for postdoctoral fellowships in the department of Ecology and Evolutionary Biology (EEB) at the University of Toronto are available to excellent researchers from all countries. Before you begin the application process for any or all of the following postdoctoral fellowship programs, Please contact potential supervisors in EEB: http://www.eeb.utoronto.ca/people/G-faculty.htm?quot;%20title 1) Banting NSERC postdoctoral fellowships: http://banting.fellowships-bourses.gc.ca/en/home-accueil.html Last year our department's first internal deadline was July 6. In mid June, check our webpage for information on deadlines and application requirements for 2017: http://www.eeb.utoronto.ca/about-us/employment/postdocs.htm 2) Liber Ero postdocs: The details of the program will be announced in late summer 2017: http://liberero.ca/fellowship-details/ 3) EEB postdoctoral fellowship(s): If funding is available, we will offer EEB postdoctoral fellowship(s) again this coming year. Information about these postdoc fellowships will be available in late October or early November here: http://www.eeb.utoronto.ca/about-us/employment/postdocs/eebpostdoc.htm (note: only faculty on the St. George campus are eligible to sponsor applications for these postdocs)

4) the U of T Faculty of Arts and Science postdoc: http://www.artsci.utoronto.ca/graduate/-postdoctoral-fellowships (note: only faculty on the St. George campus are eligible to sponsor applications for these postdocs)

nicole.mideo@me.com

## UToulouse EndophyteDiversity

Dear colleagues, chers collègues,

please find below a post-doc offer available in our lab Evolution Diversité Biologique,

best wishes, Mélanie Roy and Jerôme Chave

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*Post-doctoral research associate: diversity of endophytes in the canopy*

*One-year position, starting in December 2017. Application before 15th July 2017.*

We are seeking a skilled and enthusiastic post-doctoral research associate to collaborate on a project funded by the French ANR (Study of endophytic fungi: exploring and valorizing antibacterial metabolites; http://secil.obs-banyuls.fr). The goal of the project is to explore the biodiversity and the biochemistry of foliar endophytic fungi. We seek to test whether differences of endophytes communities among hosts reflect a strong spatial structure or host specificity, and if host specificity follows host phylogeny or correlate with functional traits. The project will be based on a sampling of over a thousand leaf samples in a primary forest canopy in French Guiana, taking advantage of the COPAS system (Nouragues station). Surface-sterilized leaf samples span a range of canopy tree species. Total DNA will be extracted and amplification will be conducted with DNA primers specific to fungi and bacteria. In addition, leaf traits will be collected. This will generate one of the largest surveys of endophytic communities ever collected in a tropical forest, and will be used to test hypotheses of community assembly and species coexistence. The applicant will be in charge of data analysis, and interpretation. Relations with the other teams in ANR SECIL will be encouraged.

The position is open at the EDB research unit (Evolution et Diversité Biologique: http://www.edb.ups-tlse.fr) located in Toulouse France. Principal collaborators will be Dr. Jérôme Chave (http://chave.ups-tlse.fr) and Dr. Mélanie Roy. The position is expected to start on December 2017 or January 2018, for one year. Salary will be commensurate with experience according to the CNRS.

*Qualifications: *The successful applicant should hold a PhD in ecology and/or environmental science, and is expected to have a good knowledge of endophytic fungi, biodiversity theory, tropical forest ecology, excellent skills in data analysis (including bioinformatics and statistical analysis), and excellent writing skills.

*How to apply:* Applicants should submit a complete application package no later than July 15th, 2017, to Jessica Delhaye, Université Toulouse III Paul Sabatier, Laboratoire EDB UMR5174, Toulouse 31062 cedex 9, France (e-mail: jessica.delhaye@univ-tlse3.fr). The application package should include two items (both in PDF format): (1) a CV, statement of research interests and accomplishments, and the contact information for three referees, (2) a statement of motivation for the project, in relation to the applicant's research interests and past experience. Incomplete applications will not be examined. If emails are rejected, please use a transfer link to send your application package.

Mela Roy <mela.roy@gmail.com>

## VanderbiltU EvolutionaryGenomicsOfPregnancy

Postdoctoral Position in the Evolutionary Genomics of Pregnancy

A joint postdoctoral position is available in the labs of Tony Capra and Antonis Rokas at Vanderbilt University in Nashville, TN.

The successful candidate will lead our efforts to integrate diverse evolutionary and 'omic data from contexts relevant to pregnancy to identify novel candidate genetic loci for preterm birth risk. The project will leverage Vanderbilt's unique BioVU biobank of more than 230,000 patient DNA samples linked to electronic health records (https://victr.vanderbilt.edu/pub/biovu/) to validate the clinical relevance of our candidates and better map the genetic architecture of preterm birth. We also collaborate closely with wet lab biologists in the March of Dimes Prematurity Research Center Ohio Collaborative, and the successful candidate will help coordinate further testing of novel findings in model systems. New algorithms and data from these projects will be integrated into our popular GEneSTATION (http://www.genestation.org/) web data portal for the study of the genetics and evolution of pregnancy. There is also substantial room for the design and leadership of new projects at the intersection of the genetics and evolution of human pregnancy.

A record of successful publications and a PhD in bioinformatics, genetics, computer science, statistics, or a similar discipline is required. Programming, analytical skills, and the ability to synthesize large omics data sets are essential for this position. Knowledge of pregnancy, reproductive biology, and evolution are preferred, but not strictly necessary.

Interested applicants should email a CV and cover letter outlining qualifications and research interests to both: Tony Capra <tony.INSERTLASTNAME@vanderbilt.edu> Antonis Rokas < antonis.INSERTLASTNAME@vanderbilt.edu>

Please include the phrase "Postdoc Application" in the subject and provide contact information for three references.

The focus of the Capra Lab is comparative and evolutionary genomics. In addition to our work on the genetics and evolution of pregnancy, we have active projects investigating gene regulatory changes in recent human evolution, modeling effects of genetic variation on protein structures, and evaluating the effects of admixture with archaic groups on modern humans. For more information about the group and our work, visit http://www.capralab.org/ . The Rokas Lab focuses on the study of the DNA record to gain insight into the patterns and processes of evolution. We do so using both computational and experimental approaches and focus on three major research themes; the evolution of human pregnancy, the evolution of fungal chemodiversity, and phylogenomics. More information is available at http://www.rokaslab.org/ . "tony.capra@vanderbilt.edu" <tony.capra@vanderbilt.edu>

## WashingtonStateU PlantDiazotrophInteractions

The Friesen lab is moving to Washington State University ( http://plantpath.wsu.edu/people/faculty/friesen/- ) Fall 2017 to continue to pursue research at the intersection of genomics, evolution, and ecology using plant-diazotroph interactions as a model system. Postdoctoral positions are available with the possibility of contributing to ongoing projects in legume-rhizobia and grass-associative nitrogen fixer interactions, with the expectation that applicants will simultaneously develop independent lines of inquiry, apply for independent funding, and contribute to collaborative proposal preparation. Solid training in (at least one of) evolution, ecology, plant biology, microbiology, modeling and/or genomics is desired, with demonstrated facility in quantitative methods and written communication, as well as interest in interdisciplinary research and excitement for contributing to a collaborative and inspiring lab environment. The lab has access to excellent facilities at WSU for plant growth, phenomics, and genomics, and there are nifty opportunities for outreach, including but not limited to evolutionary video game development. Please contact me (maren.l.friesen@gmail.com) with CV and brief statement of interest; I will be at Evolution 2017, the Microbial Population Biology GRC, and ESA 2017 this summer if you'd like to meet up to chat about opportunities in person. Current lab website: friesen.plantbiology.msu.edu

Maren L. Friesen Assistant Professor, Department of Plant Biology Program in Ecology, Evolutionary Biology and Behavior Michigan State University 612 Wilson Rd, East Lansing, MI USA 48824-6481 phone: +1 (323) 454-3023 || office: +1 (517) 844-6947 || fax: +1 (517) 353-1926 http://friesen.plantbiology.msu.edu/ ****Moving to WSU effective August 16th, 2017*** * Assistant Professor, Department of Plant Pathology & Department of Crop and Soil Sciences Washington State University 345 Johnson Hall, Pullman, WA USA 99164 http://plantpath.wsu.edu/people/faculty/-friesen/ maren.l.friesen@gmail.com

## Yale-NUS College Singapore SpiderBehaviorPhylogenomics

Postdoctoral Researcher in Spider Behavior and Phylogenomics

The Piel lab at Yale-NUS College and the National University of Singapore seeks to fill a post-doctoral position to investigate the web-building behavior of spiders in the family Pschridae within the context of lycosoid phylogenomics. The successful applicant is likely to do field work in Singapore and internationally, perform detailed study of spider behavior in the lab along with video digital analysis, use phylogenetic comparative methods, and perform basic molecular methods. The researcher will be collaborating with a bioinformatician and has the opportunity to be trained in building phylogenomic pipelines and to mentor students.

The lab facilities include a molecular lab, digital microscopes, an insectary, behavioral lab, and high-performance computers (PowerEdge R830, 64-cores, 1TB RAM and PowerEdge R730 with added GPU computation). Beyond this, the university has SEM facilities, genomics and sequencing centers, high performance computation, and free access to Singapore's National Supercomputing Centre. NUS also features other large, active research groups in arachnology, phylogenomics, and comparative methods, as well as the nearby newly-minted Lee Kong Chian Natural History Museum.

Singapore is centrally located in the South East Asian tropics with relatively inexpensive low-cost flights to neighboring destinations (e.g. roundtrip: $120 to Bali, $90 to Borneo, etc.) as well as year-round tropical weather and a perennial abundance of local invertebrate fauna. Food is fabulous and inexpensive; public transport is efficient; housing is expensive (comparable to London, New York, Zurich, etc).

The successful applicant will receive a full-time appointment on a contract basis of up to 32 months with medical benefits, ideally starting in August. Foreigners will receive a housing allowance and a one-time travel subsidy.

Qualifications: Ph.D. in biology and ideally with experience in arachnology, animal behavior, comparative methods, etc. The applicant should not have more than 6 years of postdoctoral experience as this triggers a different pay scale that has not been budgeted.

Application: Please express your interest to william.piel@yale-nus.edu.sg including a current CV with a letter of Interest and contact information for three references.

metepeira@gmail.com

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## YaleU 2 PlantEvolutionaryBiology

Two post-doctoral positions in plant evolutionary biology

The Edwards lab is moving to the Department of Ecology and Evolutionary Biology at Yale University, and we are looking for two post-doctoral research associates to join our ongoing efforts focused on the evolution of C4 and CAM photosynthesis in the Caryophyllales. One position will be primarily responsible for the molecular/phylogenomic aspects of the project, and the second will take the lead in physiological/anatomical work. The overarching goal is to develop an integrative and detailed model of C3 to CAM, C3 to C4, and CAM to C4 evolutionary trajectories that can explain the repeated emergence of C4 and CAM syndromes in particular angiosperm lineages. While some goals are quite firm (e.g., improved phylogenies for several clades within Caryophyllales), there will be plenty of opportunity to develop other projects based on the applicant's own interests- this will be actively encouraged.

The successful candidates will be highly motivated, independent, careful scientists and team players, with proven track records in creative project design, data collection, analysis, and publication. Good computing and analytical skills are essential qualities.

The position start date is flexible, and the initial appointment will be for one year, with an opportunity for extension depending on performance. To apply, please send a research statement, a current CV, and contact information for three references (and please, send this as a single PDF document) to Erika Edwards (erika.edwards@yale.edu <mailto:erika_edwards@brown.edu>). Applications will be reviewed starting immediately and accepted until the positions are filled. In accordance with Title IX policy and as delineated by federal and Connecticut law, Yale does not discriminate in admissions, educational programs, or employment against any individual on account of that individual's sex, race, color, religion, age, disability, status as a protected veteran, or national or ethnic origin; nor does Yale discriminate on the basis of sexual orientation or gender identity or expression.

"Edwards, Erika" <erika.edwards@yale.edu>

# WorkshopsCourses

## Barcelona InferenceInBiogeography Dec11-15

Dear colleagues,

This course might be of interest to the people in this list: MODEL-BASED STATISTICAL INFERENCE IN ECOLOGICAL AND EVOLUTIONARY BIOGEOGRAPHY - 2nd Ed.

Instructors: Dr. Dan Warren (Macquarie University, Australia) and Dr. Matthew Van Dam (California Academy of Sciences, USA).

Place: Els Hostalets de Pierola, Barcelona (Spain).

Dates: December 11th-15th, 2017.

PROGRAM

- Monday;

Organization and introductions.

Spatial data in R.

Point data, vector data, and raster data.

GBIF, the Global Biodiversity Information Facility.

Interacting with Google Maps.

Working with raster and vector data.

- Tuesday;

Ecological biogeography.

ENM / SDM concepts and assumptions.

Dismo.

Conceptual issues with ecological inferences from distribution data.

Simulating species occurrence data.

- Wednesday;

Testing ecological hypotheses via Monte Carlo methods.

ENMTools R package.

Ecospat.

Questions of taxonomic scale.

Incorporating niche conservatism into the modelling process.

- Thursday;

Phylogenetic biogeography.

How to read and use phylogenies.

Short history of historical biogeography methods and assumptions.

Likelihood-based statistical model choice.

New probabilistic models for historical biogeography in BioGeoBEARS.

Biogeographical stochastic mapping.

Using BioGeoBEARS and interpreting results.

Including geographical and environmental distance in models.

Using QGIS basics and creating paleo areas.

- Friday;

Integrating in phenology (NCDF & other data sources) in SDM and trait evolution.

Integrating biogeography with biotic interactions (e.g. insect host plant interactions).

Running analyses over multiPhylo objects (posterior distribution) and interpreting results.

Help session for student projects.

Wrap-up.

Organized by: Transmitting Science and the Institut Català de Paleontologia M. C.

More information: http://www.transmittingscience.org/courses/biogeography/model-based-statistical-inference-ecological-evolutionary-biogeography/ With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science http://www.transmittingscience.org Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

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## Berlin EukaryoticMetabarcoding Feb26-Mar2

Dear all,

We are pleased to announce that the 2nd edition of Eukaryotic Metabarcoding Workshop will take place from February 26th to March 2nd, 2018 in Berlin (Germany): https://www.physalia-courses.org/courses-workshops/course4/ Instructors

Dr Owen S. Wangensteen (University of Salford, UK)/ MSc Vasco Elbrecht (University of Duisburg-Essen, Germany)

Overview:

Metabarcoding techniques are a set of novel genetic tools for qualitatively and quantitatively assessing biodiversity of natural communities. Their potential applications include (but are not limited to) accurate water quality, soil diversity assessment, trophic analyses of digestive contents, diagnosis of health status of fisheries, early detection of non-indigenous species, studies of global ecological patterns and biomonitoring of anthropogenic impacts. This workshop gives an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the workshop, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, including bioinformatic data analysis and planning of laboratory work. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended audience:

This workshop is mainly aimed at researchers and technical workers with a background in ecology, biodiversity or community biology who want to use molecular tools for biodiversity research and at researchers in other areas of bioinformatics who want to learn ecological applications for biodiversity-assessment. In general, it is suitable for every researcher who wants to join the growing community of metabarcoders worldwide. This workshop will review mostly techniques and software useful for eukaryotic metabarcoding. Other workshops focused on procedures currently used in microbial metabarcoding will be available from Physalia-courses.

Teaching format:

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion.

Assumed background:

No programming or scripting experience is necessary, but some previous expertise using the Linux console and/or R will be most welcome. All examples will be run either in Linux or Mac environments, with some ssh connections to remote servers. For Windows users, a virtual box running Linux under Windows and/or the installation of an ssh client (e.g. PuTTY) will be needed. For MacOSX systems, installation of some additional Python packages might be needed for running the OBITools software suite. The syllabus has been planned for people which have some previous experience running simple commands from a terminal in Linux or Mac and using the R environment (preferently RStudio) for performing basic plots and statistical procedures. You will need to have a laptop with Python 2.7 installed for running OBITools, but no experience with Python is necessary. If in doubt, take a look at the detailed session content below or send an email to us.

Course programme:

Monday 26th - Classes from 09:30 to 17:30

Session 1. Introduction to metabarcoding procedures. The metabarcoding pipeline.

In this session students will be introduced to the key concepts of metabarcoding and the different next-generation sequencing platforms currently available for implementing this technology. Some examples of results that can be obtained from metabarcoding projects are explained. We will outline the different steps of a typical metabarcoding pipeline and introduce some key concepts. We will also explain the format of the course. In this session, we will check that the computing infrastructure for the rest of the course is in place and all the needed software is installed. Core concepts introduced: high-throughput sequencing, multiplexing, NGS library, metabarcoding pipeline, metabarcoding marker, clustering algorithms, molecular operational taxonomic unit (MOTU), taxonomic assignment.

Session 2. Molecular laboratory protocols. DNA extraction. Metabarcoding markers. Primer design. PCR and library preparation. Good laboratory practice.

In this session we will learn the basics about molecular laboratory procedures needed for metabarcoding. While there will be no hands-on laboratory practices, guidelines and best practices for all key laboratory steps will be discussed. We will explain sample collection techniques,

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## Berlin GenomicVisualizationsInR Sep11-15

Dear all,

we still have a few spots available for the Workshop “Genomic Data Visualization and Interpretation”.

11th-15th September, Berlin (Germany)

https://www.physalia-courses.org/courses-workshops/course14/ Topic: Advanced R and bioinformatics applications for visualization and interpretation of genomic data.

Length: 5 days (~ 9.30 AM to 5.30 PM with breaks)

Instructors: Dr Obi Griffith and Dr Malachi Griffith (Washington University School of Medicine)

Course overview

The advent of rapid and relatively cheap massively parallel sequencing has dramatically increased the availability of genome, transcriptome, and epigenome profiling. Analysis workflows and published best practices are also now available to process raw sequence data into alignments, variant calls, expression estimates, etc., in relatively standardized file formats. Interpretation and visualization of these data, often consisting of thousands to billions of data points, and extracting biological meaning remains a serious challenge. In this workshop we will explore a number of best-in-class visualization tools, and provide working examples that demonstrate important principles of ’omic interpretation strategies.

Workshop format

The workshop will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using a combination of tools installed on the attendees laptop computer and web resources accessed via web browser.

Who should attend

This workshop is aimed at researchers and technical workers who are analyzing some kind of omic data (e.g. WGS, exome, RNA-seq, variant files, etc.). Examples demonstrated in this course will involve primarily human genome/transcriptome data but many of the concepts learned will be applicable to model organisms, metagenomics, simulated data, etc.

Requirements

Attendees should have a background in biology and a basic knowledge of R. We will dedicate one session to a brief R/linux primer. Attendees should have also some familiarity with genomic data. The course will teach relatively advanced usage of R (especially ggplot2 and Bioconductor packages). Attendees should have a working installation of R and RStudio on their laptop.

Example data

Attendees will learn to visualize and interpret results from real human genome data sets generated at the McDonnell Genome Institute at Washington University School of Medicine. These data will be analyzed to determine previously known as well as potentially novel interpretations. Since the example data are not simulated or arbitrarily filtered, interpretation and visualization will be performed in the context of representative levels of sequence error, and other sources of technical and biological noise.

Curriculum

Monday 11th (09:30-17:30) Lecture 1: Introduction to Genomic Data Visualization and Interpretation

* Central dogma * Omic technologies and data * Reference files: GTF, BAM, VCF, MAF, BED, etc * Genome annotation resources, browsers, etc. * Introduction to demonstration data sets

Lab 1: Genome Browsing and Visualization exercises

* IGV o Basics o Creating custom genomes o Sashimi plots * UCSC * Ensembl

Lab 2: Web resources for variant annotation and visualization

* VEP/SnpEff * ProteinPaint * CBioportal * Ensembl BioMart

Tuesday 12th (09:30-17:30)

Lecture 2. Introduction to R for Genomic Data Visualization and Interpretation

Lab 3: Intro to R

* Installation * CRAN and Bioconductor * Data types * Reading and writing Data * Data Frames, slicing, and manipulation * Basic control structures * apply() family of functions * Additional resources

Lab 4: Intro to ggplot

* wide vs long format * geom and aes * axis scaling and manipulation * faceting * themes and colours * ggvis * Additional resources

Lab 5: Real world examples using ggplot

* Heatmaps * Regression lines * Survival analysis * circos

Wednesday 13th (09:30-17:30)

Lab 6. Popular genomic visualizations with GenVisR

* Waterfall plots * TvTi plots * cnSpec plots * cnView plots * lohSpec plots * genCov plots

Lecture 3: Differential gene expression and pathway analysis

Lab 7: Differential expression analysis

* DEseq2

Thursday 14th (09:30-17:30)

Lab 8: Tools and datasets for pathway analysis

* KEGG * GO * GAGE (R package)

Lab 9: Pathway visualization

* Pathview (R package) * Cytoscape

Lecture 4: Clinical interpretation of variants

Lab 10: Clinical variant interpretations

* Variant identity o HGVS o TransVar o Mutalyzer * ClinVar * CIViC

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## Berlin LandscapeGenomics Nov6-10

Dear all,

registration is now open for the course "Landscape Genomics" : https://www.physalia-courses.org/courses-workshops/course17/, https://www.physalia-courses.org/courses-workshops/course17/ 6-10 November, Berlin (Germany).

Instructors: Dr.Stéphane Joost and Oliver Salmoni, ( Laboratory of Geographic Information System (LASIG), Swiss Federal Institute of Technology of Lausanne (EPFL)). Stéphane is specialized in the contribution of Geographic Information Science for the conservation of plant and animal genetic resources. He applies spatial statistics and geocomputation methods to conservation genetics and landscape genomics (https://www.physalia-courses.org/instructors/t13/).

Course Overview

Landscape genomics is an emerging research field that studies how genetic diversity distributes across space and how environmental features can modify this structure through local adaptation. In this workshop, students will learn the basics of this approach and train using state of the art methods. The course will provide an overview of the type of dataset that can be used for a landscape genomics analysis. Firstly, students will learn how to obtain environmental data from publicly available databases, how to process it with Geographic Information Systems (GIS) and how to use the latter to produce indicators able to describe the characteristics of the landscape. Next, the course will discuss the different approaches to obtain genetic data and subsequently show how to study genetic variation and population structure across space in the R environment. Students will be given an overview of the different statistical approaches to study local adaptation, and will be trained in using two of them, Sambada and LFMM. The course will also cover the critical task of the interpretation and validation of the results. Finally, the workshop will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

Targeted Audience & Assumed Background

This workshop is aimed at all biologists, ecologists, geneticists, veterinarians that want to implement the landscape genomics approach in their own studies of evolutionary biology and conservation. Even though the course is not intended for a specialized audience, basic knowledge in evolutionary biology and population genetics would help. Students will learn how to use GIS, but basic computer skills are desirable (e.g. in the R environment). A basic understanding of statistics is also necessary.

Teaching Format

The course is organized in ten learning sessions. During the first two sessions, the course will provide a contextualization of the research field. Then, students will be guided through a landscape genomics experiment with sessions that couple brief theoretical introductions with practical work.

Programme

Monday 6th ÂC Classes from 09:30 to 17:30

Session 1-Introduction

- Overview of the course program

- Introduction on Landscape Genomics

- Examples

Session 2 - Dataset

- The environmental data

- The genetic data

Tuesday 7th ÂC Classes from 09:30 to 17:30

Session 3-Environmental Data 1

- GIS basics

- Main environmental databases

- Derived environmental variables

Session 4- Environmental Data 2

- Environmental characterization of the samples

- Point versus surface

- Analysis of environmental diversity of samples

Wednesday 8th ÂC Classes from 09:30 to 17:30

Session 5- Genetic Data 1

- Sequencing strategies

- Data filtering

Session 6- Genetic Data 2

- Spatial genetic variation

- Population structure

Thursday 9th ÂC Classes from 09:30 to 17:30

Session 7-Statistical Analysis

- Overview of statistical methods (univariate, multivariate, w/wo population structure)

- samÂ£ada: logistic regression

Session 8-InterpWarning: base64 decoder saw premature EOF! reting Results

- Spatial autocorrleation

- Process samÂ£ada output in R

- Validation of results

Friday 10th ÂC Classes from 09:30 to 17:30

Session 9- Planning a Landscape Genomics Experiment

- Scale and Resolution

- Sampling Design

Session 10-Conclusion

- Take home messages

- Question time

Application deadline is: October 6th, 2017.

Further information:

The cost is 480 euros (VAT included) including course material and refreshments. We also offer an all-inclusive package at 745 euros (VAT included), which includes course material, refreshments, accommodation and meals.

Upcoming courses

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## Berlin R Sep-Oct

Dear all,

Physalia-courses provides 3 training courses in biological data analysis, interpretation and visualization using R.

1) Genomic Data Visualization and Interpretation. 11-15 September 2017, Berlin (Germany).

Instructors: Drs Obi and Malachi Griffith (Washington University School of Medicine, US)

Course overview

The advent of rapid and relatively cheap massively parallel sequencing has dramatically increased the availability of genome, transcriptome, and epigenome profiling. Analysis workflows and published best practices are also now available to process raw sequence data into alignments, variant calls, expression estimates, etc., in relatively standardized file formats. Interpretation and visualization of these data, often consisting of thousands to billions of data points, and extracting biological meaning remains a serious challenge. In this workshop we will explore a number of best-in-class visualization tools, and provide working examples that demonstrate important principles of 'omic interpretation strategies.

For more info: https://www.physalia-courses.org/-courses-workshops/course14/ –

2) Statistics for biologists using R. 18-23 September 2017, Berlin (Germany).

Instructor: Dr Ken Aho (Idaho State University, US)

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).

For more info: https://www.physalia-courses.org/-courses-workshops/course13/ –

3) Practical GWAS using Linux and R. 23-27 October 2017, Berlin (Germany).

Instructor: Dr. Jing Hua Zhao (University of Cambridge School of Clinical Medicine, UK)

Course 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.

For more info: https://www.physalia-courses.org/-courses-workshops/course15/ –

For a full list of our training course please visit our website: https://www.physalia-courses.org/courses-workshops/ In the meantime, thank you so much for your attention and participation.

Best regards,

Carlo Pecoraro

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

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https://groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

## Berlin StatisticsForBiologistsUsingR Sep18-23

STATISTICS FOR BIOLOGISTS USING R.

https://www.physalia-courses.org/courses/course13/
Dates: 18 - 23 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.

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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 utilization and development of GUIs, and calling routines from compiled languages.

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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.

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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

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## FrenchGuiana BiodiversityRemoteSensing Sep25-29

Thematic school

Remote sensing for tropical biodiversity mapping and management across scales Faculty: David Coomes, University of Cambridge, UK Mathias Disney, University College London, UK Maria Joao Ferreira dos Santos, Universiteit Utrecht, Netherlands Jean-Baptiste Feret, IRSTEA, Montpellier, France Sassan Saatchi, NASA JPL Pasadena, USA Convenors: Jer0me Chave (CNRS, Toulouse, France) and Gregoire Vincent (IRD, Montpellier, France) Dates: 25-29 September 2017 Venue: Hotel des Roches, Kourou, French Guiana Context: Earth surface is now being sensed continuously at high temporal and spatial resolution by multiple space-borne instruments.

When combined with appropriate methodologies, these sources of information will allow monitoring biodiversity at the global scale. In addition, technologically advanced sensors such as Lidar and imaging spectrometers are becoming increasingly available on airborne platforms. They are part of the equipment dedicated to ground observation, and allow an exploration of the structural heterogeneity of the vegetation, spanning orders of spatial scale. Such technologies already proved their potential and allow multiple applications for the monitoring of complex ecosystems.

Objectives: The Thematic School is open in priority, but not exclusively, to early-career scientists (PhD students, post-doctoral associates) interested in exploring the potential of remote sensing in tropical biodiversity mapping and management. For instance, canopy heterogeneity is correlated with insect diversity in tropical forests, and canopy moisture is a proxy for amphibian diversity. Environmental variables can also be coupled with biodiversity occurrence data using species distribution modelling. Mapping of species richness derived from imaging spectroscopy is another attractive opportunity. These techniques have a direct implication for the management of tropical ecosystems, as they help prioritize areas for conservation. The week will be organized around working sessions, evening lectures and will include a visit to a field station (Paracou). The participants are expected to apply with a clearly stated research problem including already acquired datasets. During the meeting sessions, they will collaborate with other members of the group. Teachers will give evening lectures and provide guidance. Individual projects should result in publishable papers.

How to apply: Applicants should submit their application preferably before July 12th, 2017 to Jessica Delhaye (jessica.delhaye@univ-tlse3.fr). The application package should include two pdf files: (1) a curriculum vitae, (2) a motivation letter detailing your proposed research project and the nature of available datasets. This could include remote sensing data analysis, biodiversity modelling or other questions relevant to tropical forest biodiversity.

Costs: The program will cover accommodation, meals, and transport within French Guiana, but not travel costs to French Guiana.

Jessica Delhaye IR - Chargee de projet LabEx CEBA Evolution et Diversite Biologique - UMR 5174 - Universite Toulouse 3 Paul Sabatier Batiment 4R1 - Bureau 122 118 Route de Narbonne - 31062 Toulouse Cedex 9 - France jessica.delhaye@univ-tlse3.fr 0033 (0)5 61 55 74 86 Laboratoire d'Excellence - Centre d'Etude de la Biodiversite Amazonienne www.labex-ceba.fr jessica delhaye <jessica.delhaye@live.fr>

## Lausanne StatisticalGenetics Sep4-15

SWISS INSTITUTE IN STATISTICAL GENETICS

MODULE 1 - BAYESIAN STATISTICS FOR GENETICS

WHERE? University of Lausanne WHEN? 4-6 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jonathan Wakefield (University of Washington - US) & Prof. Ken Rice (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/-activity/?p28&uid350 DESCRIPTION: The use of Bayesian methods in genetics has a long history. In this introductory module we will begin by discussing introductory probability. We will then describe Bayesian approaches to binomial proportions, multinomial proportions, two-sample comparisons (binomial, Poisson, normal), the linear model, and Monte Carlo methods of summarization. Advanced topics will be touched on, including hierarchical models, generalized linear models, and missing data. Illustrative applications will include: Hardy-Weinberg testing and estimation, detection of allele-specific expression, QTL mapping, testing in genome-wide association studies, mixture models, multiple testing in high throughput genomics.

MODULE 2 - POPULATION GENETIC DATA ANALYSIS

WHERE? University of Lausanne WHEN? 6-8 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/-activity/?p28&uid351 DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests with mid-p-values and a new look at X-chromosome Hardy- Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

MODULE 3 - QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 11-13 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/-activity/?p28&uid744 DESCRIPTION: Quantitative Genetics is the analysis of complex characters where both genetic and environment factors contribute to trait variation. Since this includes most traits of interest, such as disease susceptibility, crop yield, growth and reproduction in animals, human and animal behavior, and all gene expression data (transcriptome and proteome), a working knowledge of quantitative genetics is critical in diverse fields from plant and animal breeding, human genetics, genomics, behavior, to ecology and evolutionary biology. The course will cover the basics of quantitative genetics including: genetic basis for complex traits, population genetic assumptions including detection of admixture, Fisher's variance decomposition, covariance between relatives, calculation of the numerator relationship matrix based on IBD alleles and an arbitrary pedigree, the genomic relationship matrix based on AIS alleles, heritability in the broad and narrow sense, inbreeding and crossbreeding, and response to selection. Also an introduction to advanced topics such as: Mixed Models, Best Linear Unbiased Prediction (BLUP), Genomic selection (GBLUP), Genome Wide Association Analysis (GWAS), QTL mapping, detection of selection from genomic data, correlated characters; and the multivariate response to selection.

MODULE 4 - MIXED MODELS IN QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 13-15 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/-activity/?p28&uid745 DESCRIPTION: "Mixed models" refers to the analysis of linear models with arbitrary (co)variance structures among and within random effects and may be due to such factors as relationships or shared environments, cytoplasm, maternal effects and history. Mixed models are utilized in

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## LeedsUK EssentialComputingSkillsForMolBiol Jul3-5

Reminder: only 3 days left to apply and only a few places left!

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 will be 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.

AUDIENCE

The first workshop is aimed at researchers with little or no experience in programming and data analysis who nevertheless need these approaches in their research.

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 shell, software development and best practices, delivered using Python but easily transferable to other programming languages.

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.

DATE

The first workshop will be run on the 3rd-5th July 2017 (Monday to Wednesday inclusive).

VENUE

The first workshop will take place at the University of Leeds, 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 if 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 *by midnight 15th June 2016*. The workshop will be limited to 25 participants. The selection committee will notify successful applicants by the end of 16th June.

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 :-).

University of Huddersfield inspiring tomorrow's professionals.

Jarek Bryk <J.Bryk@hud.ac.uk>

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## Leiden MicrobialDarwinianMedicine Aug14-17

Just prior to the ISEMPH and ESEB meetings, August 14th to 17th, we will host a workshop at the Lorentz Center in Leiden, called "Microbial Darwinian Medicine: A Workshop at the Interface of Medicine and Microbial Eco-Evolutionary Biology".

Please check it out and submit an application if you're interested in participating!

http://www.lorentzcenter.nl/lc/web/2017/908/-info.php3?wsid=908&venue=Oort Sandra Breum Andersen (New York, USA) Jesse Shapiro (Montreal, Canada) Christina Vandenbroucke-Grauls (Amsterdam, The Netherlands) Marjon de Vos (Wageningen, The Netherlands)

Thank you, Sandra Andersen

Sandra Breum Andersen <sandrabreumandersen@gmail.com>

## Mexico SustainableAquaticDevelopment Sep12-14

Researcher Links Workshop - Sustainable Aquatic Resource Development - Mexico

Dear colleagues,

I am pleased to announce a workshop in Mexico focussed on sustainable use of aquatic resources, including aquaculture and fisheries. Topics to be addressed will be related to invasive species, pollution, conservation, resource management and technological innovation. The workshop will address these issues from evolutionary and ecological approaches.

Dates: 12-14th September 2017, Felipe Carrillo Puerto, Quintana Roo, Yucatan Peninsula, Mexico

Number of participants: 24 (12 from Mexico, 12 from the UK).

Discussions will be used to establish the current status of aquatic resource use in Mexico, and identify opportunities for research collaboration between institutions in the UK and Mexico. A key outcome from the workshop will be a horizon-scanning paper, identifying future issues in aquatic sustainable development, accompanied by information on the solutions, collaborations and skill sets required.

We have a strictly limited number of places available - those attending will have their travel, food and accommodation expenses covered by the Newton Fund Researcher Links programme. The workshop is primarily focussed on early career researchers, defined as up to ten years post-PhD research experience accounting for career breaks. For the funded places we aim to attract researchers with a range of research expertise and viewpoints relating to the core workshop theme. Those attending should have an academic base in the UK or Mexico.

If this fits your research interests and career stage, and you are interested in attending, please complete the expression of interest form by 9th June 2017. See the workshop webpage has further details, http://-sustainableaquaticresourcesmexico.weebly.com/ Please feel free to forward this information to others who you think may be interested.

With best wishes,

Dr Martin Genner School of Biological Sciences University of Bristol Bristol Life Sciences Building 24 Tyndall Avenue Bristol BS8 1TQ

“bzmjg@bristol.ac.uk” <bzmjg@bristol.ac.uk>

## MountainLake GrantWriting Jul24-29

Grant Writing Workshop at Mountain Lake Biological Station July 24-29 2017

Mountain Lake Biological Station (MLBS) will offer a 6-day hands-on grant writing workshop targeted at junior scientists who want to learn strategies, styles, and structures to improve their grant proposals. The experience is geared toward early career proposal writers including graduate students, postdocs, and early stage faculty, and will include direct discussions and writing sessions based on participants own proposal ideas. The workshop will be led by former PI and current NSF program officer Leslie Rissler.

The workshop will take place at MLBS, a residential field station atop Salt Pond Mountain in the southern Appalachians. Cost for the workshop is $250, plus room and board. Limited financial aid to defray room and board costs is available. Space in the workshop will be limited to enable close interaction. For more information, or to enroll, please email MLBS Station Manager Jaime Jones (jjones@virginia.edu) or visit MLBS.org.

“Brodie, Edmund Darrell (Butch) (edb9j)” <edb9j@eservices.virginia.edu>

## Poznan Bioinformatics Sep4-8

Dear colleagues,

We are extremely happy to announce 12th edition of Poznan Summer School of Bioinformatics (PSSB 2017). This meeting takes place at Adam Mickiewicz University in Poznan (Poland) from 4th to 8th September 2017.

This year's topic is NGS in medical research, including subjects like:

1. Introduction to Linux 2. Introduction to next-generation sequencing 3. RNA-Seq: gene expression estimation, differential expression 4. microRNA studies 5. ChIP-Seq data analysis 6. CLIP-Seq in medical studies 7. Genome variant calling 8. Roche sequencing 9. Bioinformatics of rare mendelian disorders 10.Medical applications of Nanopore sequencer

The workshop is suitable both for beginners and for those who already have some basic knowledge in computational biology and find it necessary and interesting to learn more about bioinformatic applications related to Next Generation Sequencing in medical research. Our school consists of lectures and hands-on - this combination should fit best your needs as you have a chance to try out the discussed methods yourself.

The deadline for REGISTRATION is August 25th.

For further information, please visit our website: http://bioinformatics-school.pl Please forward this announcement to anyone who might be interested. Best regards, PSSB Organizing Committe Contact: genomics@amu.edu.pl

Bioinfo School <genomics@amu.edu.pl>

## Sicily EnvDNAMetabarcoding Sep3-9 DeadlineExt

Dear All,

Great news!

The deadline to apply for the Environmental DNA and Metabarcoding Course in Sicily has been extended. Now you can apply until June 16th at info@sciecenter.org .

Don't miss out this great opportunity to come to SCIE Center to learn a novel approach to study aquatic ecosystems.

Below the course information:

Dates 3-9 September

Program - 7 days/6 nights

Number of participants - (25 max)

Program Fee per Student - euro 1290

Venue - SCIE Center, Sicily, Italy www.sciecenter.org

Course Description:

Environmental DNA (eDNA) coupled with metabarcoding represents a powerful tool to investigate ecosystem complexity and reveal hidden biodiversity.

This novel approach is revolutionising the way we assess and monitor aquatic ecosystems.

This course will provide the students with the basic knowledge and skills required to apply the eDNA metabarcoding approach in aquatic environments.

The course program includes a combination of lectures, field activities in the Plemmirio Marine Protected Area, lab-work and data analysis to provide

the students with a thorough understanding of the use of eDNA in molecular ecology, with hands-on experience.

This program is aimed to postgraduate students (masters and PhD students), postdoctoral and early-career researchers.

The course will be held on the scenic island of Ortigia, the historic centre of Siracusa in Sicily, Italy.

Course Lecturers:

Prof. Stefano Mariani, University of Salford, United Kingdom

http://www.marianilab.org/stefano-mariani Dr. Owen S. Wangensteen, University of Salford, United Kingdom

http://www.marianilab.org/owen-wangensteen-1 Judith Bakker, MSc., University of Salford, United Kingdom

http://www.marianilab.org/judith-bakker Dr. Alexia Massa-Gallucci, SCIE Center, Italy

http://sciecenter.org/about/

Course Content:

What is eDNA. The role and usefulness of eDNA for the study of aquatic biodiversity. Application of eDNA.

Sampling methods and strategies. Sample storage, transport and processing.

Analysis of samples: extraction of DNA. Choice of primers, species-specific vs multispecies approaches. Metabarcoding. PCR-free approaches.

eDNA metabarcoding: library preparation and sequencing.

eDNA metabarcoding: bioinformatics.

Down-stream ecological analysis.

Powers and pitfalls of eDNA. The Future of eDNA.

Application and Course Fees:

Application by June 16th 2017 at info@sciecenter.org

To apply send a letter of support from your academic supervisor and a half page letter of intention detailing your research interests and experience and

how you would envisage employing eDNA in your current or future project.

Fee per student euro 1290 includes:

Accommodation in B&B, welcome and farewell dinners, refreshments during the course, transport to the fieldwork site, general liability insurance,

certificate of participation, tuition, SCIE Center 24 hour support.

For more information, enquiries and booking:

Email: info@sciecenter.org web: www.sciecenter.org tel.: +39 366 1907984

Spread the information among your colleagues and all those who might be interested.

Best regards,

Dr. Alexia Massa-Gallucci.

Dr. Alexia Massa-Gallucci Lecturer in Marine Biology, Course Coordinator for Environmental Science, SCIE (Sicily Centre for International Education), Via Landolina 5, 96100 Siracusa Italy

massagalluccia@sciecenter.org

www.sciecenter.org

Alexia Massa Gallucci <alexia.massagallucci@gmail.com>

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## Siegen Germany
## ComputerAnimatedFishModels
## Oct20-22

Are you interested in using computer animated fish models in animal behavior research? Then our software FishSim might be the key to expand your scientific toolset for future research. Join our workshop to get to know the software and to discuss your ideas and work using computer animation!

Workshop: "Discovering FishSim in 3 days - new software for computer-animated 3D fish stimuli for innovative research in animal behavior"

When? October, 20th - 22nd 2017 Where? University of Siegen, Hölderlinstr. 3, 57076 Siegen, Germany Participants: 10 Language: English Costs: 50 euro (Students), 70 euro (Postdocs and senior researchers)

Contact: virtual.fish.project@gmail.com Website: https://virtualfishproject.wixsite.com/fishsim Application deadline: Friday, 30th June 2017

BACKGROUND Within the scope of the DFG funded Virtual Fish Project at University of Siegen (Germany), we developed the free and open-source "FishSim Animation Toolchain" (FishSim) which combines easy creation, animation and presentation of realistic 3D computer-animated fish stimuli for the use in experiments with live test fish (Müller et al. 2016, doi: 10.1093/cz/zow106; Gierszewski et al. 2016, doi: 10.1093/cz/zow108). FishSim was specifically designed for behavioral experiments using common one-choice and two-choice set-ups, as in studies on visual signaling and mate choice. FishSim provides various possibilities to experimentally manipulate morphology and behavior of any number of virtual 3D fish with presentation via monitors. Since FishSim is based on a computer game engine, it offers a unique way for animating 3D fish via real-time input from an external video-game controller.

To introduce FishSim and to assist in the implementation of our toolchain, we would like to welcome you to join a 3-day international workshop for behavioral biologists on "Discovering FishSim in 3 days - new software for computer-animated 3D fish stimuli for innovative research in animal behavior". The workshop will be held at University of Siegen in Siegen, Germany, from October 20-22, 2017, and is organized by Dipl.-Biol. Stefanie Gierszewski (Institute of Biology, University of Siegen), Prof. Dr. Klaudia Witte (Institute of Biology, University of Siegen), Dipl.-Inform. Klaus Müller (Institute of Real-Time Learning Systems, University of Siegen) and BSc. Jan-Marco Hütwohl (Institute of Real-Time Learning Systems, University of Siegen).

The goal of this 3-day workshop is to provide detailed information on the free and open-source FishSim Basic and its integrated tools FishCreator, FishSteering and FishPlayer in both theory and practice. DOs and DON'Ts for implementation of FishSim Basic in future research are discussed. Working computers with all software installed will be provided but it is also possible to use personal laptops. Assistance and advice for working with own data will be given.

Please visit our website https://virtualfishproject.wixsite.com/fishsim for more information about the software, the preliminary program and the application procedure.

We hope to welcome you in Siegen!

Cheers, The Organizing Team

"Gierszewski, Stefanie" <gierszewski@chemie-bio.uni-siegen.de>

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## ThunderBay Ontario PracticalDNATrainingProgram

Practical DNA Training Program:

A two-week (9 business days) intensive laboratory-based training program designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training program is offered at various times throughout the year and we will work with you to find a suitable time for training. The cost of the training program is now $2500.00.

The next scheduled time for the Practical DNA Training Program is: August 14-24, 2017

For more information please contact us at 807-343-8877 or email paleodna@lakeheadu.ca or visit our website at www.ancientdna.com and click on 'Training Programs'.

Thank you.

Karen.

– Karen Maa Administrative Assistant Paleo-DNA Laboratory 1294 Balmoral Street, 3rd Floor Thunder Bay, ON P7B 5Z5

Telephone: 1-866-DNA-LABS

Karen Maa <kmaa@lakeheadu.ca>

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## UExeter Falmouth ButterflyGenomics Jul27-28

Butterflies as Genomic Models in Ecology & Evolution

27-28 July 2017

Centre for Ecology & Conservation, University of Exeter, Penryn Campus, Cornwall, UK

Two day international workshop centred on addressing the challenges involved in whole genome sequencing to achieve novel high impact insights in ecology and evolution using butterflies as a model system. The workshop will feature presentations from leading international research groups in the field, providing examples of how genomic data can be used to tackle fundamental questions in evolutionary ecology.

Please email requests for attendance, and presentation titles/abstracts (up to 150 words), by 20th June to: exeterbutterflies@gmail.com

Successful requests for attendance and presentations will be notified by 27th June.

List of invited speakers and provision titles:

Professor Haruhiko Fujiwara, University of Tokyo, Japan - Molecular biological and genomics approach to reveal the genetic mechanism and evolution of Batesian mimicry supergene in Papilio butterflies.

Dr Krushnamegh Kunte, National Centre for Biological Sciences, Bangalore, India - The Evolution and Genetics of an Iconic Adaptation: A Population Genomics Story in 40 Parts.

Dr Niclas Backström, University of Uppsala, Sweden - Genomic approaches to investigate adaptation, speciation and karyotype evolution in wood-white.(Leptidea) butterflies

Professor Jim Mallet, Harvard University, USA - Heliconius butterfly genomics is messing up our understanding of species.

Dr Mattieu Joron, University of Montpellier, France - The ecology of chromosomal inversions: introgression, demography, and the maintenance of polymorphism.

Dr Beatriz Vicoso, Institute of Science and Technology, Austria - Sex chromosome evolution in Lepidoptera.

Dr Simon Martin, University of Cambridge, UK - Suppressed recombination in the African Queen hybrid zone and the origin of a neo-W.

Dr Konrad Lohse, University of Edinburgh, UK - Are speciation islands real? A test in Heliconius butterflies.

Professor Mark Blaxter & LepBase, University of Edinburgh, UK - LepBase: a community database for lepidopteran genomics.

Dr Richard Merrill, Ludwig-Maximilians-Universität, Munich, Germany - Genetic dissection of assortative mating behaviour.

Dr Marcus Kronforst, University of Chicago, USA - TBA.

Dr Alexander Hayward Room 3052a, Daphne du Maurier Building Centre for Ecology and Conservation University of Exeter, Penryn Campus alex.hayward@exeter.ac.uk Tel: +44 (0) 1326 259147

“Hayward, Alex” <Alex.Hayward@exeter.ac.uk>

## UGothenburg Sweden BioinformaticPipelines Nov6-10

Dear all,

Please find below the preliminary schedule and general aims of the course, “An introduction to bioinformatic tools for population genomic data analysis”, offered November 6-10 2017 at the Sven Lovén Centre for Marine Sciences on the island of Tjärnö outside of Strömstad on the Swedish West Coast (http://loven.gu.se/english/about_the_loven_centre/tjarno).

There is no course fee. Accommodation and meals for students are provided by the Royal Academy of Sciences of Sweden. Students will need to provide their own means of transportation to and from the course, however.

The course will be open to a maximum of 18 students, as large parts of the course will consist of hands-on exercises. The aim is a broad mix of students both from the University of Gothenburg and from the outside, mainly PhD students but postdocs are also welcome to apply.

Knowledge of general molecular biology and genetics is necessary, as is some previous experience with command-line interfaces. Previous experience working on a remote server will also be beneficial. No previous bioinformatics skills are needed, however.

For more information and registration, please visit the course web site at: https://sites.google.com/view/bioinformaticpipelines2017 Deadline for registration is September 15th 2017.

Please note that ALL students must bring their own computers.

Best wishes,

Pierre De Wit

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An introduction to bioinformatic tools for population genomic data analysis, 2.5 higher education credits Third Cycle

Faculty of Science; Department of Marine Sciences

The Swedish Royal Academy of Sciences

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1. Course content

This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one“s own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of whole genome / exome / restriction site digested (RAD) DNA for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises using a remote server. The course introduces bioinformatics software for analysis of RAD-data, and downstream population genetic analysis of genotype data. The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, alignment/mapping, differential Gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests. The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

2. Outcomes

1. Knowledge and understanding 1a. Demonstrate advanced knowledge of experimental strategies, applications and bioinformatic tools for population genomics. 1b. Demonstrate advanced knowledge of the potential of genomics approaches to answer ecosystem-wide questions, in particular for biodiversity monitoring.

2. Skills and abilities 2a. Ability to use basic commands in the Unix command line environment (reformatting data with regular expressions, basic scripting, running python scripts from the unix shell)

2b. Ability to use different software tools to analyse sequence data from restriction-site digested DNA (data cleaning steps, clustering of reads, mapping to reference genomes, extracting and filtering genotype data.

2c. Ability to use population genomics software tools to assemble and a genome/transcriptome, and perform gene alignment/mapping, differential gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests.

3. Judgement and approach 3a. Formulate one's own research questions, identify data and tools needed to answer these questions and critically evaluate and analyse the results.

4. Required reading

Part 1: General computing tools. This will be the main textbook for the introduction to general computing tools: - Haddock and Dunn (2010). Practical computing for Biologists. Sinauer Associates.

Part 2: RAD data analysis. - Wang et al. (2012). 2b-RAD: a simple and flexible method for genome-wide genotyping. Nature Methods 9, 808-810. - Davey et al. (2011). Genome-wide genetic marker discovery and genotyping

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## UK BioinformaticsCourseScholarships Jul3-7

PR INFORMATICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE

"Bioinformatics for geneticists and biologists (BIGB02)" This course will run from 3rd - 7th July at SCENE field station, Loch Lomond, Scotland.

SCHOLARSHIPS CONTRIBUTE TOWARDS TUITION FEES WITH 5 PLACES' AVAILABLE

AT 310.00 (Fees have been subsidised by 50% from 620.00). Accommodation packages can be added for an additional 260.00 for the week including all meals etc.

Applications should be sent to oliverhooker@prinformatics.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 18th June 2017 We still have 'normal' places available for anyone else interested. Full course details are given below https://www.prinformatics.com/course/bioinformatics-for-geneticists-and-biologists-bigb02/ Oliver Hooker <oliverhooker@prinformatics.com>

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## UK EukaryoticMetabarcoding Jul23-28

"Intro to Eukaryotic Metabarcoding" Delivered by Dr. Owen Wangensteen an expert in eukaryotic metabarcoding.

https://www.prinformatics.com/course/eukaryotic-metabarcoding-eukb01/ This course will run from 23rd - 28th July 2018 at Margam Discovery Centre, Wales.

Prices start at Â£400 (approx. 450 euros), accommodation packages available for Â£260 (approx. 295 euros) Metabarcoding techniques are a set of novel genetic tools for assessing biodiversity of natural communities. Their potential applications include (but are not limited to) accurate water quality, soil diversity assessment, trophic analyses of digestive contents, early detection of non-indigenous species, studies of global ecological patterns and biomonitoring of anthropogenic impacts. This course will give an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the course, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, using bespoke primer sets and custom reference databases. 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.

Course content is as follows full syllabus available on the course page; https://www.prinformatics.com/course/-eukaryotic-metabarcoding-eukb01/ Monday 20th Session 1. Introduction to metabarcoding procedures. The metabarcoding pipeline.

Session 2. Metabarcoding markers. Primer design. PCR and library preparation protocols.

Tuesday 21st Session 3. The OBITools pipeline. First steps and quality control.

Session 4. Clustering algorithms. Constant and variable identity thresholds.

Wednesday 22nd Session 5. Taxonomic assignment. The ecotag algorithm. Reference databases.

Session 6. Generating, improving and curating reference databases.

Thursday 23rd Session 7. Refining and analysing the final dataset. Collapsing, renormalising and blank correction. Î±- and ß- diversity patterns.

Session 8. Presenting the final results. Online resources and future developments.

Friday 24th Session 9. Customization.

Session 10 Optional free afternoon to cover previous modules, discuss data or continue with the customization session.

Please email oliverhooker@prinformatics.com with any question or visit our website www.prinformatics.com Please feel free to distribute this material anywhere you feel is suitable

Upcoming PR informatics courses 1. BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS #BIGB 3rd - 7th July 2017, Scotland, Dr. Nic Blouin, Dr. Ian Misner http://www.prinformatics.com/course/-bioinformatics-for-geneticists-and- biologists-bigb02/ 2. INTRODUCTION TO BIOINFORMATICS USING LINUX #IBUL 16th - 20th October, Scotland, Dr. Martin Jones http://www.prstatistics.com/course/-introduction-to-bioinformatics-using -linux-ibul02/ 3. INTRODUCTION TO PYTHON FOR BIOLOGISTS #IPYB 27th Nov - 1st Dec, Wales, Dr. Martin Jones http://www.prinformatics.com/course/-introduction-to-python-for-biologis ts-ipyb04/ 4. INTRODUCTION REMOTE SENSING AND GIS APPLICATIONS FOR ECOLOGISTS #IRMS 27th Nov - 1st Dec, Wales, Dr Duccio Rocchini, Dr. Luca Delucchi http://www.prstatistics.com/course/-introduction-to-remote-sensing-and-g is-for- ecological-applications-irms01/ 5. DATA VISUALISATION AND MANIPULATION USING PYTHON #DVMP 11th - 15th December 2017, Wales, Dr. Martin Jones http://www.prinformatics.com/course/data-visualisation-and-manipulation -using-python-dvmp01/ 6. EUKARYOTIC METABARCODING 23rd - 27th July 2018, Scotland, Dr. Owen Wangensteen http://www.prinformatics.com/course/eukaryotic-metabarcoding-eukb01/ 7. CODING, DATA MANAGEMENT AND SHINY APPLICATIONS USING RSTUDIO FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS #CDSR Dr. Aline Quadros —– Upcoming PR statistics courses 1. MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA #MASE

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## UK LandscapeGenomicsUsingR Nov6-10

“Landscape genomics/genetics using R”

Delivered by Dr. Rodney Dyer a leading expert in landscape genetics.

http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/ This course will run from 6th - 10th November 2016 at Margam Discovery Centre, Wales.

The term 'landscape genetics' has been applied studies that integrate ecological context and intervening landscape into population genetic analyses of contemporary processes such as gene flow and migration. This course will cover the basics of both quantitative landscape ecology and population genetics, focusing on how we develop and evaluate spatial/genetic analyses using the R platform

Course content is as follows Day 1 - Spatial & Ecological Data - Installation & configuring R & RStudio -

Acquiring spatial data, projections, and visualization - Vector and raster data

Day 2 - Genetic markers and basic analyses - Genetic markers and sampling - Genetic distance, diversity, and structure - Ordination techniques based upon genetic markers

Day 3 - Integrating spatial and genetic data - Barrier detection & population division - Resistance Modeling - Mantel and distance regressions - Remote sensing - LiDAR and Hyperspectral data

Day 4 - Integrating spatial and genetic data - Spatial autocorrelation - Network Approaches - PCMN & Redundancy

Day 5 - Adaptive Genetic Variance - Outliers & gradients - Quantitative genetics, why we should care. - Chromosome walking

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Upcoming PR statistics courses

1. MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA #MASE 19th - 23rd June, Canada, Prof. Subhash Lele, Dr. Peter Solymos http://www.prstatistics.com/course/multivariate-analysis-of-spatial-ecological-data-using-r-mase01/ 2. TIME SERIES MODELS FOR ECOLOGISTS USING R (JUNE 2017 #TSME 26th - 30th June, Canada, Dr. Andrew Parnell http://www.prstatistics.com/-course/time-series-models-foe-ecologists-tsme01/ 3. META-ANALYSIS IN ECOLOGY, EVOLUTION AND ENVIRONMENTAL SCIENCES #METR01 24th - 28th July, Scotland, Prof. Julia Koricheva, Prof. Elena Kulinskaya http://www.prstatistics.com/course/-meta-analysis-in-ecology-evolution-and-environmental-sciences-metr01/ 4. SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R #SPAE 7th - 12th August 2017, Scotland, Prof. Jason Matthiopoulos, Dr. James Grecian http://www.prstatistics.com/-course/spatial-analysis-ecological-data-using-r-spae05/ 5. 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/ 6. GENETIC DATA ANALYSIS AND EXPLORATION USING R #GDAR 23rd - 27th October, Wales, Dr. Thibaut Jombart, Zhian Kavar http://-/www.prstatistics.com/course/genetic-data-analysis-exploration-using-r-gdar03/ 7. STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR 23rd - 27th October, Wales, Prof Jarrett Byrnes, Dr. Jon Lefcheck http://www.prstatistics.com/-course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ 8. LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R #LNDG 6th - 10th November, Wales, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/ 9. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS #ABME 20th - 25th November 2017, Scotland, Prof. Jason Matthiopoulos, Dr. Matt Denwood http://www.prstatistics.com/course/applied-bayesian-modelling-ecologists-epidemiologists-abme03/ 10. ADVANCING IN STATISTICAL MODELLING USING R #ADVR 11th - 15th December 2017, Wales, Dr. Luc Bussiere, Dr. Tom Houslay, Dr. Ane Timenes Laugen,

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## Vienna ExperimentalEvolution Nov6-10

The Vienna Graduate School of Population Genetics is now accepting applications for the course “Experimental evolution: From theory to practice” at the University of Veterinary Medicine in Vienna, November 6-10, 2017.

Experimental evolution is extensively used to address questions of evolutionary biology by exposing evolving populations to different environmental conditions. It offers the opportunity to replicate experiments and test for convergent outcomes. With the recent drop in DNA sequencing cost and the advance of sequencing technologies, the combination of experimental evolution with next generation sequencing of pools of individuals (Evolve & Resequence) has become a state-of-the-art method to link phenotypic responses to genetic changes. Although the availability of replicated time series data is one key advantage of E&R, the analysis of such data sets is still in its infancy. This course will introduce the participants to several new approaches for the analysis of genomic time series data covering the latest software tools as well as required statistical and computational skills.

The course is targeted towards researchers interested in experimental evolution combined with NGS and will cover the design of experimental evolution studies as well as the analysis of Pool-Seq time series data.

The course aims to introduce participants to:

State-of-the-art software packages Modeling of neutral data Identifying selected regions Comparison of n-point analysis with time series data Inferring linkage structure of Pool-Seq data Estimating selection coefficients Calling transposable elements in time series data Inferring selection in transcriptomics data

Morning lectures by internationally renowned faculty will be followed by computer practicals on the analysis of experimental evolution data in the afternoon.

Faculty:

Jeffrey E. Barrick (The University of Texas at Austin, US) Anthony M. Dean (University of Minnesota, US) Tadeusz J. Kawecki (University of Lausanne, CH) Christian Schlotterer (Vetmeduni Vienna, A) Marina Telonis-Scott (Monash University, AUS) Olivier Tenaillon (French Institute for Medical Research, FR) Henrique Teotonio (IBENS, FR)

The course is free but will be restricted to a maximum of 15 participants for the practical sessions (hands on computer lab). Additional seats will be available for attending the lectures, only. Students and researchers are invited to apply by submitting a single .pdf file containing 1) a short CV, 2) a motivation letter and a statement of computer skills to popgen.vienna@gmail.com by August 15, 2017. Confidence in working with Unix command line as well as in R, is strongly recommended for the practicals. Participants are expected to arrange their own accommodation.

Further information and updates available at http://www.popgen-vienna.at/training/-experimental-evolution-2017.html Julia Hosp <julia.hosp@gmail.com>

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# 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 notifcation 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 formated) the message will be send 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 preformating 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.