# EvolDir

April 1, 2019

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.

—— / ——

Foreword ..... 1

Conferences ..... 2

GradStudentPositions ..... 31

Jobs ..... 62

Other ..... 78

PostDocs ..... 88

WorkshopsCourses ..... 124

Instructions ..... 143

Afterword ..... 144

# Conferences

Ankara EvolutionaryBiol Jul10-12 .................. 3
Asilomar ASN Jan3-7 CallSymposia ................ 3
Basel EvolutionComparativeGenomics Jul21-25 ..... 4
Berlin WildlifeConservation Sep30-Oct2 ............ 4
Bristol Systematics Jun17-19 ........................ 5
BrownU EvolutionMimulus Jun21 .................. 5
Buffalo GLAM-EvolutionaryGenomics May31 ...... 6
Cambridge EvolutionaryGenetics Apr16-18 ......... 6
Cambridge UK EvolutionEvolving Apr1-4 RegistrationMar15 ........................................ 7
Cartagena Colombia EvolutionCorals Jul29-Aug2 ... 7
Hamburg Hybridization Jun12-14 ................... 8
Hinxton MathMolBiol Apr25-26 .................... 8
Hinxton UK CancerEvolution Jul17-19 ............. 9
Huesca Spain PlantEvolution Jun25-28 ............. 9
KansasStateU ArthorpodGenomics Jun12-14 Absts . 9
Malawi SMBE EvolGenomics Sep18-22 ............ 10
Manchester SMBE2019 Jul21-25 AncientDnaForSelection ............................................ 11
Manchester SMBE 2019 Jul21-25 CallForAbstractsAndAwards ........................................ 11
Manchester SMBE2019 Jul21-25 DetectingSelection 12
Manchester SMBE2019 Jul21-25 MutationRateEvolution ............................................ 13
Manchester SMBE2019 Jul21-25 PolygenicAdaptation 13
Manchester SMBE Jul21-25 CallForAbstractsAndAwards ........................................ 14
Manchester SMBE Jul21-25 EvolutionOfSenescence 14
Manchester SMBE Jul21-25 FitnessLandscapes .... 15
Manchester SMBE Jul21-25 Microbiomes ......... 15
Manchester SMBE Jul21-25 MoleculesNeuronsBehavior 16
Manchester SMBE Jul21-25 MSC-Phylogenomics .. 16
Manchester SMBE Jul21-25 OutreachInMolEvol ... 17
Manchester SMBE Jul21-25 RegistrationAndAbstractSub ............................................ 17
Manchester SMBEMajorTransitions Jul21-25 ...... 18
Manhattan Kansas ArthropodGenomics Jun12-14 . 19
Manhattan Kansas ArthropodGenomics Jun12-14 TravelGrantApplications .............................. 20
Marseilles 23rdEvolutionaryBiology Sep24-27 ...... 20
Maryland Batrafest2019 May3 .................... 21
MexicoCity PoeciliidEvolution Sep24-26 ........... 21
Montpellier DomesticationEvolution Jun3-7 ....... 22
Nottingham UK EndosymbiontEvolution Apr25-26 22
Portland Oregon Sex Asex Jun2-4 ................. 22
PrincetonU EvolutionInfectiousDiseases Jun10-13 . 23
Roscoff France VirusEvolution Oct21-25 ........... 23
Toulouse CulturalEvolution May23-24 ............. 24
Tucson PlantEvol Jul27-31 ........................ 24
Turku ESEB PolygenicAdaptation Aug19-24 ...... 25
Turku Finland ESEB2019 AbstractDeadline31Mar . 26
Turku Finland ESEB2019 AbstractDeadline3Weeks 27
UCambridge EcologicalGenetics Apr16-18 ......... 28
UCambridge EcologicalGenetics Apr16-18 AbstDeadline 28
UppsalaU ConflictAndCooperation May21-22 ...... 29
YaleU SMBE EvolutionOfCancer Apr12-13 ........ 29
Zurich Evolutionandmedicine Aug13-16 ........... 30

## Ankara EvolutionaryBiol Jul10-12

Dear Colleagues,

We would like to remind you to the Ecology and Evolutionary Biology Symposium, Turkey (EEBST), which will take place this year on 10-12 July 2019 at Ankara University, in Ankara.

More information and registration information can be found at the

symposium web site:

http://eebst.org/ Abstracts submission deadline is 15 April 2019.

Keynote Speakers;

Douglas J. Futuyma, Stony Brook University, USA

Olivia Roth, GEOMAR, Germany

Dieter Ebert, Universität Basel, Switzerland

Laurent Duret, Universitê Claude Bernard, France

Lucie Zinger, Ãcole Normale Supérieure, France

EEBST'19 will be the sixth in a series of symposia organized annually by the Ecology and Evolutionary Biology Society of Turkey ( www.ekoevo.org/en ) . The language of symposium is English, and is well attended by diverse international faculty, post-docs and students from all around the world.The symposia also aims to stimulate international collaborations and it offer great opportunity to interact other researchers.

Hope to see you in Ankara

On behalf of the EEBST'19 Organizing Committee

Metehan Arıkan <arikanmetehan@gmail.com>

---

## Asilomar ASN Jan3-7 CallSymposia

*The American Society of Naturalists*

Call for Symposia to be held at the

ASN meeting at Asilomar, California 3-7 Jan 2020

*Due March 31, 2019*

The American Society of Naturalists invites proposals for symposia at its stand-alone meeting at Asilomar, in Monterey, California, 3-7 January 2020. Two symposia will be selected.

Symposium topics should support the Societys goal to advance the conceptual unification of the biological sciences and to further knowledge in evolution, ecology, behavior, and organismal biology. Proposals are encouraged on topics that are synthetic and interdisciplinary, or that address important emerging issues in evolution, ecology, and behavior.

Proposals should include (1) a title; (2) a description of the symposium topic (one page); (3) a tentative list of speakers, including institutional affiliations; (4) a justification for the symposium explaining why the topic and speakers are appropriate for an ASN meeting, keeping in mind the broader goals of the society ( http://www.amnat.org/about/about-the-society.html); and (5) a statement that all proposed invited speakers have agreed to participate. Organizers should plan the symposia to run from approximately 1:30-5:30 pm, and may allocate this time amongst speakers as they wish, reserving time for a coffee break.

Proposals must be submitted by midnight Eastern Standard Time on March 31, 2019 by email to kmkay@ucsc.edu as a single pdf attachment and under the subject heading: *ASN Asilomar Symposium Proposal*. Proposals that include women, young investigators, and individuals from underrepresented groups are especially encouraged.

Please note that, as with previous Asilomar meetings, the society does not have funds to pay for travel or lodging expenses of speakers. However, we may consider requests to waive conference registration costs for junior participants in symposia in cases of financial hardship. Nevertheless, speakers should assume that they will likely have to cover their own travel costs.

The Societys selection committee will evaluate proposals based on the likelihood of attracting a substantial audience, the significance and timeliness of the topic, and on the topics differing substantively from recent symposia hosted by the Society. All applicants will be notified of the committees decision by late April 2019.

Kathleen M. Kay

ASN Symposium Committee Chair

Department of Ecology and Evolutionary Biology

University of California, Santa Cruz

kmkay@ucsc.edu

– Kathleen Kay Associate Professor Ecology and Evolutionary Biology Coastal Biology Building 130 McAllister Way UC Santa Cruz Santa Cruz, CA 95060

831-459-3446 http://kay.eeb.ucsc.edu/ Kathleen Kay <kmkay@ucsc.edu>

---

## Basel EvolutionComparativeGenomics Jul21-25

ISMB/ECCB 2019 EvolCompGen COSI: Call for abstracts

We are soliciting abstract submissions for talks or posters at the Evolution and Comparative Genomics Community of Interest (EvolCompGen COSI) track at ISMB/ECCB 2019, which will take place July 21-25, 2019 in Basel, Switzerland. https://evolcompgen.org/meetings/ismb-eccb_2019 The goal of the track is to foster exchange and collaborations between developers and users of computational methods in evolution and comparative genomics within the ISCB.

The track will feature a mix of proceedings talks (for which the submission deadline has already passed) and contributed talks from the submitted abstracts (deadline: April 11th). In addition, there will be a poster session.

To make the most of the limited time, contributed talks will be 10 minutes including Q&A. Talks can be on unpublished work or work published after January 1, 2018, and delivered by speakers at any career stage.

The selection will be made by a committee chaired by Aïda Ouangraoua and Lars Arvestad, based on the following criteria: (i) significance and novelty of the contribution; (ii) completeness of the description of methods, data, and analysis; (iii) quality of the presentation.

Travel fellowships will be available for presenting students and postdocs. The procedure for application will be communicated to the relevant people in the talk/poster acceptance email.

Information on abstract submission deadline and guidelines can be found here: https://www.iscb.org/ismbeccb2019-submit/abstracts#deadlines Applications should be submitted here: https://easychair.org/conferences/?conf=ismbeccb2019abstract For more information on the EvolCompGen COSI, consult our website at: https://EvolCompGen.org? Aïda Ouangraoua <Aida.Ouangraoua@USherbrooke.ca>

---

## Berlin WildlifeConservation Sep30-Oct2

Dear colleagues,

we wish to extend a cordial invitation to you to participate in Wildlife Research and Conservation 2019 (WRC2019)! The conference will be held from September 30th to October 2nd, 2019 in Berlin, Germany. WRC2019 is jointly organised by the Leibniz Institute for Zoo and Wildlife Research (Leibniz-IZW), the European Association of Zoos and Aquaria (EAZA) and WWF Germany; it is the successor of the International Conference on Behaviour, Physiology and Genetics of Wildlife.

Online registration and abstract submission are open! We welcome contributions to the following topics:

- Behaviour, life history and phenotypic plasticity - Social behaviour and mating systems - Hormones, individual plasticity and fitness - Defaunation: species functional extinctions and their socio-ecological consequences - Importance of social behaviour and application of social networks across wildlife biology and conservation - Human-Wildlife Interactions: Coming from both sides - Advances in gamete preservation for assisted reproduction - Smart tags for smart animals; but are we being smart about what we are doing with them?

Deadline for abstract submission and early bird registration is April 30th, 2019! To register for the conference and submit your abstract, go to: https://www.bayceer.uni-bayreuth.de/wrc2019/en/ Plenary speakers and main sessions: - Prof. Dr. Barbara Taborsky (Institute of Ecology and Evolution, University of Bern, Switzerland): Behaviour, life history and phenotypic plasticity - Prof. Dr. Michael Cant (Centre for Ecology and Conservation, University of Exeter, UK): Social behaviour and mating systems - Prof. Dr. Michaela Hau (Max Planck Institute for Ornithology and University of Konstanz, Germany): Hormones, individual plasticity and fitness - Prof. John E. Fa (Manchester Metropolitan University, UK/Center for International Forestry Research, Indonesia): Defaunation: species functional extinctions and their socio-ecological consequences - Prof. Mike Bruford (School of Biosciences and Sustainable Places Institute, Cardiff University, UK): Conservation Genetics

Parallel sessions and workshops: - An introduction to the ctmmweb R package for movement analysis - Importance of social behaviour and application of social networks across wildlife biology and conservation - Human-Wildlife Interactions: Coming from both sides - Recent advances in capture-recapture studies with applications in wildlife research and conservation - Advances in gamete preservation for assisted reproduction - Smart tags for smart animals; but are we being smart about what we are doing with them? - Defaunation - from conservation science to conservation action

Please visit our conference website for further information: http://www.izw-berlin.de/welcome-234.html . Sponsorship opportunities: If you are interested in sponsoring our conference, please contact us at symposium@izw-berlin.de.

We look forward to welcoming you in Berlin!

Sarah Benhaiem, Anne Berger, Oliver Honer, Conny Landgraf, Josepha Prugel and Viktoriia Radchuk

Contact: Leibniz Institute for Zoo and Wildlife Research (IZW) Conference Organisation Alfred-Kowalke-Str. 17 10315 Berlin Germany

Phone: +49 (0) 30 5168 127 Fax: +49 (0) 30 5126 104 E-mail: symposium@izw-berlin.de Conference website: http://www.izw-berlin.de/welcome-234.html Online registration: http://www.bayceer.uni-bayreuth.de/wrc2019/en/ "Prugel, Josepha" <pruegel@izw-berlin.de>

---

## Bristol Systematics Jun17-19

*** EARLY BIRD CLOSING THIS SUNDAY 31st MARCH!! ***

We would like to invite you to the 10th Biennial Conference of the Systematics Association. The meeting will take place in the vibrant city of Bristol from 17th to 19th June 2019. Keynote speakers include Fredrik Ronquist, Tandy Warnow, and Tom Brooks.

A preliminary program can be seen here: https://systass.org/wp-content/uploads/2018/12/2018_Biennial_Preliminary_programme.pdf Key dates: - Abstracts submission is open until 26th April. - Early bird registration ends in 31 March 2019

There are special rates for students and attendants from developing countries, and there is a limited number of student bursaries available.

More information can be found here: https://systass.org/events-2019/biennial-2019/ . You can also follow the Systematics Association twitter (@SystAssn) for update announcements.

Looking forward to welcoming you in Bristol!

The Systematics Association Biennial Organising Team

Karen Siu Ting, M.Sc., Ph.D. Postdoctoral fellow

Ecological and Evolutionary Genomics Lab Institute for Global Food Security Queen's University Belfast

Karen Siu Ting <agalychnica@gmail.com>

---

## BrownU EvolutionMimulus Jun21

Mimulus Meeting 2019

June 21, 2019

Brown University, Providence, RI

This is an informal meeting with the goal of bringing together scientists interested in the biology of Mimulus for discussions, sharing of ideas, and community building. The meeting will occur just prior to the International Evolution Meeting, which begins the evening of June 21st at the Rhode Island Convention Center in Providence.

There is no registration fee, but sign up here if youd like to receive information and updates about the meeting: https://docs.google.com/spreadsheets/d/1tzyZlR6CHDeI_NHS7V4pjilj3goGtPPxy_XeyH5PrIw/edit#gid=0 . Food and lodging will not be provided, but we will be going out to meals together if you want to join.

We hope to see you there!

Andrea

Andrea L. Sweigart Department of Genetics 120 East Green Street Davison Life Sciences Building, C218 University of Georgia Athens, GA 30602-7223

office phone: (706)-542-7001 sweigart@uga.edu

Andrea Sweigart <sweigart@uga.edu>

## Buffalo GLAM-EvolutionaryGenomics May31

The inaugural Great Lakes Evolutionary Genomics Symposium (GLAM - evogen) will be held on May 31, 2019, at the Center of Arts located in the University at Buffalo. We aim to bring together faculty and trainees from a range of backgrounds with a particular focus on work at the interface between genomics and evolutionary biology. We strongly encourage faculty to encourage their trainees to attend and present. There will be no fee for participation. The deadline for abstract submission is May 10th.

More information can be found at https://-gokcumenlab.org/glam-evogen/ For questions, please contact Omer Gokcumen - gokcumen@gmail.com

Omer Gokcumen <gokcumen@gmail.com>

## Cambridge EvolutionaryGenetics Apr16-18

Hi All,

Registration is now open but will be closing soon (29th March) for this years annual Ecological Genetics Group meeting, in association with the British Ecological Society and Genetics Society. So getting registering so you don't miss out!

This years conference is to be held on the 16th to the 18th of April at the stunning Downing College, University of Cambridge. There will be a full scientific and social programme throughout the conference to bring together those with an interest in population genetics and ecology and evolution. The programme will include a series of talks and a poster session on relevant topics including talks by our two confirmed guest speaks,

Dr Matt Davey, Department of Plant Sciences, University of Cambridge https://www.plantsci.cam.ac.uk/-directory/davey-matthew Dr Matthew Davey X Department of Plant Sciences www.plantsci.cam.ac.uk Biography: Dr Matt Davey is a plant and algal physiologist at the Department of Plant Sciences, University of Cambridge. His key interests are in understanding the diversity of metabolism in natural ecosystems and controlled environments and how such knowledge can be translated for innovation purposes by collaborating with industrial partners involved in bioenergy and natural high value products.

And Prof Bill Amos, Department of Zoology, University of Cambridge https://www.zoo.cam.ac.uk/directory/-william-amos Professor William Amos | Department of Zoology www.zoo.cam.ac.uk I am interested in many aspects of evolutionary genetics. My early work focused on using techniques such as DNA fingerprinting to investigate breeding behaviour and population structure in marine mammals, particularly the long-finned pilot whale and the grey seal.

There will also be the opportunity for a behind the scenes tour of the Sainsbury Laboratory Herbarium at the University. A collection dating back 300 years that will allow you to get up close to specimens collected by the Grandfathers of evolutionary theory, Darwin and Wallace. The Cambridge Genomics Services will a be holding a Genomics and Bioinformatics session to help with all your Next-Gen needs. And our postgrad student workshop this year it will be on 'How to review a paper.'

Let us not forgot the now famous EGG-Heads quiz which will be held after the conference dinner.

Full Conference details can be found here

https://www.britishecologicalsociety.org/event/-ecological-genetics-group-63rd-annual-meeting/ Ecological Genetics Group 63rd Annual Meeting - British Ecological Society www.britishecologicalsociety.org Join us for the 63rd Meeting of the Ecological Genetics Group at the University of Cambridge for this 3-day conference sponsored by the British Ecological Society and the Genetics Society. There will be a full scientific and social programme throughout the conference, where we hope to bring together those working in the fields of population K

All Welcome, from any career stage.! Please note - All poster slots for the conference are now filled but was can squeeze in one or two more talk slots. Send abstracts to geb3@aber.ac.uk asap.

Looking forward to seeing you in Cambridge.

Cheers

Gemma

Dr Gemma Beatty Lecturer Institute of Biological, Environmental and Rural Sciences Aberystwyth University Penglais Aberystwyth Ceredigion SY23 3DA Email:

geb3@aber.ac.uk

Prifysgol Aberystwyth www.aber.ac.uk Prifysgol y Flwyddyn ar gyfer Ansawdd Dysgu - The Times & The Sunday Times 2019.

Aberystwyth University www.aber.ac.uk University of the Year for Teaching Quality - The Times & The Sunday Times 2019.

"Gemma Beatty [geb3]" <geb3@aber.ac.uk>

---

## Cambridge UK EvolutionEvolving Apr1-4 RegistrationMar15

Evolution Evolving: Process, Mechanism and Theory < https://evolutionevolving.org/ > is an international evolutionary biology conference taking place in Cambridge, UK, 1-4 April at Churchill College. You are invited!

***Registration closes in two weeks V Friday 15th March***

The conference program is now online. Invited speakers include Alex Badyaev, Renee Duckworth, Laurel Fogarty, Jukka Jernvall, Alan C Love, Joanna Masel, Armin Moczek, Angela Potochnik, Sean Rice and Jessica Riskin.

Evolutionary biology is a vibrant field with a theoretical framework that itself evolves. The Evolution Evolving conference will focus on some emerging themes in the relationship between development and evolution. Topics include the evolutionary causes and consequences of developmental bias, plasticity, niche construction and extra-genetic inheritance V all of which contribute to an understanding of evolvability. The conference will feature a balanced program of talks and poster sessions spanning three days, and be a mix of empirical and theoretical work, as well as contributions to the history and philosophy of evolutionary biology.

website: https://evolutionevolving.org/ registration: https://evolutionevolving.org/registration/ twitter: @EvoEvolving < https://twitter.com/EvoEvolving/ > email: evoevolving@st-andrews.ac.uk

The organising committee look forward to seeing you there! Prof Paul Brakefield, Prof Kevin Laland, Prof Tobias Uller, Dr Andrew Buskell, Dr Katrina Falkenberg

Katrina Falkenberg <kjf5@st-andrews.ac.uk>

---

## Cartagena Colombia EvolutionCorals Jul29-Aug2

7th International Symposium on Deep-Sea Corals, Cartagena, Colombia ' July 29 - August 2, 2019

We are pleased to announced that, thanks to our sponsors, we are able to maintain early registration rates for the regular registration period, which ends on April 16th, 2019. Register now!

In addition, the information on how to book discounted-rate rooms at the venue hotel (InterContinental Cartagena) is now available at https://www.deepseacoral2019.org/logistics.html Other important reminders:

Travel awards (Application deadline: April 1st, 2019) The Deep-Sea Biology Society (DSBS) will be sponsoring travel awards to the 7th International Symposium on Deep-Sea Corals (ISDSC7) in Cartagena, Colombia. These awards are open to any members of the society and can be used towards any costs associated with attendance and presentation (oral or poster) at the symposium. If you are not a member yet, you can become one at https://dsbsoc.wildapricot.org. The maximum amount that can be requested is pounds 750 (GBP). Awards will be based on both the quality of the abstract and evidence of financial need. Awards are open to participants from all career levels, not limited to students. Successful applicants will be required to write a short blog post, report or video blog for the Society website about their experience at the Symposium. More information at https://www.deepseacoral2019.org/awards.html Abstracts (Abstract submission deadline: April 16th, 2019) Abstracts summarizing new advances in deep-sea coral systems ' from the hadal to the mesophotic, and inclusive of sponges ' will be considered for oral or poster presentations in the following topical areas: Systematics & evolution (taxonomy, fossil record, molecular phylogenetics, and macroevolutionary patterns) Organismal biology & natural history (reproduction, development, growth, behavior, disease, physiology, and microbiome) Ecological interactions (biogeochemical cycling, alterations of ocean chemistry, and carbon sequestration; links with surrounding ecosystems; hydrodynamics and food supply, trophic ecology, and bentho-pelagic coupling; habitat provision, symbiotic relationships, parasites, microbial ecology) Biogeography and connectivity (patterns of community composition, diversity, and distribution; habitat mapping and suitability modeling; population genetics, phylogeography and microevolutionary patterns; larval dispersal) Corals and changing ocean environments (paleo-oceanography and historical environmental reconstructions; biomineralization; modeling impacts of climate change, ocean acidification, and future habitat suitability) Technical advances and novel methods (experimental design, eDNA, omics, imaging technologies, machine learning/AI, photogrammetry, time-series; marine natural product discovery, biotechnology) Anthropogenic stressors (impacts from single to multiple stressors on organisms, communities and ecosystems [e.g. warming, oxygen decrease, ocean acidification, pollution, physical damage]; resilience and recovery; restoration) Conservation and management of deep-sea coral and sponge ecosystems (identification of vulnerable biogenic habitats [VMEs, EBSAs, etc.], biodiversity conservation, fisheries MPA design, legal instruments and governance [national or high seas e.g., ABNJ]; deep-sea mining) More information at https://-www.deepseacoral2019.org/abstracts.html Looking forward to seeing you in Cartagena!

Santiago Herrera, PhD Lehigh University

Juan Sanchez, PhD Universidad de los Andes

Luisa Dueñas, PhD Universidad Nacional de Colombia

7th International Symposium on Deep-Sea Corals

Santiago Herrera <tiagohe@gmail.com>

## Hamburg Hybridization Jun12-14

Dear evolutionary biologists,

we would like to draw your attention to a conference on hybrids to be held in Hamburg/Germany from June 12 to 14, 2019. The meeting will bring together researchers working on a wide range of animal and plant systems studying different aspects of hybridization. It will start with an opening lecture by Jim Mallet and be closed by a lecture of Rosemary Grant. In between the two we have further excellent speakers and offer several additional slots for oral presentations of selected poster contributions.

Thanks to a federal grant supporting our local initiative on hybrids, we could keep the registration costs very low. Further information and the registration form can be found at:

www.biologie.uni-hamburg.de/hybridsymposium < http://www.biologie.uni-hamburg.de/hybridsymposium >

We are looking forward to an exciting conference and hope to welcome you here in Hamburg in June.

Susanne Dobler & Arp Schnittger

Prof. Dr. Susanne Dobler Universität Hamburg Institute of Zoology Martin-Luther-King Pl. 3 20146 Hamburg

Tel: +49-40-42838-4288 Fax: +49-40-42838-3937 email: susanne.dobler@uni-hamburg.de web: www.biologie.uni-hamburg.de/molevol Dobler Susanne <susanne.dobler@uni-hamburg.de>

## Hinxton MathMolBiol Apr25-26

Dear all,

This is a reminder that the registration deadline for MASAMB (Workshop on Mathematical and Statistical Aspects of Molecular Biology) 2019 is in one week, on Friday 15th of March 2019.

Registration links and other information are available here: https://www.ebi.ac.uk/about/events/2019/-workshop-mathematical-and-statistical-aspects-molecular-biology Please hurry to register if you want on-site accommodation, as there are a limited number of available rooms.

Thanks to the Genetics Society, we still have some limited funds available for bursaries to potential attendees who need support. Please emaildemaio@ebi.ac.ukto express your interest.

With best wishes from the Local Organising Committee: — — —Nick Goldman (EMBL-EBI) — — —Gos Micklem (CCBI, University of Cambridge) — — —Nicola De Maio (EMBL-EBI)

demaio@ebi.ac.uk

## Hinxton UK CancerEvolution Jul17-19

Dear colleagues,

We are pleased to announce that registration is now open for 'Evolution and Ecology of Cancer'. The conference will be held 17-19 July in Hinxton, near Cambridge, UK.

The meeting is organised in collaboration with the International Society for Evolution, Ecology and Cancer (ISEEC). It aims to bring together evolutionary biologists, ecologists, cancer researchers and cancer clinicians, highlighting that evolution and ecology are fundamental to both the basic science and the clinical management of cancer.

The conference will discuss the evolution and ecology of cells in tumours, as well as the interaction of cancer with the evolution and ecology of organisms. The main focus of this year's meeting is on Cooperation, Conflict and Parasitism, including cellular competition, multicellularity and mathematical models. There will also be an extensive session on the new and exciting field of transmissible cancers.

For more information and registration please visit the event website: https://coursesandconferences.wellcomegenomecampus.org/our-events/evolutionecologycancer2019/ Nicole Schatlowski <nicole.schatlowski@wellcomegenomecampus.org>

## Huesca Spain PlantEvolution Jun25-28

Dear colleague,

You are cordially invited to participate in the 4th International Brachypodium Conference on 25-28 June 2019, in Huesca, Spain. You can visit our 4th IBC 2019 web site (http://brachypodium2019.unizar.es/) to get updated information on the conference. The registration period is open from January to May 2019.

Brachypodium has proven to be an outstanding model system for functional, comparative, and other studies in plant biology and crop improvement. We will gather to share and discuss the latest discoveries, tool and resource developments, establish collaborations and identify avenues for future research.

New Phytologist (IF 7.43) has agreed to publish a special issue containing papers from the Brachypodium 2019 conference. This is an excellent opportunity to highlight your best work together with a critical mass of thematically linked papers that will ensure wider exposure than individual publications. We look forward to meeting you at Huesca next June.

Sincerely,

The Fourth International Brachypodium Conference Organizing Committee

– Prof. Pilar Catalan Escuela Politecnica Superior de Huesca Universidad de Zaragoza Ctra. Cuarte km 1 22071 Huesca (Spain) phone +34 974232465/+34 974239301 fax +34 974239302

pcatalan <pcatalan@unizar.es>

## KansasStateU ArthorpodGenomics Jun12-14 Absts

REGISTRATION is OPEN! Accepting ABSTRACTS for Oral Presentation Consideration! TRAVEL GRANT information NOW available! V June 12-14, 2019 V 12th Annual Arthropod Genomics Symposium at KSU Manhattan, KS

PLEASE SHARE THIS ANNOUNCEMENT WITH COLLEAGUES AND STUDENTS!

Hi All:

In 2019 the AGS returns to KSU in Manhattan, KS. Visit our website at www.k-state.edu/agc/ags for more details about the symposium.

REGISTRATION Register online at the Symposium website, www.k-state.edu/agc/ags! KEY DEADLINES Monday, March 11 V Abstracts due for Oral Presentation consideration Sunday, March 31 V Travel Grant Applications for Vector Biologists due Monday, May 20 - Abstracts due for Poster Presentations

OVERVIEW The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, welcome reception and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions begin Wednesday evening, June 12, with a Welcome Reception featuring our Keynote Speaker and conclude Friday evening, June 14, with a walk and dinner on Konza Prairie.

SPEAKERS Keynote Speaker: Denise Montell, Duggan Professor and Distinguished Professor from University of California Santa Barbara

Featured Speakers Include: + Kerri Coons, University of Wisconsin-Madison, USA + Conor McMeniman, John Hopkins Bloomberg School of Public Health, USA + Shahideh Nouri, Kansas State University, USA + Luisa Orsini, University of Birmingham, UK + Mark Rebeiz, University of Pittsburgh, USA + Stephane Rombauts, Ghent University, Belgium + Surya Saha, Boyce Thompson Institute, USA + Nick Teets, University of Kentucky, USA + Yoshi Tomoyasu, Miami University, USA + Jamie Walters, University of Kansas, USA

ABSTRACT PRESENTATIONS Abstract presentations will be scheduled throughout the sessions on Thursday and Friday of the symposium. This years sessions include: i5K/Comparative Genomics, Stress Response, Microbiome, Evo/Devo, Vector Biology & Bioinformatics. If interested in submitting an abstract for oral consideration during one of these sessions, visit the website at www.k-state.edu/agc/ags. Abstracts are due Monday, March 11 for oral presentation consideration.

TRAVEL GRANTS Arthropod Genomics Symposium Travel Grants are being offered to support registration, lodging, and transportation to attend the 12th Arthropod Genomics Symposium held at the Kansas State University from June 12 - June 14, 2019. Early stage investigators whose research focuses on arthropod vectors of disease will be eligible to apply for funding; applications from individuals who do not have other financial support for the meeting will be favored. Vector biology travel grants are sponsored by the University of Notre Dames Eck Institute for Global Health. More information on the travel grants can be found at https://www.k-state.edu/agc/ags/travel_grants/index.html . QUESTIONS: Contact Symposium Coordinator, Kascha Johnson at kascha@k-state.edu

If you would like to join the ArthropodNews to ensure receiving future notices, please send an email with your name and email address to kascha@k-state.edu.

>From the 2019 SYMPOSIUM ORGANIZING COMMITTEE:

Sue Brown, Neal Dittmer, Maureen Gorman, Mike Kanost, Berlin Londono, Jocelyn McDonald, Mary Ann McDowell, Kristin Michel, Yoonseong Park, Mike Pfrender, Hugh Robertson, Gene Robinson, Molly Scheel

kascha@ksu.edu

---

## Malawi SMBE EvolGenomics Sep18-22

We are happy to announce the SMBE Regional Meeting - Evolutionary genomics at the human-environment interface taking place in Malawi, Africa from September 18-22, 2019.

https://smbe-malawi.org/ Keynote speakers

Romulus Abila, Maasai Mara University Alex Cagan, Wellcome Sanger Institute Anne Charmantier, University of Montpellier Richard Durbin, University of Cambridge Sophie van der Heyden, University of Stellenbosch Cyprian Katongo, University of Zambia Eline Lorenzen, Natural history Museum of Denmark Peter Visscher, University of Queensland Naomi Wray, University of Queensland

Topics

- Genomics of invasive or alien species - Genomics of hybridization and introgression - Selection and adaptation - Population genetic inference - Meta-genomics - Genomics and resource management - The future of conservation genetics in Africa

Register now at https://smbe-malawi.org/ Abstract Deadline: May 15, 2019

Summary

Most natural systems are impacted by human activities such as resource extraction, habitat perturbation, and the introduction of alien species. While human impact poses a serious threat to many of these systems, it can also generate testable hypotheses about the process of molecular evolution. In this meeting, we will bring together African and international researchers that use genetics or genomics (in the broad sense) to study natural systems impacted by human activities. We will discuss how the study of such systems can help us understand the process of evolution in general, and also how this understanding can be applied to both natural conservation and resource management. We will focus on the genomic effects of hybridisation between native and alien species, and the impact of human-induced selection on genomes (be it directly through hunting or fishing, or indirectly through environmental perturbation). Furthermore, we will discuss population genomic techniques to infer human-induced population changes and the use of (meta-) genomics to monitor ecosystems.

Registration fee: — 150/250 USD per person for African/international researchers

Travel grants available at — https://smbe-malawi.org/ For the organising committee, Hannes Svardal

– Hannes Svardal Research Professor in Evolutionary, Ecological and Environmental Omics Department of Biology University of Antwerp

Campus Groenenborger, room U758 hannes.svardal@uantwerpen.be

Hannes.Svardal@uantwerpen.be

## Manchester SMBE2019 Jul21-25 AncientDnaForSelection

Dear colleagues,

We would like to invite you to the symposium titled "Using Ancient DNA to Study Natural Selection: New Models and New Data", to be held during the SMBE meeting in Manchester (21-25 July).

More information about the SMBE symposia can be found here: http://smbe2019.org/programme/symposia-overview/ As the number of published ancient genomes is growing rapidly, there is also increasing interest in going beyond demographic inference and using this new information for studying past and present adaptation. The temporal dimension provided by the incoming aDNA data can boost power to identify selection signatures. For instance, ancient genomes can be used to study soft sweeps affecting polygenic traits, difficult to investigate using present-day genomic variation only. Increased time resolution can further facilitate testing hypotheses on the ecological drivers of past selection events. But despite all its lure, using aDNA to study selection also involves considerable obstacles, including low coverage or partial genomes, typically small sample sizes, post-mortem damage confounding polymorphism, and other hurdles such as combining data produced using different strategies. This session will be an opportunity to start discussing these issues to promote the wider employment of aDNA in studying adaptation. We particularly invite talks describing novel methodology to most efficiently use available data to capture selection signatures. We also invite researchers studying adaptive processes using ancient genomes to share exciting new examples of adaptation in humans, domestic species, and natural populations, including selection on multigenic traits and adaptive introgression.

Invited speakers: Dr Beth Shapiro, UC Santa Cruz, USA Dr Fernando Racimo, University of Copenhagen, Denmark

Organizers: Anders Gotherstrom, Stockholm University, Sweden ( anders.gotherstrom@arklab.su.se) Matteo Fumagalli, Imperial College London, UK (m.fumagalli@imperial.ac.uk) Mehmet Somel, Middle East Technical University, Ankara, Turkey ( msomel@metu.edu.tr)

The abstract submission deadline is 17th March ( http://smbe2019.org/abstracts/). More information on the meeting can be found here: http://smbe2019.org/ Looking forward to seeing you in Manchester!

Anders, Matteo and Mehmet

– Mehmet Somel METU Dept. Biology / ODTÜ Biyoloji Bolumu 06800 Ankara, Turkey Tel: +90-543-9799060; Office: +90-312-2106460 Email: msomel@metu.edu.tr Lab: compevo.bio.metu.edu.tr aDNA Lab: http://adna.bio.metu.edu.tr/ Eco-Evo Society of Turkey: https://ekoevo.org somel.mehmet@googlemail.com

## Manchester SMBE 2019 Jul21-25 CallForAbstractsAndAwards

SMBE 2019, 21-25 July 2019, Manchester, UK V Call for Abstracts and Awards

Society for Molecular Biology & Evolution

smbe@allenpress.com

Dear SMBE Members,

We are delighted to announce that abstracts are now being accepted for SMBE 2019, here (https://t.e2ma.net/click/1w5iy/9yk2r1/hhsebg). The deadline for abstracts is midnight GMT on Sunday 17 March 2019. Please be aware that the deadline will not be extended. Abstracts should be no longer than 2500 characters (~250 words), with a title no longer than 300 characters.

SMBE 2019 is taking place in Manchester, UK on 21-25 July 2019 at the state of the art venue in Manchester Central. Full details on the symposia programme and confirmed keynote speakers can be viewed here (https:/-

/t.e2ma.net/click/1w5iy/9yk2r1/x9sebg).

A range of awards can be applied for during Abstract submission, all of which require SMBE membership (costing only $10/$30 for 3 years for students/others at https://www.smbe.org/smbe/MEMBERSHIP.aspx (https://t.e2ma.net/click/1w5iy/9yk2r1/d2tebg)) at the time of application.

Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society may apply for the Fitch award (https://t.e2ma.net/click/1w5iy/9yk2r1/tuuebg). Extended abstracts are no longer required this year, just the conference abstract and a cv. Unsuccessful Fitch applicants will automatically be considered for Young Investigator and Registration awards.

Any graduate student or postdoc may apply for the Young Investigator Award (https://t.e2ma.net/click/1w5iy/9yk2r1/9mvebg), which substantially funds the cost of attending. Application materials are the same as for the Fitch, i.e. abstract and cv. Unsuccessful applicants for both will automatically be considered for Registration-only awards.

Undergraduates (including Masters students under a 3+2 system) can apply for the Undergraduate Travel & Mentoring award (https://t.e2ma.net/click/1w5iy/9yk2r1/pfwebg). In addition to presentation title and abstract, this requires a short explanation (250 words) of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university. You also need to arrange to have a short letter of support (250 words) sent from your academic supervisor to masel@email.arizona.edu , confirming that you are undergraduate or a Masters student under 3+2, and that the research is your own.

Carer Travel Awards (https://t.e2ma.net/click/1w5iy/9yk2r1/57webg) can be applied as part of conference registration rather than abstract submission, or by email to Nicolas Galtier .fr if an earlier response is needed. SMBE will make available up to $2000 to SMBE members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as they wish to facilitate the members attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while youre at the meeting, or extra help paying for on-site daycare.

A range of sponsorship opportunities have been developed for the meeting, if interested please contact SMBE2019@mci-group.com .

For any queries over abstracts or registration, please contact SMBE2019@mci-group.com .

Society for Molecular Biology & Evolution <smbe@allenpress.com>

---

## Manchester SMBE2019 Jul21-25 DetectingSelection

We would like to invite you to the symposium on "Genome-wide methods for detecting selection" to be held during the SMBE19 meeting in Manchester (21-25 July).

Natural selection is a key process in evolutionary biology, and despite being a well-established concept in evolutionary theory, detecting and measuring selection signatures genome-wide remains still challenging. In the last two decades, many probabilistic models have helped us to investigate different types such as purifying, positive or balancing selection. However, the debate on how complex these models should be to adequately describe the selection mechanisms while considering confounding factors such as demography and fixation biases (e.g., biased gene conversion) is still ongoing. Recently, approaches to detect signatures of selection that are based on machine learning techniques have been developed. Deep-learning algorithms generally incorporate fewer explicit assumptions about the genetic signatures of natural selection than mechanistic models and were shown useful for discovering subtle patterns hidden in large amounts of data. However, these methods cannot be used for inference are rather descriptive and less suitable for predictions. In this symposium, we will bring together researchers of both mechanistic and machine learning approaches, and we hope to enable a discussion that will benefit the evolutionary community.

Invited speakers Maria Anisimova, Zurich University of Applied Sciences, Switzerland Nicolas Galtier, Université de Montpellier, France

Organizers Rui Borges (ruiborges23@gmail.com), Vetmeduni, Austria Carolin Kosiol (ck202@st-andrews.ac.uk), St Andrews University, UK

The deadline for Abstract submission is 17th March ( http://smbe2019.org/abstracts/). More information about the SMBE symposia can be found here: http://smbe2019.org/programme/symposia-overview/ Looking forward to seeing you in Manchester!

ruiborges23@gmail.com

## Manchester SMBE2019 Jul21-25 MutationRateEvolution

SMBE 2019, 21-25 July 2019, Manchester, UK

We would like to invite you to submit abstracts to symposium “Mutation Rate Evolution”.

Symposium overview: There is a long-standing interest in the study of mutations. Knowledge of how quickly mutations accumulate is critical to many areas of evolutionary genetics, ranging from the quest to improve evolutionary inference to the genetic basis of disease to the advancement of our understanding of the chronology of human evolution to the characterization of relationships among populations and species. While there is considerable uncertainty in historical mutation rate estimates obtained from indirect methods, recent advances in high-throughput sequencing have made it possible to directly estimate mutation rates from parent-offspring trios and multi-generation pedigrees. As a result of these methodological breakthroughs, novel insights into the genomic distribution of mutations as well as potential underlying molecular mechanisms have recently emerged in a number of different species. This symposium will provide a forum to discuss novel scientific findings in this timely area of research.

Invited speakers: Aylwyn Scally, University of Cambridge, United Kingdom Peter Keightley, University of Edinburgh, United Kingdom

The deadline for abstracts is midnight GMT on Sunday 17 March 2019. Submit your abstract here: https://b-com.mci-group.com/AbstractSubmission/SMBE2019.aspx Looking forward to seeing you in Manchester!

Organizers: Kelley Harris, University of Washington, United States Susanne Pfeifer, Arizona State University, United States

– Susanne P. Pfeifer Assistant Professor Arizona State University School of Life Sciences http://spfeiferlab.org spfeife1@asu.edu

## Manchester SMBE2019 Jul21-25 PolygenicAdaptation

SMBE 2019, 21-25 July 2019, Manchester, UK

We would like to invite you to submit abstracts to symposium ’The genetic architecture of polygenic adaptation: sweeps, small shifts and everything in between’.

Symposium overview: For decades the identification of selected loci built on population genetic theory predicting “selective sweep” signatures for selection targets and flanking sequences. Many empirical studies found genomic patterns that are compatible with predictions for hard, soft or incomplete sweeps. Nevertheless, most traits are polygenic as demonstrated by many QTL and GWAS studies. Empirical evidence for genomic signatures of polygenic adaptation has been considered difficult since only small shifts in the allele frequency of (very) many contributing loci are expected. Recent theoretical and empirical work demonstrated, however, that the selection signature of polygenic adaptation can result in substantial allele frequency changes-similar to selective sweeps. Hence, the dynamics of alleles contributing to polygenic adaptation can be traced experimentally, leading to novel insights about adaptive processes. This symposium brings together empirical and theoretical researchers with the intention to explore the genomic signatures of polygenic adaptation. Combining theory with empirical data from natural populations and experimental populations this symposium will provide an important contribution to develop new approaches for the detection of polygenic adaptation.

Invited speakers: Samuel Yeaman, University of Calgary, Canada Kavita Jain, Jawaharlal Nehru Centre for Advanced Scientific Research, India Jonathan Pritchard, Stanford University, USA

The deadline for abstracts is midnight GMT on Sunday 17 March 2019. Submit abstracts here: http://smbe2019.org/abstracts/ Looking forward to seeing you in Manchester!

Organizers: Christian Schli Âand Neda Barghi, Institute of Population Genetics, Vetmeduni, Vienna, Austria

Neda Barghi, Ph.D.

Institut fi Â¼r Populationsgenetik

Department fi Â¼r Biomedizinische Wissenschaften

Veterini Ârmedizinische Universiti Ât Wien, i-sterreich

Neda Barghi <barghi.neda@gmail.com>

## Manchester SMBE Jul21-25 CallForAbstractsAndAwards

We are delighted to announce that abstracts are now being accepted for SMBE 2019, at http://smbe2019.org/-abstracts/. The deadline for abstracts is midnight GMT on Sunday 17 March 2019. Please be aware that the deadline will not be extended. Abstracts should be no longer than 2500 characters (˜250 words), with a title no longer than 300 characters.

SMBE 2019 is taking place in Manchester, UK on 21-25 July 2019 at the state of the art venue Manchester Central. Full details on the symposia programme and confirmed keynote speakers can be viewed at http:/-/smbe2019.org/scientific-programme/ . A range of awards can be applied for during Abstract submission, all of which require SMBE membership (costing only $10/$30 for 3 years for students/others at https://-www.smbe.org/smbe/MEMBERSHIP.aspx) at the time of application.

Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society may apply for the Fitch Award ( https://www.smbe.org/smbe/-AWARDS/TheWalterMFitchAward.aspx). Extended abstracts are no longer required this year, just the conference abstract and a cv. Unsuccessful Fitch applicants will automatically be considered for Young Investigator and Registration awards.

Any graduate student or postdoc may apply for the Young Investigator Award (

https://www.smbe.org/smbe/AWARDS/-AnnualMeetingTravelAwards/-YoungInvestigatorTravelAward.aspx ), which substantially funds the cost of attending. Application materials are the same as for the Fitch, i.e. abstract and cv. Unsuccessful applicants for both will automatically be considered for Registration-only awards.

Undergraduates (including Masters students under a 3+2 system) can apply for the Undergraduate Travel & Mentoring Award (

https://www.smbe.org/smbe/AWARDS/-AnnualMeetingTravelAwards/-UndergraduateTravelandMentoringAward.aspx ). In addition to presentation title and abstract, this requires a short explanation (250 words) of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university. You also need to arrange to have a short letter of support (250 words) sent from your academic supervisor to masel@email.arizona.edu, confirming that you are undergraduate or a Masters student under 3+2, and that the research is your own.

The Carer Travel Award (

https://www.smbe.org/smbe/AWARDS/-AnnualMeetingTravelAwards/CarerTravelAward.aspx ) can be applied for as part of conference registration rather than abstract submission, or by email to Nicolas Galtier nicolas.galtier@umontpellier.fr if an earlier response is needed. SMBE will make available up to $2000 to SMBE members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as they wish to facilitate the member attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while youre at the meeting, or extra help paying for on-site daycare.

A range of sponsorship opportunities have been developed for the meeting, if interested please contact SMBE2019@mci-group.com.

For any queries over abstracts or registration, please contact SMBE2019@mci-group.com.

"Lulu Stader (SMBE admin)" <smbe.contact@gmail.com>

## Manchester SMBE Jul21-25 EvolutionOfSenescence

Dear All,

We would like to invite you to the symposium on "The Evolution of Senescence: From Theory to Molecular Data", to be held during the SMBE meeting in Manchester (21-25 July).

More information about the SMBE symposia can be found here: http://smbe2019.org/programme/symposia-overview/ Senescence (or ageing) is the progressive and time-dependent decline in physiological function that affects most organisms, leading to decreased rates of survival and reproduction and, eventually, to death. Senescence is a fascinating evolutionary problem and, given an ageing population worldwide, it is arguably the major biomedical challenge of the 21st century. Many theories have been proposed to explain how senescence evolves. The best known and widely accepted ones are the Mutation Accumulation and the Antagonistic Pleiotropy theories. However, the sheer diversity of ageing patterns across the tree of life, including organisms that do not appear to experience senescence, suggests that there is no single theory that can be reconciled with all the data. Many theoretical and empirical studies have tried to unravel the evolutionary and mechanistic underpinnings of senescence, ranging from novel mathematical models to comparative studies of long and short-lived organisms, including human supercentenarians. We aim to bring together recent contributors of innovative models, novel datasets and new experimental and analytical approaches. Together, we will examine how the latest developments can shed light on our understanding of the evolutionary and mechanistic causes of ageing and, perhaps, how can they suggest strategies to deal with ageing in our species.

Invited speakers: Emma Telling, University College Dublin, Ireland Jacob Moorad, University of Edinburgh, UK

Organizers: Arcadi Navarro, Universitat Pompeu Fabra, Spain (arcadi.navarro@upf.edu) Joao Pedro de Magalhaes, University of Liverpool, UK (aging@liverpool.ac.uk)

The deadline for Abstract submission is 17th March (http://smbe2019.org/abstracts/), more information on the meeting can be found here: http://smbe2019.org/ Looking forward to seeing you in Manchester!

Joao Pedro & Arcadi

Arcadi Navarro i Cuartiellas, PhD ICREA Research Professor

Departament of Experimental and Health Sciences Universitat Pompeu Fabra

Dr. Aiguader, 88 +34 93 3160844 ph E-08003 Barcelona +34 93 3960901 fax

email: arcadi.navarro@upf.edu web: http://-biologiaevolutiva.org/anavarro/ Arcadi Navarro Cuartiellas <arcadi.navarro@upf.edu>

---

## Manchester SMBE Jul21-25 FitnessLandscapes

We invite abstract submissions for talks and poster for our symposium “Insights from Fitness Landscapes into Evolutionary Pathways” at SMBE in Manchester 21-25 July 2019.

Deadline for abstracts 17th March. Submit your abstracts here: http://smbe2019.org/abstracts/ Symposium overview: A question of central importance in evolutionary genetics concerns how pathways and directions of evolutionary change are affected by the mapping function between genotype and phenotype. This question can now be addressed in earnest. The advent of new experimental methods based on deep mutational scanning has enabled direct high-throughput measurements of fitness for vast libraries of mutant genotypes. In parallel, new theoretical research predicts how the fitness landscape should shape trajectories of evolutionary change. Reconstruction of the roads actually taken by evolution, and comparisons to the roads not taken, allows us to test hypotheses about the factors that influence pathways of change. Finally, patterns of sequence divergence at large evolutionary timescales can provide an independent view of the fitness landscape shape and dynamics. With this symposium, we will provide a comprehensive perspective on how this combination of approaches deepens our understanding of evolutionary pathways over different timescales.

Invited speaker: Claudia Bank, Instituto Gulbenkian de Ciência, Portugal - https://evoldynamics.org/people/-claudia-bank-2/ Organisers: Georgii A Bazykin, Skolkovo Institute of Science and Technology, Russia Jay Storz, University of Nebraska, USA

Georgii Bazykin <g.bazykin@skoltech.ru>

G.Bazykin@skoltech.ru

---

## Manchester SMBE Jul21-25 Microbiomes

We invite abstract submissions (for talks and poster) for our symposium on the application of evolutionary approaches to the study of microbial communities and microbiomes at SMBE in Manchester 21-25 July 2019.

Deadline for abstracts 17th March. Submit your abstracts here: http://smbe2019.org/abstracts/ Symposium overview: Microbial communities (i.e. microbiomes) shape ourselves and our environments. Our interactions with these communities can alter our health, our food sources, and the marine and soil environments around which we live. In order to better understand these communities, we must understand the evolution of individual strains and species within them, the evolutionary interactions (i.e. cooperation and competition) between members, as well as how these collective communities have evolved to interact with their environment and/or host organism. Evolutionary studies of microbial communities have historically been neglected. As such, the aim of this symposia is to highlight those whose research is making strides in combining the fields of evolution and microbiology towards the study of microbial communities. This symposia will focus on fostering the novel approaches in this field, including research which may not be getting enough attention in the broader field of microbiome research. Talks will combine evolution, ecology, and microbiology, in order to shape our understanding of the microbial communities which live in us, around us, and in symbiosis with us.

Invited speaker: Nicola Segata (CIBIO - University of Trento) - http://segatalab.cibio.unitn.it/index.html Organisers: Fiona J Whelan, University of Nottingham, UK Chris Creevey, Queen's University Belfast, UK

Chris Creevey <chris.creevey@gmail.com>

## Manchester SMBE Jul21-25 MoleculesNeuronsBehavior

This is a callout to evolutionary biologists interested in the molecular and neural basis of behavioral evolution. We would like to encourage you to consider submitting an abstract for our symposium at this year's SMBE meeting in Manchester (July 21-25).

Deadline is coming up soon: 17th March Submission link: http://smbe2019.org/abstracts/ Symposium overview: Underlying the diversity of animal sensory capabilities and behaviors are fascinating differences that have evolved within their nervous systems. While there has been steady progress in understanding foundational neurophysiology principles in model organisms, only recently have the tools and resources become available to study neural circuit evolution among diverse species. These tools and approaches are now allowing comparative studies aimed at integrating questions about fine-scale molecular changes, neural architecture modifications, and behavioral evolution. As a result of these rapidly developing methodologies and growing applications, a symposium on the molecular basis of neural circuit and behavioral evolution would provide an opportune time to share recent results from these research avenues. Our goal with the symposium will be to highlight interdisciplinary work existing at the interface between evolutionary thought (theory and inference-based analyses) and functional characterization (neurogenetics, molecular biology). We believe that the symposium will be of general interest to the conference attendees as it has great potential to be informative on fundamental evolutionary topics including the relationship between genotypic and phenotypic variation, the genetics of adaptation, speciation biology, and behavior.

Invited speakers: Ralf J. Sommer Max Planck Institute for Developmental Biology, Germany http://www.sommerlab.org/members/ralf-sommer.html Sylvie Rétaux, Evo Neuroscience Paris-Saclay Institute CNRS, France http://neuro-psi.cnrs.fr/spip.php?article144&lang=fr Organisers: Lucia Prieto-Godino, The Francis Crick Institute, England Roman Arguello, University of Lausanne, Switzerland

roman.arguello@unil.ch

## Manchester SMBE Jul21-25 MSC-Phylogenomics

Dear all,

We are excited to invite you to submit abstracts of your research to the symposium on "Phylogenomics under the Multispecies Coalescent", to be held during the SMBE meeting in Manchester, UK (21-25 July).

Invited speakers: Ziheng Yang, University College London, United Kingdom Anne D. Yoder, Duke University, USA The deadline for Abstract submission is 17th March (http://smbe2019.org/abstracts/). For more information please visit: http://smbe2019.org/ Symposium Overview: The coalescent has played a pivotal role in molecular population genetics and has been widely used for estimating population genetic parameters (i.e., population size, migration and recombination rates) from sequence data. The natural extension to multiple species, the multispecies coalescent (MSC), has marked a paradigm shift in molecular systematics by using gene-tree heterogeneity across the genome as a source of information for species-tree inference. Using MSC methods appears important when the species arose through a radiative speciation process, perhaps accompanied by migration or introgression between species, because those processes generate short branches in the species tree and thus widespread species tree-gene tree discordance. In the past 10 years, heuristic and full likelihood (such as Bayesian MCMC) approaches under the MSC have been developed. In this symposium we will discuss the latest advances in MSC methods, such as the development of new computational MCMC algorithms, improvements to summary methods, divergence time estimation, and large-scale analysis of real data.

We are looking forward to seeing you in Manchester!

The symposium organizers,

Tomas Flouri, Mario dos Reis Barros, Paschalia Kapli

Paschalia Kapli <k.pashalia@gmail.com>

---

## Manchester SMBE Jul21-25 OutreachInMolEvol

Dear all,

Are you interested in the practices and challenges of communicating molecular evolution to broad audiences? Join us at the symposium " Outreach in Molecular Biology and Evolution - good practices and challenges" taking place the SMBE

meeting in Manchester (21-25 July).

A key aspect of current research in the field of Evolution is the proper dissemination to stakeholders, politicians, general public, and also other scientists. Successful outreaching may help solve various societal issues particularly in an era of fake news: scientifically literate public are for example more supportive of the public funding of science and of scientifically driven practices such conservation policies. Unfortunately, scientists often fail to properly reach the public (or even a general academic audience) particularly for what concerns molecular evolutionary concepts. The communication of Molecular Evolution concepts is extremely important, but can be challenging. With this symposium we would like to inspire the SMBE audience on how to do better outreach by providing with examples of great communicators and outreach practices on a variety of molecular evolutionary topics. We aim at providing concrete tools and examples on how to best communicate research by selecting talks from proven excellent SMBE outreachers, by pointing toward pitfalls that should be avoided, and to good practices that should be followed. We also aim at providing with examples of alternative ways than conference talks such as public engagement, citizen science, media and social networking. We welcome contributions from enthusiast molecular evolutionists, ranging from student with new outreaching unconventional ideas to mature academics with long history of communication.

For more information (including invited speakers):

http://smbe2019.org/programme/symposia-overview/ And for registration:

http://smbe2019.org/registration/ Hope to see you there!

The organizers,

Omar Rota Stabelli, Fondazione Edmund Mach, Italy

omar.rota@fmach.it

Heloise Dufour, Cercle FSER, France

heloise.dufour@cerclefser.org

Rita Ponce, Polytechnic Institute of Setubal, Portugal

ana.ponce@ess.ips.pt

Rita Ponce <anaritaponce@gmail.com>

---

## Manchester SMBE Jul21-25 RegistrationAndAbstractSub

We are delighted to announce that registration for SMBE 2019 is now live. SMBE 2019 is taking place in Manchester, UK on *21-25 July 2019* at the state of the art venue Manchester Central. Full details on the symposia programme and confirmed keynote speakers can be viewed at http://smbe2019.org/programme/ . Information on the registration fees can be viewed at http://smbe2019.org/registration/registration/. Register before the early bird deadline on Wednesday 8 May in order to secure discounted registration rates.

You can book your accommodation from a range of city centre properties from inside the registration system.

Delegates requiring a VISA in order to attend SMBE 2019 can select this option within the registration system. The registration team will be able to assist in creating the documentation in order to support your VISA application.

Carer Travel Awards (https://www.smbe.org/smbe/AWARDS/AnnualMeetingTravelAwards/UndergraduateTravelandMentoringAward.aspx) can be applied for as part of conference registration. SMBE will make available up to $2000 to SMBE members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as they wish to facilitate the members attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while youre at the meeting, or extra help paying for on-site daycare.

*Abstract and Award submission deadline.*

The abstract submission deadline is fast approaching. *The deadline for abstracts is midnight GMT on Sunday 17 March 2019.* Please be aware that *the deadline will not be extended*. Abstracts should be no longer than 2500 characters (~250 words), with a title no longer than 300 characters. Full details on abstract topics, guidance and the submission portal can be found at http://smbe2019.org/abstracts/ . A range of awards (https://www.smbe.org/smbe/AWARDS/) can be applied for during Abstract submission, all of which require SMBE membership (costing only $10/$30 for 3 years for students/others at https://www.smbe.org/smbe/MEMBERSHIP.aspx) at the time of application.

Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society may apply for the Fitch award < https://www.smbe.org/smbe/AWARDS/TheWalterMFitchAward.aspx >. Extended abstracts are no longer required this year, just the conference abstract and a cv. Unsuccessful Fitch applicants will automatically be considered for Young Investigator and Registration awards.

Any graduate student or postdoc may apply for the Young Investigator Award < https://www.smbe.org/smbe/AWARDS/AnnualMeetingTravelAwards/YoungInvestigatorTravelAward.aspx >, which substantially funds the cost of attending. Application materials are the same as for the Fitch, i.e. abstract and cv. Unsuccessful applicants for both will automatically be considered for Registration-only awards.

Undergraduates (including Masters students under a 3+2 system) can apply for the Undergraduate Travel & Mentoring award < https://www.smbe.org/smbe/AWARDS/AnnualMeetingTravelAwards/UndergraduateTravelandMentoringAward.aspx >. In addition to presentation title and abstract, this requires a short explanation of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university. You also need to arrange to have a short letter of support (250 words) sent from your academic supervisor to masel@email.arizona.edu, confirming that you are undergraduate or a Masters student under 3+2, and that the research is your own.

A range of sponsorship opportunities have been developed for the meeting, if interested please contact SMBE2019@mci-group.com.

For any queries over abstracts or registration, please contact SMBE2019@mci-group.com.

"Lulu Stader (SMBE admin)" <smbe.contact@gmail.com>

---

## Manchester SMBEMajorTransitions Jul21-25

We would like to invite you to the symposium on "The molecular basis of major transition in evolution", to be held during the SMBE meeting in Manchester (21-25 July). More information about the SMBE symposia can be found here: http://smbe2019.org/programme/symposia-overview/ The history of life on Earth shows major evolutionary transitions, shifts in which new biological features emerged that dramatically changed the biology of organisms. The endless forms most beautiful we observe today are the result of these revolutions that shaped the biology of the planet. These innovations were at the centre of the seminal book "The Major Transitions in Evolution" by John Maynard Smith and Eörs Szathmáry, published nearly 25 years ago. They include the origins of cells and sex, major endosymbiotic events, or the rise of multicellularity and societies among others. The abundance of genomic data, new evolutionary algorithms, and emerging technologies - such as single-cell sequencing - offer a timely opportunity to study the molecular changes underlying most of these major transitions. Recent research has showed the importance of gene duplication (e.g., the origins of multicellularity), the evolution of cell types (the rise of animals or the nervous system), or the fusion of genomes from different organisms (eukaryotes and photosynthesis). In this symposium we will explore the molecular basis associated with these transitions at different organisation levels, from genes and cells to complete organisms.

Invited speakers Eörs Szathmáry, Biological Institute, Eötvös University, Hungary Purificacion Lopez-Garcia, CNRS, University of Paris Sud, France

The deadline for Abstract submission is 17th March. (http://smbe2019.org/abstracts/), more information on the meeting can be found here: http://smbe2019.org/ Looking forward to see you in Manchester!

Signed the symposium organising team (Mary O'Connel, Roberto Feuda, Jordi Paps)

Jordi Paps Montserrat <jordi.paps@bristol.ac.uk>

---

## Manhattan Kansas ArthropodGenomics Jun12-14

NEW TRAVEL GRANT information available! Accepting ABSTRACTS for Oral Presentation Consideration! REGISTRATION is OPEN! V June 12-14, 2019 V 12th Annual Arthropod Genomics Symposium at KSU Manhattan, KS Hi All:

In 2019 the AGS returns to KSU in Manhattan, KS. Visit our website at www.k-state.edu/agc/ags for more details about the symposium.

TRAVEL GRANTS V Applications Due March 31 + Vector biology travel grants are sponsored by the University of Notre Dames Eck Institute for Global Health. + Postdoc & student travel grants are sponsored by the Kansas State University Arthropod Genomics Center. + More information on the travel grants can be found at https://www.k-state.edu/agc/ags/travel_grants/index.html.

REGISTRATION Register online at the Symposium website, www.k-state.edu/agc/ags! KEY DEADLINES Monday, March 11 V Abstracts due for Oral Presentation consideration Sunday, March 31 V Travel Grant Applications Due Monday, May 20 - Abstracts due for Poster Presentations

OVERVIEW The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, welcome reception and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions begin Wednesday evening, June 12, with a Welcome Reception featuring our Keynote Speaker and conclude Friday evening, June 14, with a walk and dinner on Konza Prairie.

SPEAKERS Keynote Speaker: Denise Montell, Duggan Professor and Distinguished Professor from University of California Santa Barbara

Featured Speakers Include: + Kerri Coons, University of Wisconsin-Madison, USA + Conor McMeniman, John Hopkins Bloomberg School of Public Health, USA + Shahideh Nouri, Kansas State University, USA + Luisa Orsini, University of Birmingham, UK + Mark Rebeiz, University of Pittsburgh, USA + Stephane Rombauts, Ghent University, Belgium + Surya Saha, Boyce Thompson Institute, USA + Nick Teets, University of Kentucky, USA + Yoshi Tomoyasu, Miami University, USA + Jamie Walters, University of Kansas, USA

ABSTRACT PRESENTATIONS Abstract presentations will be scheduled throughout the sessions on Thursday and Friday of the symposium. This years sessions include: i5K/Comparative Genomics, Stress Response, Microbiome, Evo/Devo, Vector Biology & Bioinformatics. If interested in submitting an abstract for oral consideration during one of these sessions, visit the website at www.k-state.edu/agc/ags. Abstracts are due Monday, March 11 for oral presentation consideration.

QUESTIONS: Contact Symposium Coordinator, Kascha Johnson at kascha@k-state.edu

If you would like to join the ArthropodNews list to ensure receiving future notices, please send an email with your name and email address to kascha@k-state.edu.

>From the 2019 SYMPOSIUM ORGANIZING COMMITTEE:

Sue Brown, Neal Dittmer, Maureen Gorman, Mike Kanost, Berlin Londono, Jocelyn McDonald, Mary Ann McDowell, Kristin Michel, Yoonseong Park, Mike Pfrender, Hugh Robertson, Gene Robinson, Molly Scheel

Kascha Johnson Symposium Coordinator 2019 Arthropod Genomics Symposium Division of Biology Kansas State University kascha@k-state.edu

Kascha Johnson <kascha@ksu.edu>

## Manhattan Kansas ArthropodGenomics Jun12-14 TravelGrantApplications

TRAVEL GRANT applications DUE March 31! Accepting ABSTRACTS for Poster Session! REGISTRATION is OPEN! V June 12-14, 2019 V 12th Annual Arthropod Genomics Symposium at KSU Manhattan, KS

PLEASE SHARE THIS ANNOUNCEMENT WITH COLLEAGUES AND STUDENTS!

Hi All:

Planning is well underway for the 2019 AGS that is returning to KSU in Manhattan, KS. Visit our website at www.k-state.edu/agc/ags for more details about the symposium.

TRAVEL GRANT V Applications Due March 31 + Vector biology travel grants are sponsored by the University of Notre Dames Eck Institute for Global Health. + Postdoc & student travel grants are sponsored by the Kansas State University Arthropod Genomics Center. + More information on the travel grants can be found at https://www.k- state.edu/agc/ags/travel_grants/index.html.

REGISTRATION Register online at the Symposium website, www.k-state.edu/agc/ags! KEY DEADLINES Sunday, March 31 V Travel Grant Applications Due Sunday, May 19 V Early Registration Deadline Monday, May 20 - Abstracts Due for Poster Sessions

OVERVIEW The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, welcome reception and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions begin Wednesday evening, June 12, with a Welcome Reception featuring our Keynote Speaker and conclude Friday evening, June 14, with a walk and dinner on Konza Prairie.

SPEAKERS Keynote Speaker: Denise Montell, Duggan Professor and Distinguished Professor from University of California Santa Barbara

Featured Speakers Include: + Yehuda Ben-Shahar, Washington University in St Louis, USA + Kerri Coon, University of Wisconsin-Madison, USA + Nsa Dada, US Centers for Disease Control and Prevention, USA + Conor McMeniman, John Hopkins Bloomberg School of Public Health, USA + Shahideh Nouri, Kansas State University, USA + Luisa Orsini, University of Birmingham, UK + Mark Rebeiz, University of Pittsburgh, USA + Stephen ¥Fringy Richards, University of California Davis, USA + Stephane Rombauts, Ghent University, Belgium + Surya Saha, Boyce Thompson Institute, USA + Nick Teets, University of Kentucky, USA + Yoshinori Tomoyasu, Miami University, USA + James Walters, University of Kansas, USA

POSTER SESSION Poster session will be scheduled for both Thursday and Friday of the symposium. This years sessions include: i5K/Comparative Genomics, Stress Response, Microbiome, Evo/Devo, Vector Biology & Bioinformatics. If interested in submitting an abstract for the poster session, please visit the website at www.k-state.edu/agc/ags. Abstracts are due for the Poster Session on Monday, May 20.

QUESTIONS: Contact Symposium Coordinator, Kascha Johnson at kascha@k-state.edu

If you would like to join the ArthropodNews list to ensure receiving future notices, please send an email with your name and email address to kascha@k-state.edu.

2019 SYMPOSIUM ORGANIZING COMMITTEE:

Sue Brown, Neal Dittmer, Maureen Gorman, Mike Kanost, Berlin Londono, Jocelyn McDonald, Mary Ann McDowell, Kristin Michel, Yoonseong Park, Mike Pfrender, Hugh Robertson, Gene Robinson, Molly Duman-Scheel

Kascha

Kascha Johnson Symposium Coordinator 2019 Arthropod Genomics Symposium Division of Biology Kansas State University kascha@k-state.edu

Kascha Johnson <kascha@ksu.edu>

---

## Marseilles 23rdEvolutionaryBiology Sep24-27

We are organizing again the evolutionary biology meeting at Marseilles ( 24-27 2019 )

The DL is end of june

more info aeeb.fr and twitter :EvolBiolMeetingMarseilles

The Evolutionary Biology Meeting at Marseilles is an annual congress which has gathered high level experts in evolutionary biology since its creation in 1997.

If the congress was initially a local meeting, it quickly gained an important weight in the scientific life. Indeed, whereas the number of participants has been increasing, the geographical origin of the researchers has been diversifying and widening year by year.

Today, the Evolutionary Biology Meeting at Marseilles has reached a worldwide dimension and plays a paramount role in the international scientific life: allowing the gathering of high level specialists, it encourages the exchange of ideas and stimulates the works of the researchers all through the world.

The following subjects will be discussed:

* Evolutionary biology concepts and modeling; * Biodiversity and Systematics; * Comparative genomics ans post-genomics (at all taxomic levels); * Functional phylogeny; * Environment and biological evolution; * Origin of life and exobiology; * Non-adaptative versus adaptative evolution; * The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge; * Convergent evolution * Evolution of complex traits (Evo-Devo)

Best regards

Pierre

< https://twitter.com/pontarotti >

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

---

## Maryland Batrafest2019 May3

Subject: Batrafest 2019, A Symposium for Dr. Suzanne Batra. May 3, 2019, Maryland, USA

Join us and Dr. Suzanne Batra for a Symposium honoring Suzanne's long and varied career, from pioneering work with eusocial bees to numerous applied and fundamental discoveries in bees and the environment. As a bonus, Suzanne will give the final word on what she meant when she coined the term "eusocial" 55 years ago! May 3, 2019, USDA Log Lodge, Beltsville, MD 20705

- 8:30-9:30- Signing in and Coffee, USDA Log Lodge, Beltsville, MD USA - 9:30 Dr. Jay Evans, USDA-ARS Bee Research Lab, "Suzanne at the USDA" - 9:45: Dr. Francisco Posada-Florez, USDA-ARS Bee Research Lab, "Suzanne's diverse contributions to bee science" - 10:00- Plenary Lecture: Dr. Miriam Richards, Brock University, " "Sweat bees, carpenter bees, and the (slowly) evolving definition of insect sociality" - 10:30-10:45 Break - 10:45- Plenary Lecture: Dr. Sarah Kocher, Princeton University, "The interplay of genes and ecology in the evolution of eusociality". - 11:15 Dr. Suzanne Batra "You say Eusocial: what did I say? And a life with bees" - 12:00 ' 1:00 Lunch, sandwiches - 1:00-3:00 10 additional speakers (selected from attendees) - 3:00-5:00 Discussions and a tour of Suzanne's bee pastures and nesting sites - 5:00- 7:00 Catered Dinner, Indian food - Optional field trips on May 4

$50 FOOD AND DRINK CONTRIBUTION, $20 FOR STUDENTS https://www.tickettailor.com/-events/awoolfarm/247858 Jay Evans and Francisco Posada-Florez (USDA), Miriam Richards (Brock Univ), Sarah Kocher (Princeton Univ)

Dr. Jay Evans Research Leader USDA-ARS Bee Research Lab BARC-E Bldg 306 Beltsville, MD 20705 USA Ph 301-504-5143 FX 301-504-8736, jay.evans@ars.usda.gov https://-/orcid.org/0000-0002-0036-4651 "Evans, Jay" <Jay.Evans@ARS.USDA.GOV>

---

## MexicoCity PoeciliidEvolution Sep24-26

This informs of the incoming Conference of Poeciliid Biologists. This is a specialists meeting with a strong focus on evolution, and indeed some Poeciliid fish such as the guppy and the swordtail are paradigmatic species in the study of the evolutionary consequences of sexual selection and on the evolution of life histories.

Dear all

We are organising the 8th Conference of Poeciliid Biologists, to take place on the 24-26 of September 2019 in Mexico City, at the main campus of the Universidad Nacional Autonoma de Mexico (UNAM).

As in previous editions, this meeting will gather experts who use species of Poeciliid fishes to address, mainly, evolutionary questions, or questions about other issues (e.g. conservation) seen through an evolutionary optic. Information on the venue, program, submission and registration forms can be found here:

https://biologia-ue.fciencias.unam.mx/-poeciliidconference/index.php There are still places available for the conference, and we will inform in the above page if and when vacancies are exhausted.

Please address any questions to:

poeciliids.mex@iecologia.unam.mx

On behalf of Los Poecilistas

Constantino

Constantino Macas Garcia Director Instituto de Ecologa, UNAM (http://web.ecologia.unam.mx/) Phone: +5255 56229044 Fax: +5255 56161976

maciasg <maciasg@unam.mx>

## Montpellier DomesticationEvolution Jun3-7

Harlan III Symposium 3-7 June 2019, Montpellier - Extended deadline 25th March

Dear Colleagues,

The Call for abstracts for the Third Harlan Symposium Dedicated to the Origins of Agriculture and the Domestication, Evolution, and Utilization of Genetic Resources is still open : the deadline is extended until the 25th of March !

Do not hesitate to come and share your work and results with the community : four sessions cover a broad range of research Session 1 : History of Agriculture Session 2 : Diversity and Adaptation Session 3 : Mobilizing genetic resources Session 4 : Agrosystem services and functioning

We also strongly encourage students, PhDs and post-docs to submit their work - all career stages welcome !

Visit the symposium website for more information and details : https://www.alphavisa.com/harlan/2019/-index.php Hope to see you all in June in Montpellier,

Anne-Céline THUILLET On behalf of the organizing committee

Anne-Céline THUILLET <anne-celine.thuillet@ird.fr>

## Nottingham UK EndosymbiontEvolution Apr25-26

On behalf of the organising committee we would like to invite you to the Joint Insect Endosymbiont and Infection and Immunity meeting due to be held between the 25th and 26th of April 2019 at the University of Nottingham, UK.

We are pleased to announce our invited speakers for this meeting are Lucy Weinert, University of Cambridge (Insect Endosymbionts) and Sheena Cotter, University of Lincoln (Insect Infection and Immunity).

The conference websites and registration information can be found here (both sites contain the same text): https://www.royensoc.co.uk/meeting/-endosymbiont https://www.royensoc.co.uk/meeting/-infection-immunity The deadline for registration and abstract submission will be the 7th April 2019.

Venue: School of Life Sciences, University Park, University of Nottingham

All communication should be made using the gmail address provided: insectinfect19@gmail.com

We hope to see you there!

Ella Deutsch <Ella.Deutsch1@nottingham.ac.uk>

## Portland Oregon Sex Asex Jun2-4

Don't forget to register for AGA2019! Early bird registration ends on April 15.

Sex & Asex: The Genetics of Complex Life Cycles American Genetic Association President's Symposium 2-4 June 2019, Portland, Oregon

Many organisms across the tree of life have complex life cycles that include both sexual and asexual reproduction or are obligately asexual. Recently, scientists have been applying both theory and empirical work, including genomic and genetic studies, to untangle the evolutionary effects of the amount and timing of sexual and asexual reproduction.

Join AGA President Maria Orive at beautiful McMenamins Edgefield. AGA symposia are small, friendly gatherings and provide wonderful opportunities for researchers and students to engage with one another and share their science.

Details on the AGA website: http://www.theaga.org . Speakers include: Key Distinguished Lecturer Sally Otto Rebecca Zufall, University of Houston Stacy Krueger-Hadfield, University of Alabama at Birmingham Matthew Hartfield, University of Edinburgh Laura Katz, Smith College Tanja Schwander, University of Lausanne, Switzerland Curt Lively, Indiana University Catherine Rushworth, UC Davis Solenn Stoeckel, INRA Rennes, France Jennifer Anderson, Uppsala University, Sweden Mercedes Burns, University of Maryland Jeannette Whitton, University of British Columbia

ccough-schulze@cvm.tamu.edu

---

## PrincetonU EvolutionInfectiousDiseases Jun10-13

Dear all,

Registration and abstract submission are now open for the 2019 conference on the Ecology and Evolution of Infectious Disease (EEID), to be held at Princeton University, New Jersey, USA, from 10-13 June. Please see this URL for more info and instructions on how to register and to submit an abstract: http://ideas.princeton.edu/eeid-2019/ Please note that the abstract submission deadline is 15 April. We will accept registrations until we reach conference capacity (@0) or 15 May, whichever comes first.

Contributed talks and posters on any topics in infectious disease ecology and evolution are welcome. By design and due to its modest size, the EEID conference provides plenty of opportunities to interact one-on-one with other researchers.

The conference will also offer invited talks on behavioral, genetic, and environmental drivers of disease dynamics, plus talks on within-host competition and evolution in response to medical interventions. A related pre-EEID workshop V Evolutionary Consequences of Feedbacks Between Within-host Competition and Disease Control X is available by application: http://ideas.princeton.edu/future-workshops-2/ Looking forward to seeing you in June!

All the best, Andrea L Graham, on behalf of the Princeton Disease Group

algraham@Princeton.EDU

---

## Roscoff France VirusEvolution Oct21-25

Dear all,

we are please to anounce that the Jacques Monod Conference entitled “Virus evolution on the mutualist - parasite continuum” will be held in Roscoff (Britany, France) on October 21-25, 2019.

The deadline for abstract submision is June 21st.

More details about the conference can be found here: https://www.insb.cnrs.fr/virus-evolution-mutualist-parasite-continuum The list of invited speakers is the following:

Samuel Alizon (Montpellier, France), chairperson Raul Andino (San Francisco, USA) Megan Baldridge (St Louis, USA) Monsef Benkirane (Montpellier, France) Ignacio Bravo (Montpellier, France) Siobain Duffy (Rutgers, USA) Christophe Fraser (Oxford, United Kingdom) Fernando Garcia-Arenal (Madrid, Spain) Clement Gilbert (Gif-sur-Yvette, France) Katia Koelle (Emory, USA) Eugene Koonin (Bethesda, USA) Philippe Lemey (Louvain, Belgium) Alice McHardy (Helmholtz, Germany) Yannis Michalakis (Montpellier, France) Marie-Agnes Petit (Jouy-en-Josas, France) Gwenael Piganeau (Banyuls, France) Thomas Pradeu (Bordeaux, France) Andrew Read (Penn State, USA) Roland Regoes (Zurich, Switzerland) Marilyn Roossinck (Penn State, USA) Carla Saleh (Paris, France) Rafael Sanjuan (Valencia, Spain) Pauline Scanlan (Cork, Ireland) Manuela Sironi (Bosisio Parini, Italy) Paul Turner (Yale, USA), vice-chairperson Stineke van Houte (Exeter, UK) Anne-Nathalie Volkoff (Montpellier, France) Lena Wilfert (Ulm, Germany)

Please do not hesitate to circulate this announcement!

- Samuel

– Samuel Alizon

MIVEGEC, CNRS, IRD, Université de Montpellier IRD, 911 Avenue Agropolis, BP 64501 34394 Montpellier Cedex 5, France

Phone: +33 4 48 19 18 67 Fax: +33 4 67 41 62 99

http://alizon.ouvaton.org/ Samuel Alizon <samuel.alizon@cnrs.fr>

## Toulouse CulturalEvolution May23-24

Dear colleagues,

Registrations for the 7th Toulouse Economics and Biology Workshop - Cultural Evolution, May 23-24, 2019 are now open. Please register HERE < https://www.iast.fr/registration_form_eco_bio_workshop >

We will circulate a preliminary program shortly.

The speakers are: Erol Ak??ay < https://www.bio.upenn.edu/people/erol-akcay >, University of Pennsylvania

??ric Crub??zy < http://amis.cnrs.fr/?Crubezy-Eric >, CNRS - AMIS Universit?? Paul Sabatier

Maxime Derex < https://lillethics.com/maxime-derex/ >, University of Exeter and Universit?? Catholique de Lille

Marcus Feldman < https://www-evo.stanford.edu/marc.html >, Standford University

Herb Gintis < https://people.umass.edu/gintis/ >, UMass Amherst and Santa Fe Institute

Barry Hewlett < http://anthro.vancouver.wsu.edu/faculty/hewlett/ >, Washington State University Vancouver

Sabine N??bel < https://scholar.google.de/citations?hlÃ&user=ZjLy_H4AAAAJ&view_op=list_works&sortby=pubdate >, IAST

Pete Richerson < http://www.des.ucdavis.edu/faculty/richerson/richerson.htm >, University of California Davis

Mohamed Saleh < https://www.tse-fr.eu/people/mohamed-saleh >, TSE, Universit?? Toulouse Capitole, and IAST

Paola Sapienza < https://www.kellogg.northwestern.edu/faculty/directory/sapienza_paola.aspx >, Northwestern Univesity

Jean Tirole < https://www.tse-fr.eu/people/jean-tirole >, TSE, EHESS, and IAST

Thierry Verdier < https://www.parisschoolofeconomics.eu/en/verdier-thierry/ >, Paris School of Economics

Besides the plenary sessions, there will be a poster session to which post-docs and Ph.D. students are most welcome to submit applications (abstract + CV + cover letter) to econbio_poster@iast.fr no later than March 30, 2019.

For any further information please contact us directly at econbio@iast.fr

We look forward to seeing you in May!

Organizers: Ingela Alger and J??rgen Weibull,

Co-organizers: Francesca De Petrillo and Victor Gay

Val??rie Nowaczyk Administrative and Scientific Assistant Assistante Administrative et Scientifique

IAST & TSE Manufacture des Tabacs 21 all??e de Brienne B??t. E - 5e ??tage - ME 503.6 F-31015 Toulouse Cedex 6 Tel.: +33(0) 5 61 12 85 24

The Toulouse Economics and Biology Workshop <econbio@iast.fr>

## Tucson PlantEvol Jul27-31

PLANTS Undergraduate travel awards enhancing diversity at BOTANY 2019 meetings, July 27-31, 2019, Tucson, Arizona botanyconference.org Target date for travel grant applications: April 10, 2019, with a rolling review after that date until all available slots have been filled. Apply soon! Application: https://cms.botany.org/home/awards/travel-awards-for-students/plants-grants.html PLEASE SHARE THIS ANNOUNCEMENT WITH COLLEAGUES AND STUDENTS

PLANTS Grants: Undergraduate Travel Awards Enhancing Diversity at the Botanical Society of America Conferences PLANTS (Preparing Leaders and Nurturing Tomorrow's Scientists: Increasing the diversity of plant scientists) is a program to bring diverse and talented undergraduates to the BOTANY 2019 meeting July 27-31, 2019, in Tucson, Arizona. Funded by the National Science Foundation and Botanical Society of America, the program will support up to 12 undergraduates to attend the entire meeting, discuss scientific talks with mentors (grad student, postdoc, professionals), and participate in networking, professional development, and career-oriented events. The program covers the normal costs of travel, registration, food and accommodation at the meeting. An overview of the scientific conference is available at: botanyconference.org

Topics at the conference range across all levels of botany and include presentations on conservation, biodiversity, plant genomics, evolution, plant systematics, and botanical education. There are also a number of social functions, specifically targeted at students for networking and fun. The meetings are a great way to understand the breadth of botanical research and education, to meet undergraduate and graduate students with similar interests, and to network with professionals in your area of interest. This is really a friendly community, so please consider joining us!

DEADLINE: Target date of April 10, 2019 with a rolling review after that date until all available slots have been filled.

APPLICATIONS: Applications will be accepted with a target date of APRIL 10, 2019 and a rolling review after that date until all available slots have been filled. The application includes completion of the online form providing your statement of interest, a letter of recommendation, and unofficial transcripts. Applications are welcome from all domestic undergraduates from the US and Puerto Rico (we are unable to accept applications from international students) who have interest in plant science; the admissions goal is to create a diverse pool of students attending the conference. The application form is located online at https://cms.botany.org/home/awards/travel-awards-for-students/plants-grants.html We encourage you to review the online form thoroughly before filling it out. Please have letters of recommendation and unofficial transcripts sent directly to Heather Cacanindin at HCacanindin@Botany.org.

CONTACTS: If you have questions, please contact one of the organizers: Anna Monfils – anna.monfils@cmich.edu Heather Cacanindin – hcacanindin@botany.org Ann Sakai' aksakai@uci.edu

aksakai@uci.edu

---

## Turku ESEB PolygenicAdaptation Aug19-24

We would like to invite you to submit abstracts to symposium S18 ÕThe genetic architecture of polygenic adaptation: sweeps, small shifts and everything in betweenÕ.

Symposium overview: For decades the identification of selected loci built on population genetic theory predicting Ôselective sweepÕ signatures for selection targets and flanking sequences. Many empirical studies found genomic patterns that are compatible with predictions for hard, soft or incomplete sweeps. Nevertheless, most traits are polygenic as demonstrated by many QTL and GWAS studies. Empirical evidence for genomic signatures of polygenic adaptation has been considered difficult since only small shifts in the allele frequency of (very) many contributing loci are expected. Recent theoretical and empirical work demonstrated, however, that the selection signature of polygenic adaptation can result in substantial allele frequency changes-similar to selective sweeps. Hence, the dynamics of alleles contributing to polygenic adaptation can be traced experimentally, leading to novel insights about adaptive processes. This symposium brings together empirical and theoretical researchers with the intention to explore the genomic signatures of polygenic adaptation. Combining theory with empirical data from natural populations and experimental populations this symposium will provide an important contribution to develop new approaches for the detection of polygenic adaptation.

Invited speakers: Catherine Peichel, University of Bern, Switzerland Joachim Hermisson, University of Vienna, Austria

Abstracts can be submitted up until 23:59 EET on 31.3.2019 (note that Finland is one hour ahead of central Europe!). Submit abstracts here: https://eseb2019.fi/symposia-and-abstracts Looking forward to seeing you in Turku!

Organizers: Christian Schloetterer and Neda Barghi, Institute of Population Genetics, Vetmeduni, Vienna, Austria

Neda Barghi, Ph.D.

Institut für Populationsgenetik

Department für Biomedizinische Wissenschaften

Veterinärmedizinische Universität Wien, Ã-sterreich

ESEB (European Society for Evolutionary Biology) 2019, 19-24 August 2019, Turku, Finland

Neda Barghi <barghi.neda@gmail.com>

## Turku Finland ESEB2019 AbstractDeadline31Mar

This is the final reminder of the ESEB2019 abstract deadline, which is 23.59 on Sunday 31.3 Finnish time (EET)

Finland commences daylight savings time on this day: so equivalent global times are 21.59 in the UK, 22.59 in central Europe, 16.59 in New York, 13:59 in California, 05:59 on 1.4 in Tokyo, 07:59 on 1.4 in Melbourne, Australia

Full details are below

The European Society for Evolutionary Biology (ESEB) organizes Europe's largest evolutionary biology conference every 2nd year. The 17th ESEB congress will be held from 19-23 August 2019 in Turku, Finland, the gateway to the Finnish archipelago. There will be five plenary speaker, as well as 8 concurrent sessions covering 35 themed symposium topics (full list below) plus an open symposium. Each symposium has two invited speakers plus a number of presenters selected from the submitted abstracts. There is a cap of 1300 participants. More details about the congress can be found at https://eseb2019.fi/ The ESEB2019 call for abstracts closes at 23:59 EET on 31.3.2019 (note that Finland is one hour ahead of central Europe!). Submitted abstracts can be modified up until the deadline. The titles of all 36 symposia can be found at the end of this message. More detailed descriptions of each symposium and their invited speakers, as well as the abstract submission system itself can be accessed via the conference web page:

https://eseb2019.fi/symposia-and-abstracts Each congress participant is permitted to submit only one (max. 250 word abstract, max. 15 word title) abstract as a presenter (co-authorships in other abstracts are allowed). The only exception to this rule is that participants can submit a second abstract as a presenter to Symposium 35: Evolution outreach projects: Keep SCREAMing. Submitters have the opportunity to select a first and second preference symposium for their abstract.

Researchers submitting to Symposium 36: Open Symposium are encouraged to read the symposium description for more details about additional information required when submitting to this symposium. This information will assist organisers in arranging Open Symposium presentations into sub-themes not covered by the 35 themed symposia.

The expected length of presentation slots is 15 minutes (10+3+2) for regular presentations and 30 minutes (23+5+2) for invited speakers. Due to the tighter timeline being implemented for abstract submission (in previous ESEB meetings, abstract submissions closed in January), there will be no extension to this deadline.

Abstracts will be blind-evaluated by symposium organisers during April. All abstract submitters will be notified of the fate of their abstract by the end of April, and those being accepted for oral or poster presentations are required to register for the congress by May 10. If they do not register by this date, their talk/poster slot will be offered to other participants, who will have the chance to register prior to general earlybird registration opening on May 15.

Details of grants available for supporting travel and family arrangements can be found on the ESEB website https://eseb.org/prizes-funding/equal-opportunities-initiative/ Equal opportunities initiatives being implemented at ESEB2019 can be found here: https://eseb2019.fi/equal-opportunities We look forward to seeing many of you in Turku in August!

Craig Primmer (on behalf of the organizing committee)

ESEB2019 symposium titles

1. Trans generational plasticity in animals 2. Evolution in real time: experimental evolution approaches 3. Exploring the role of nongenetic inheritance in evolution 4. Cognitive evolution and environment 5. Aging & cancer through the lens of evolution 6. Eco-evolutionary approach to the antimicrobial resistance problem 7. Human-induced evolution 8. Genetics of small populations 9. Microbial genome and community evolution in food environments 10. Rapid Evolutionary Adaptation: Potential and Constraints 11. Quantitative trait effect size distributions and their impact on evolutionary processes 12. Quantifying selection and evolvability in wild plant populations: methods and measurements 13. Genetics and genomics of adaptation 14. The mechanisms of evolutionary change: moving from genomic signatures to functional validation 15. Tracing evolution through time using ancient DNA 16. Mito-nuclear interactions across levels of biological organisation 17. Selfish genetic elements 18. The genetic architecture of polygenic adaptation: sweeps, small shifts and everything in between 19. "Gene-phenotype associations across evolutionary scales 20. The evolutionary consequences of social transmission and animal culture

— / —

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

---

## Turku Finland ESEB2019 AbstractDeadline3Weeks

The European Society for Evolutionary Biology (ESEB) organizes Europe's largest evolutionary biology conference every 2nd year. The 17th ESEB congress will be held from 19-23 August 2019 in Turku, Finland, the gateway to the Finnish archipelago. There will be five plenary speaker, as well as 8 concurrent sessions covering 35 themed symposium topics (full list below) plus an open symposium. Each symposium has two invited speakers plus a number of presenters selected from the submitted abstracts. There is a cap of 1300 participants. More details about the congress can be found at https://eseb2019.fi/ The ESEB2019 call for abstracts is now open for about 3 more weeks, and closes at 23:59 EET on 31.3.2019 (note that Finland is one hour ahead of central Europe!). Submitted abstracts can be modified up until the deadline, and therefore early submission of first drafts is encouraged. The titles of all 36 symposia can be found at the end of this message. More detailed descriptions of each symposium and their invited speakers, as well as the abstract submission system itself can be accessed via the conference web page:

https://eseb2019.fi/symposia-and-abstracts Each congress participant is permitted to submit only one (max. 250 word abstract, max. 15 word title) abstract as a presenter (co-authorships in other abstracts are allowed). The only exception to this rule is that participants can submit a second abstract as a presenter to Symposium 35: Evolution outreach projects: Keep SCREAMing. Submitters have the opportunity to select a first and second preference symposium for their abstract.

Researchers submitting to Symposium 36: Open Symposium are encouraged to read the symposium description for more details about additional information required when submitting to this symposium. This information will assist organisers in arranging Open Symposium presentations into sub-themes not covered by the 35 themed symposia.

The expected length of presentation slots is 15 minutes (10+3+2) for regular presentations and 30 minutes (23+5+2) for invited speakers. Due to the tighter timeline being implemented for abstract submission (in previous ESEB meetings, abstract submissions closed in January), there will be no extension to this deadline.

Abstracts will be blind-evaluated by symposium organisers during April. All abstract submitters will be notified of the fate of their abstract by the end of April, and those being accepted for oral or poster presentations are required to register for the congress by May 10. If they do not register by this date, their talk/poster slot will be offered to other participants, who will have the chance to register prior to general earlybird registration opening on May 15.

Details of grants available for supporting travel and family arrangements can be found on the ESEB website https://eseb.org/prizes-funding/equal-opportunities-initiative/ Equal opportunities initiatives being implemented at ESEB2019 can be found here: https://eseb2019.fi/equal-opportunities We look forward to seeing many of you in Turku in August!

Craig Primmer (on behalf of the organizing committee)

ESEB2019 symposium titles

1 Trans generational plasticity in animals 2 Evolution in real time: experimental evolution approaches 3 Exploring the role of nongenetic inheritance in evolution 4 Cognitive evolution and environment 5 Aging & cancer through the lens of evolution 6 Evo-evolutionary approach to the antimicrobial resistance problem 7 Human-induced evolution 8 Genetics of small populations 9 Microbial genome and community evolution in food environments 10 Rapid Evolutionary Adaptation: Potential and Constraints 11 Quantitative trait effect size distributions and their impact on evolutionary processes 12 Quantifying selection and evolvability in wild plant populations: methods and measurements 13 Genetics and genomics of adaptation 14 The mechanisms of evolutionary change: moving from genomic signatures to functional validation 15 Tracing evolution through time using ancient DNA 16 Mito-nuclear interactions across levels of biological organisation 17 Selfish genetic elements 18 The genetic architecture of polygenic adaptation: sweeps, small shifts and everything in between 19 "Gene-phenotype associations across evolutionary scales

— / —

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

## UCambridge EcologicalGenetics Apr16-18

Dear All,

The countdown is on! ONE week to go to get those abstracts submitted for #EGG2019 < https://twitter.com/hashtag/EGG2019?src=hash >

Talks and Posters welcomed from all career stages! Email them to geb3@aber.ac.uk by the 17th March.

This years conference is to be held on the 16th to the 18th of April at the stunning Downing College, University of Cambridge. There will be a full scientific and social programme throughout the conference to bring together those with an interest in population genetics, ecology and evolution. The programme will include a series of talks and a poster session on relevant topics, as well as a conference dinner and, of course, the now famous EGG-Heads quiz. There will also be the opportunity for a behind the scenes tour of the Sainsbury Laboratory Herbarium at the University. A collection dating back 300 years that will allow you to get up close to specimens collected by the Grandfathers of evolutionary theory, Darwin and Wallace.

Please use the link below for more information.

https://www.eventbrite.co.uk/e/ecological-genetics-group-63rd-annual-meeting-tickets-56404440199?ref=estw Ecological Genetics Group 63rd Annual Meeting Tickets, Tue 16 Apr 2019 at 13:00 | Eventbrite < https://www.eventbrite.co.uk/e/ecological-genetics-group-63rd-annual-meeting-tickets-56404440199?ref=estw > www.eventbrite.co.uk Eventbrite, and certain approved third parties, use functional, analytical and tracking cookies (or similar technologies) to understand your event preferences and provide you with a customised experience.

NB. students you will be in the running for the best student talk/ poster prizes. A nice addition to anyone s CV.

Hope to see you all in Cambridge,

BW

Dr Gemma Beatty (Chair of EGG and past best student poster prize at EGG- many moons ago)

Dr Gemma Beatty

Lecturer in Agri-Environment and Grassland Ecosystems

Institute of Biological, Environmental and Rural Sciences

Aberystwyth University

Penglais

Aberystwyth

Ceredigion SY23 3DA

Email: geb3@aber.ac.uk

Prifysgol Aberystwyth www.aber.ac.uk Prifysgol y Flwyddyn ar gyfer Ansawdd Dysgu - The Times & The Sunday Times 2019.

Aberystwyth University www.aber.ac.uk University of the Year for Teaching Quality - The Times & The Sunday Times 2019.

"Gemma Beatty [geb3]" <geb3@aber.ac.uk>

## UCambridge EcologicalGenetics Apr16-18 AbstDeadline

Hi All,

The abstract deadline, on the 17th March* is fast approaching for EGG2019! So get those talk and poster abstracts rolling in and come and join us at Downing College, University of Cambridge. All welcome! If you work on any aspect of the field of Molecular Ecology, from Population Genetics to Metabarcoding then is a conference not to be missed.

And students do not forget about the prizes for best student talk and poster!

*Send abstracts to geb3@aber.ac.uk

Full conference details cab be found here < https://w/ >

https://www.britishecologicalsociety.org/event/ecological-genetics-group-63rd-annual-meeting/ Ecological Genetics Group 63rd Annual Meeting - British Ecological Society www.britishecologicalsociety.org Join us for the 63rd Meeting of the Ecological Genetics Group at the University of Cambridge for this 3-day conference sponsored by the British Ecological Society and the Genetics Society. There will be a full scientific and social programme throughout the conference, where we hope to bring together those working in the fields of population $B!D(B

Cheers

Gemma

Dr Gemma Beatty Lecturer in Agri-Environment and Grassland Ecosystems Institute of Biological, Environmental and Rural Sciences Aberystwyth University Penglais Aberystwyth Ceredigion SY23 3DA Email: geb3@aber.ac.uk

“Gemma Beatty [geb3]” <geb3@aber.ac.uk>

---

## UppsalaU ConflictAndCooperation May21-22

Just a reminder, registration is open for The Evolution of Cooperation and Conflict: from theory to experimental evaluation.

Research on conflict and cooperation has recently gained momentum due to major theoretical and genomic breakthroughs that have expanded the research horizon. Interestingly, even though the conflict and cooperation communities employ many of the same research tools and frameworks, they often proceed independently of each other. Our goal in this conference is to integrate these two complimentary communities to build new and productive links between them. More details are available at: https://-evolutioncoopconflictconference.wordpress.com/ The conference will take place May 21-22 2019 at Uppsala University.

Registration is free, at: https://www.eventbrite.co.uk/-e/the-evolution-of-cooperation-and-conflict-from-theory-to-genomes-to-phenotypes-tickets-54725551598 There are opportunities for contributed talks and posters. If you would like to contribute a talk, please email a 200 word abstract by April 1 to mank@zoology.ubc.ca. Decisions on talks will be made soon after. If you would like to present a poster, please email the title (no need for an abstract) to mank@zoology.ubc.ca by April 1. In selecting talks, preference will be made for early career researchers.

We have a great list of invited speakers:

Duur Aanen - Associate Professor, Department of Plant Sciences, Wageningen University, Netherlands. Mutualisms, evolution of cooperation.

Sylvia Cremer - Professor, Institute of Science and Technology, Austria. Social insects and social immunity.

Kelly Dyer - Associate Professor, Department of Genetics, University of Georgia, USA. Meiotic drive and intra-genomic conflict.

Urban Friberg - Senior Lecturer, Department of Physics, Chemistry and Biology, Linkoping University, Sweden. Mito-nuclear interactions, sexual conflict over ageing.

Harmit Malik - Group Leader, Basic Sciences Division, Fred Hutchinson Cancer Research Center, USA. Transposable elements and centromere interactions.

Marcus Roper - Professor, Department of Mathematics, University of California, Los Angeles. Cooperation in fungal mycelia.

Tanja Schwander - Assistant Professor, Department of Ecology and Evolution, University of Lausanne, Switzerland. The genomics of sexual conflict and mating system evolution.

Joan Strassmann - Charles Rebstock Professor, Department of Biology, Saint Louis University, USA. Cooperation in Dictystelium.

Stuart West - Professor, Department of Zoology, Oxford University. Theoretical aspects of social cooperation.

Sarah Zanders - Assistant Professor, Department of Molecular and Integrative Physiology, University of Kansas. Meiotic drive and selfish genes.

We look forward to seeing you in Uppsala!

Hanna Johannesson & Judith Mank

Judith Mank Professor and Canada 150 Chair in Evolutionary Genomics Department of Zoology and Biodiveristy Research Centre University of British Columbia

http://www.zoology.ubc.ca/mank-lab/ Judith Mank <mank@zoology.ubc.ca>

---

## YaleU SMBE EvolutionOfCancer Apr12-13

*SMBE Satellite Workshop on the Molecular Biology and Evolution of Cancer*

*Dates:* April 12 and 13, 2019

*Location:* Winslow Auditorium, 60 College Street, Yale University, New Haven, CT

*Meeting description:* More than 1 in 3 people will be diagnosed with cancer during their lifetime, and deaths from the disease were estimated to reach nearly 600,000 in the U.S. alone in 2017. The vast majority of cancer deaths are due to the evolution of therapeutic resistance and metastasis. This emergence of therapy-resistant, metastatic cancer is an evolutionary process, in which a genetically diverse population of cancer cells is subject to selective forces within the body.

This meeting seeks to bridge the gap between the molecular evolutionary community and the cancer biology field. It brings together experts and thought leaders from diverse fields, including molecular biology, cancer biology, genomics, phylogenetics, and evolutionary biology, to address a significant health issue. It will be of interest to cancer biologists and evolutionary biologists alike!

*Website:* https://smbe-cancerandevolution.org/ *Registration is free and space is limited! *

*Organizers: *

*Jeffrey P. Townsend*, Elihu Associate Professor of Biostatistics and of Ecology & Evolutionary Biology, Yale University

*Jason Somarelli*, Medical Instructor, Department of Medicine and Director of Research, Duke Comparative Oncology Group, Duke Cancer Institute

"Lulu Stader (SMBE admin)" <smbe.contact@gmail.com>

---

## Zurich Evolutionandmedicine Aug13-16

April 1 ABSTRACT DEADLINE

The Fifth Annual Meeting of the International Society for Evolution, Medicine, and Public Health will be in Zurich, Switzerland, August 13-16. Students, researchers and clinicians from medicine, nursing, evolutionary biology, ecology, genetics, anthropology, psychology, behavioral ecology and epidemiology are all welcome. Full information at https://isemph.org/2019-Meeting KEYNOTE SPEAKERS

Prof. Dario Valenzano, Max Planck Institute for Biology of Ageing, Germany: African killifishes shed light on the genomic basis of life history trait evolution in vertebrates.

Prof. Verena Schunemann, University of Zurich, Switzerland: Ancient DNA and pathogens: uncovering the past of human diseases

Prof. Bernard J. Crespi, Simon Fraser University, Canada: How evolutionary biology can frame a unified theory for understanding human mental illness.

Prof. Kayla King, University of Oxford, UK: Protectors vs. killers: microbes within the host as drivers of pathogen evolution.

PLENARY TALKS BY PRIZE WINNERS

G.C Williams $5000 Prize winner: Dr. Jessica Marie Hoffman: Is antagonistic pleiotropy ubiquitous in aging biology?

Gilbert Omenn $5000 Prize winner: TBA (Nominate your paper now!)

SYMPOSIA

The Normal and the Pathological: Paul Griffiths

Translational and clinical applications of evolutionary medicine: Nicole Bender

Human Animal Health: Barbara Natterson-Horowitz and Nicole Bender

How does the microbiome affect the brain to moderate neurological disease risk and aetiology? :Molly Fox

Using evidence from the learning sciences to develop effective evolutionary medicine resources: Jay Labov

Palaeopathology and Evolutionary Medicine: Kimberley Plomp, Gillian Bentley, Charlotte Roberts & Sarah Elton

PRECONFERENCE WORKSHOP Oxytocin and social disorders: from evolutionary perspectives to clinical applications

SOCIAL PROGRAM

Tuesday August 13, afternoon: Individual visit of several museums in the near of the University main building, for example the museum of wax moulages https://www.moulagen.uzh.ch/en.html, the zoological museum https://www.zm.uzh.ch/en.html, or the anthropological museum https://www.uzh.ch/cmsssl/en/outreach/museums/anthropologisches-museum.html . Tuesday August 13, evening: Welcome reception with bratwurst and beer (and vegetarian alternatives) on the University main building terrace

Wednesday August 14, evening: Make your own Swiss chocolate! Chocolate factory on the University main building terrace

Thursday August 15, evening: Conference Dinner

Friday August 16, evening: Farewell Dinner

Friday August 16, late evening: Guided night city tour

Saturday August 17, all day: Individual excursions in the surroundings of Zurich. Please visit the Zurich Tourism website https://www.zuerich.com/en . Randolph Nesse <nesse@asu.edu>

# GradStudentPositions

Australia SeastarGenomics . . . 31
Brazil MetagenomicsOfStinglessBees . . . 32
Czechia PopulationGenomicsOfParasites . . . 32
EBI Hinxton Bioinformatics . . . 33
HumboldtU Berlin ParasiteLifeCycleEvolution . . . 33
LundU SpeciesExtinction . . . 34
MacquarieU BehaviouralEvolution . . . 35
MainzU Germany ComputationalPaleogenomics . . . 35
MaxPlanck EvolBio ModelingRapidAdaptation . . . 36
MaxPlanckInst Ploen EvolutionIndividuality . . . 37
MississippiState EvolDefensiveSymbiosis . . . 37
MonashU SexDifferencesAndAdaptation . . . 37
NTNU Trondheim ReindeerPaleoGenomics . . . 38
Paris PlanktonPopulations . . . 39
QueenMaryU AnnelidBacterialSymbiosis . . . 40
Rennes France EvolutionaryBiol . . . 41
SorbonneU Paris EvolutionaryGenomics . . . 42
StockholmCPG AncientMicrobiomes . . . 43
Switzerland ComputationalPhylogenetic . . . 44
Sydney ForestAdaptation . . . 44
Sydney NationalTreeGenomics . . . 45
UAberdeen MicrobialEvolution . . . 46
UAdelaide AncientMarineDNA . . . 47
UBath EvolutionIntelligence . . . 47
UBergen Norway EvolutionaryEcology . . . 48
UExeter CaptivityAdaptation AvianConservation . 49
UExeter SexualSelectionTheoryBacteria . . . 50
UGeneva EvolutionaryBiol . . . 50
UGreifswald Biomathematics . . . 51
UIceland EvolutionCodMovement . . . 51
UIdaho EcologicalGenomicsModeling . . . 52
ULisboa QueensU EvolutionaryBiology . . . 53
UmeaU LandscapeGenomics . . . 53
UNeuchatel MicrobialInteractions . . . 54
UPadova SturgeonConservation . . . 55
UPorto EvolutionaryBiology . . . 56
UPotsdam EvolutionaryRescue . . . 56
UppsalaU ComputationalGenetics . . . 57
UTartu HumanPopGenomics . . . 58
UTechnologySydney RealTimePhylogenetics . . . 59
UVictoria PhytoplanktonBiodiversity . . . 60
UWyoming SalmonidEvolutionAlpineLakes . . . 60
ZFMK Bonn InvertebrateMetabarcoding . . . 61

## Australia SeastarGenomics

We are seeking expressions of interest for two PhD positions for a project investigating genomic patterns of population outbreak dynamics in Crown-of-Thorns Seastars on the Great Barrier Reef, Australia.

Crown-of-Thorns Seastars (CoTS) are among the greatest threats to the corals of the Great Barrier Reef. These coral predators follow a boom-bust cycle and diminish live coral abundance in locations suffering CoTS outbreaks. An Australian Research Council funded project will be examining key hypotheses regarding the spatio-temporal dynamics of outbreaking populations, drawing upon genomic and eDNA enabled tools and methodologies. We are seeking highly motivated individuals with experience or strong interests in some combination of population genomics, landscape genetics, invasive species/pathogen spread dynamics, and population modelling. There may be opportunities to participate in field collections dependant on interest and research diving qualifications. This project is an international collaboration between Cynthia Riginos (University of Queensland, Australia), Sven Uthicke (Australian Institute of Marine Sciences), and Gert Worheide (Ludwig Maximilians Universität Munc hen, Germany).

PhD students would be enrolled and primarily based at the University of Queensland in Brisbane, Qld, Australia. PhD students are likely to take primary responsibility for empirical genomic components of the project with one student focusing on larval quantification of plankton samples via qPCR and spending substantial time at AIMS in Townville, Qld, and a second student focusing on population genomics of the current outbreak. Competitive applicants would have demonstrated relevant research experience in evolution and population genetics (Masters or Honours degree with associated publications) and some experience with bioinformatics and computer scripting (R, python, perl or other relevant language). Full funding (living expenses and fees) for one international student will be provided by UQ. Strongly qualified domestic (Australian and New Zealand) applicants will also be considered but must be eligible and competitive for obtaining an Australian Postgraduate Award. Expression s of interest should include a CV including 3 potential referees and an undergraduate transcript.

Please contact Cynthia Riginos (c.riginos@uq.edu.au) for further details. Review of expressions of interest will start at the end of March and final candidates will be invited to apply to UQ.

c_riginos@icloud.com

---

## Brazil MetagenomicsOfStinglessBees

Graduate Research: Pathogenomics of Stingless Bees Karen L. Haag Lab, Department of Genetics, Post Graduation Program of Genetics and Molecular Biology (PPGBM) Federal University of Rio Grande do Sul - Porto Alegre - Brazil

I am seeking one highly motivated Ph.D. student interested in the evolutionary genomics of host-parasite systems.

The project focuses on the use of large scale sequencing and metagenomics to study the dynamics of the pathogens found in several species of the genus Melipona of Brazil.

Positions are available for 2019. The student in my lab will be supported by CNPq scholarship. Support is guaranteed for four years, contingent upon performance.

Basic knowledge of Portuguese is required.

Please visit: http://www.ufrgs.br/ppgbm/?lang=en for departmental information and www.ufrgs.br/-genomicaevolutiva for information on my research interests.

Inquiries are welcome via email to: karen.haag@ufrgs.br

Karen Haag <karen.haag@ufrgs.br>

---

## Czechia PopulationGenomicsOfParasites

A four year grant-supported phd position is available in the Laboratory of Molecular Ecology and Evolution (at the Biology Centre CAS and University of S. Bohemia in Ceske Budejovice, Czechia). http://jstefka.info The phd applicant will work on two related projects, studying patterns of population genomic diversity modulated by adaptation to parasitism.

- we seek for a candidate interested in population genetics and demography, evolution of pesticide resistance and the role of selection in host-parasite co-evolution. The candidate will work closely with a collaborator in Prague (at the Czech Univ. of Life Sci. https://-

bedbugs.fzp.czu.cz/). - we seek for a person willing to pick up new skills and apply them to solving wetlab and bioinformatic problems as they emerge. The candidate will be encouraged to use his/her own creativity to shape the topic according to their own interests. Upon starting the position, the candidate should hold a master degree in biology (or a related field). Previous bioinformatic and wetlab experience is desirable but not compulsory.

Come to study and do research at a highly international research facility, located in a charming historical city in the south of Czechia within an easy reach of Prague and Vienna, whilst with great outdoors nearby! The offered stipend and salary covers all living costs with a comfortable margin!

To apply, send a motivation (cover) letter and a CV to stefka@paru.cas.cz Applications are welcome until May 30. Ideal position start is July 2019, but later date is negotiable.

For more information go to: http://jstefka.info/Homepage_of_Jan_Stefka/Welcome_files/2019_newPHD.pdf Jan ©tefka, PhD Assistant professor Laboratory of Molecular Ecology and Evolution Institute of Parasitology, Biology Centre, CAS & Faculty of Science, Univ. S. Bohemia Branisovska 31, Ceske Budejovice 37005, CZ

tel.: +420 387 775 409 e-mail: jan.stefka@gmail.com web: www.jstefka.info jan.stefka@gmail.com

---

## EBI Hinxton Bioinformatics

Nick Goldman's research group is recruiting a PhD student at EMBL-EBI, Cambridge. Please pass this on to any likely candidates, or post to any other forums that you think are appropriate. Can be from anywhere, especially EMBL's member nations. Candidates must register by 25 March, and complete applications by 1 April.

We're hoping to recruit a maths/computing/algorithms-savvy student to work on sequence alignment/algorithms for next-gen sequencing.

> programme at @emblebi: https://www.ebi.ac.uk/research/eipp > our group: https://www.ebi.ac.uk/research/goldman > one of our students: https://www.ebi.ac.uk/about/jobs/career-profiles/umberto-perron-phd-student > & another: https://www.ebi.ac.uk/about/jobs/career-profiles/conor-walker-phd-student > EMBL's international PhD programme as a whole: https://www.embl.de/training/eipp > EMBL: https://www.embl.de Nick Goldman http://www.ebi.ac.uk/research/goldman European Molecular Biology Laboratory tel: +44-(0)1223-492530 European Bioinformatics Institute tel: +44-(0)1223-494522 Wellcome Genome Campus, Hinxton, Cambridge CB10 1SD, UK

Nick Goldman <goldman@ebi.ac.uk>

---

## HumboldtU Berlin ParasiteLifeCycleEvolution

POSITION A PhD position in parasite genetics and evolution is available at the Humboldt University in Berlin. The position is grant funded for up to 3 years (65% on payscale E13 TV-L HU).

PROJECT Many parasites have bizarre life cycles in which they infect very different hosts in succession, e.g. an invertebrate, then a fish, and then a bird. How do they survive and thrive in dissimilar hosts? What genetic mechanisms enable these massive ontogenetic niche shifts? The applicant will investigate these questions with experiments using parasitic worms and transcriptomic methods. A primary goal will be to understand the genetic mechanisms enabling parasites to infect very different kinds of hosts within a life cycle. The project provides the opportunity to develop skills in experimental design, next-generation sequencing, big data manipulation, advanced analytics, reproducible research, and scientific publishing. The position is funded for 3 years by the DFG and can serve as the basis for a doctoral dissertation.

REQUIREMENTS Completed degree in Biology, Molecular Biology, Bioinformatics, Genetics, or a related discipline Strong interest in parasites, evolutionary biology, and/or genetics Affinity for statistics, data analysis, and programming (in R or Python) Previous work with NGS data a plus Experience with animal experiments and fine motor skills to handle small organisms Creativity and a willingness to develop ideas independently Excellent English skills, German helpful

LOCATION The project is based at the Institute for Molecular Parasitology at the Humboldt University-Berlin and includes collaborators from the Leibniz-Institute of Freshwater Ecology and Inland Fisheries, the University of Münster, and the University of Edinburgh. The Institute for Molecular Parasitology is in central Berlin and located near the University's medical school and other research institutions. The labs are equipped for nearly all types of molecular biology studies. The successful candidate will be part of a small, new research group led by Dan Benesh, while at the same time having access to institutional resources and a larger network of students and researchers. Berlin is the largest city in Germany and it offers something for every taste ' a unique history, world-renowned museums, a hub of creative industries, legendary nightlife, and large green spaces.

APPLICATION DEADLINE 18.04.19

START DATE As soon as possible, though this is somewhat negotiable.

APPLICATION PROCESS Send applications (cover letter, CV, contact info for two references) to Dr. Dan Benesh at Institut für Biologie, Molekulare Parasitologie, Philippstr. 13, Haus 14, 10115 Berlin, or preferably by email as a PDF file to dbenesh82@gmail.com

Dan Benesh <daniel.benesh@hu-berlin.de>

---

## LundU SpeciesExtinction

Doctoral student in Biology

Lunds Universitet, Naturvetenskapliga fakulteten, Biologiska institutionen

Lund University was founded in 1666 and is repeatedly ranked among the world??s top 100 universities. The University has 40 000 students and 7 400 staff based in Lund, Helsingborg and Malm??. We are united in our efforts to understand, explain and improve our world and the human condition.

The Faculty of Science conducts research and education within Biology, Astronomy, Physics, Geosciences, Chemistry, Mathematics and Environmental Sciences. The Faculty is organized into nine departments, gathered in the northern campus area. The Faculty has approximately 1500 students, 330 PhD students and 700 employees.

Project description: The fact that climate change can cause extinction of species is established, but our ability to study and quantify causality of such effects is challenging. Reliable predictions about future extinctions are thus also elusive. The aim of this project is to develop theory and quantitative methods that can improve our understanding and prediction of ecological and evolutionary processes that structures and maintains biological communities. The Ph.D. student should thus have basic knowledge of how ecological interactions, evolutionary processes, and dispersal of organisms in a variable environment can affect the structure and dynamics of communities. A particular focus will be on the phylogenetic difference between communities (phylobetadiversity), a metric of community structure that contains signals of both ecological, evolutionary and biogeographical processes. The student will formulate general theory of the causal link between process and phylobetadiversity through analysis of spatially explicit eco-evolutionary models. Theory will also be tested against empirical patterns through parametrization and validation of the models, given available data. There will be a particular focus on hummingbird community data from the Andes, which is a global biodiversity hotspot. By fitting models to hummingbird data, we aim to quantify the processes that have structured this unique ecosystem, and possibly predict how this system may respond to future conditions.

The project is at its start-up phase and part of the start-up of Dr. Mikael Pontarp??s research group at Lund University. The student will thus have the opportunity to contribute to the profile of the project as well as the direction it may take. To be able to utilize such an opportunity the student needs to be independent and persistent. In addition, to succeed in a theoretical and quantitative project like this, the student needs experience in and interest of differential equation models, agent-based simulations, evolutionary analysis, and statistics. The project is expected to be carried out in collaboration with Prof. ??ke Br??nnstr??m at Ume?? Univeristy, Sweden who will serve as assistant supervisor.

Requirements and qualifications: The candidate should have a Masters degree in ecology/evolutionary biology. Alternatively, the candidate may have a degree in Physics, Mathematics or computer science. Knowledge of interacting ecological, evolutionary and biogeographical processes that underpin community structure and dynamics is desirable. Candidates also need to have proficiency, but not necessarily documented, in working with mathematical modeling, computation and computers and programming, e.g. in Matlab, Python, Julia, C++, etc. Knowledge of model parameterization and validation and Bayesian statistics is also desirable. Important qualities in a successful candidate are outgoing, curiosity, problem-solving, structured, independent and persistent.

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

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

Type of employment: Limit of tenure, four years according to HF 5 kap 7??.

Application: The application should include: * a personal letter with a brief description of qualifications, research interests, motivations, and contact information * a curriculum vitae * authenticated copies of degree certificates and copies of relevant work such as master??s thesis or articles that you have authored or

— / —

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

---

## MacquarieU BehaviouralEvolution

1 PhD position in Behavioural Ecology The Fish Lab, Department of Biological Sciences, Macquarie University, Sydney, Australia.

We are looking for a PhD student to join The Fish Lab for a 3 year project investigating the fitness consequences of laterality and personality in rainbowfish.

Start date: Semester 2 2019

Background:

We are looking for a student to be based at Macquarie University with a one year stint at Groningen as part of a Cotutelle agreement. The project in Sydney, primarily supervised by Prof. Culum Brown, will focus on the cognitive consequences of laterality and personality. Our artificial streams and ponds lend themselves to the possibility of examining the long-term fitness consequences of behaviour under semi-natural conditions.

Macquarie has a 3 year PhD program thus the student can enrol any time from mid 2019. The student will join a large, collaborative lab ( www.thefishlab.com) which specialises in studying the behaviour, ecology and evolution of a range of marine and freshwater species.

MQ has strict PhD entry requirements ( https://www.mq.edu.au/research/phd-and-research-degrees/how-to-apply) and the candidate must demonstrate English proficiency.

Contact: Prof. Culum Brown. Culum.Brown@mq.edu.au

– Prof. Culum Brown Director HDR Biology Dpt Biological Sciences Macquarie University Assistant Editor Journal of Fish Biology thefishlab.com

Culum Brown <culumbrown@gmail.com>

---

## MainzU Germany ComputationalPaleogenomics

1 PhD position in Computational Palaeogenemocis Palaeogenetics Research Group, Institute of Organismic and Molecular Evolution, Johannes Gutenberg University Mainz, Germany.

I am looking for a PhD student to join my research group in Mainz Germany. PhD position (3 years): genome-wide view of human adaptation to novel selective environments using ancient genomes

Start October 2019 Application deadline: May 22 - 2019

Scientific Background - Recent studies have shown significant differences in DNA methylation patterns between different ethnic groups and life-styles. - DNA post-mortem damage patterns in ancient genomes can be used to computationally infer genome wide cytosine methylation maps. Palaeogenomes therefore provide the opportunity to study genetic and epigenetic variation in extinct populations and to make inference on recent selective processes in human populations.

The Palaeogentics Group of the University of Mainz, Germany (http://palaeogenetics-mainz.de) is looking to recruit a PhD Students to begin in fall 2019. The PhD will be under the supervision of Joachim Burger. The student will study evolutionary trajectories of adaptive regulatory region variation by analysing time-series of prehistoric genomes extracted from archaeological skeletons.

We are seeking a highly motivated person with a strong interest in human evolution, statistical genomics, computer tools, and anthropology in general. The successful candidate is expected to have a background in computational genetics, bioinformatics, statistics, or population genetics. He/she will be part of a larger research team with a strong focus on the evolution of regulatory mechanisms.

Requirements: Master degree in biology, mathematics, informatics, statistics, or equivalent; Skills in population genetics, biostatistics, bioinformatics Skills in modelling and programing are an asset

Interested students are encouraged to (also) apply to the International PhD Programm (IPP) at https://www.imb.de/students-postdocs/international-phd-programme/ deadline: May 22 2019

Joachim Burger Professor of Anthropology jburger@uni-mainz.de +49 - (0)6131 V 3924489 http://-palaeogenetics-mainz.de "Burger, Prof. Dr. Joachim" <jburger@uni-mainz.de>

---

## MaxPlanck EvolBio ModelingRapidAdaptation

PhD position in Mathematical Evolutionary Biology, Research Group Stochastic Evolutionary Dynamics, Max Planck Institute for Evolutionary Biology

I am looking for a PhD student to join my research group at the Max Planck Institute for Evolutionary Biology.

PhD position (3 years): Rapid adaptation to environmental change

Populations that are threatened by environmental change may escape extinction through adaptive evolution ("evolutionary rescue"). The goal of the project is to develop mathematical models to describe the eco-evolutionary dynamics of rapid adaptation and to determine the probability of evolutionary rescue. Depending on the interests of the students, the models can be situated in an ecological context or in a medical context (evolution of drug resistance, see also below).

The ideal student will be one who is interested in applying mathematical modeling to gain insights into biological problems and is enthusiastic about math as well as about biology. The successful student will learn how to set up and analyse theoretical models to describe biological processes and become skilled in using branching process theory as a modeling tool. Applicants should have a background in mathematics, physics, biology, computer science or a related field. Good quantitative skills are essential. Prior experience in mathematical modeling and knowledge of a programming language (C, C++, Java, R, Python...) is an advantage.

Association with the International Max Planck Research School (IMPRS) for Evolutionary Biology is possible.

Interested students are encouraged to (also) apply to the International Max Planck Research School for Evolutionary Biology (deadline: March 24): www.evolbio.mpg.de/imprs Working environment

The student will join a young group at the Max Planck Institute for Evolutionary Biology. In our group, we focus on exploring the role of stochasticity in evolution. In the context of resistance evolution, we closely collaborate with experimental microbiologists at the University of Kiel. The group is part of the Department of Evolutionary Theory. The student will hence be part of a larger community of researchers working at the intersection of mathematics and biology with many opportunities to take part in journal clubs, reading groups etc.

The Max Planck Institute is a lively institute with three departments (Evolutionary Theory, Microbial Population Biology, Evolutionary Genetics) and several additional research groups. It hosts several workshops per year and continuously welcomes international short-term and long-term visitors, creating a stimulating and positive research environment. We maintain close interactions with Kiel University and belong to the Kiel Evolution Center. The area is a center of evolutionary biology in Germany.

Plön

Plön is a small town, embedded into a beautiful landscape with innumerous lakes and close to the Baltic Sea. The area provides ample opportunity for free time activities such as swimming, canoeing, or biking in a stunning environment. At the same time, the cities of Kiel and Lübeck (â¥200,000 inhabitants) are only half an hour train ride away. Hamburg (Germany's second largest city) can be reached within 1.5h by train.

Application Interested students should send their application (motivation letter, CV, copies of certificates, contact details of two references) by email to uecker@evolbio.mpg.de. Please use the code PhD2019/Postdoc2019 in the subject line.

Application deadline is April 7, 2019. However, the position will remain open until filled by a qualified candidate.

Contact: Dr. Hildegard Uecker Research group Stochastic Evolutionary Dynamics Department of Evolutionary Theory Max Planck Institute for Evolutionary Biology Website: web.evolbio.mpg.de/stochdyn Email: uecker@evolbio.mpg.de Phone: + 49 4522 763-536

Hildegard Uecker <uecker@evolbio.mpg.de>

---

## MaxPlanckInst Ploen EvolutionIndividuality

Ecological Scaffolding and the Evolution of Individuality

A graduate position is available for a highly motivated, career-minded individual at the Max Planck Institute for Evolutionary Biology (Department of Microbial Population Biology), in Plön, Germany.

The successful candidate will be intrigued by questions posed by major evolutionary transitions. S/he will have a background in quantitative biology / biophysics / engineering. The project will centre around experimental bacterial populations and involve a combination of millifluidics, genomics and theory. Ability to script is essential; a sense of humour, a bonus.

For further information contact Paul Rainey (rainey@evolbio.pmg.de). Applications comprising CV, letter of motivation and short essay (no more than 1,000 words) on “why major evolutionary transitions matter” should be sent to Britta Baron (baron@evolbio.mpg.de).

Paul B Rainey <rainey@evolbio.mpg.de>

---

## MississippiState EvolDefensiveSymbiosis

A Ph.D. position in the evolution of parasite-host interactions is available in the Department of Biological Sciences at Mississippi State University. We seek a motivated student interested in interactions between insects, microbial and multicellular parasites, and defensive symbionts.

Understanding how parasites interact with the insect innate immune system is fundamental to our knowledge of insect health and disease transmission. These interactions are often thought of as antagonistic, but in many insects, microbes help defend the host against infection. In our lab, we use Drosophila as a model system to investigate partnerships between insects and defensive microbes. We work to understand the mechanisms underlying microbe-conferred defenses, how they have evolved, and how they impact the evolution of parasites and pathogens.

Available projects focus on the evolution of toxin specificity in Drosophila-Spiroplasma defensive symbiosis, the role of domesticated RNA virus genes in insect immunity, and the evolution of Wolbachia-mediated RNA virus defense in insects.

Interested applicants should contact Dr. Matthew Ballinger (ballinger@biology.msstate.edu) with a description of research interests, experience, and a CV. Questions and discussion prior to submission of the application materials are welcome. Support is available through both teaching and research assistantships. For full consideration for the fall semester, applications should be submitted to the department by July 1, 2019. More information about graduate studies in the Department of Biological Sciences can be found at https://-www.biology.msstate.edu/degrees/graduate/ . Matthew Ballinger Mississippi State University Dept. of Biological Sciences 295 E Lee Blvd. Mississippi State, MS 39762 Email: ballinger@biology.msstate.edu Phone: (662) 325-0177

ballinger@biology.msstate.edu

---

## MonashU SexDifferencesAndAdaptation

An opportunity is available for a PhD student to join the research groups of Carla SgrÃÂ$^2$ and Tim Connallon at Monash University (Melbourne, Australia).

We are seeking a creative and motivated student who wishes to carry out original research on the evolution of local adaptation. Species with broad geographic ranges have evolved the capacity to thrive under a wide range of environmental conditions that vary with latitude, altitude, and seasonality. Each species must therefore cope with variable climatic conditions (e.g., heat stress, water availability) and variation in resources, predators, prey, and parasites. Environmental differences among locations in a species' range generate local patterns of natural selection, which drive evolutionary diversification among populations of a species.

Processes of local adaptation are more complex ’ and interesting ’ in species with separate sexes. Females and males interact with their environments in different ways, which can generate different patterns of selection between the sexes. Sex differences in selection and the genetic basis of ecologically important traits directly impact the capacity of populations to adapt to local conditions, with potential ecological consequences for species' range limits and extinction susceptibility.

We have an ongoing collaboration that seeks to address several open-ended questions about the roles of sex differences and environmental change in adaptive evolution. These questions include: Â To what extent do geographically variable patterns of natural selection differ between the sexes, and do such differences promote or inhibit local adaptation? Â What are the contributions of different regions of a genome ’ including sex chromosomes, autosomes, and the mitochondrial genome ’ to local adaptation? Â To what extent do the sexes differ in phenotypic plasticity, and how do such differences affect population persistence, the evolution of species' range limits, and the expression of sexual dimorphism? Â How do variable environmental conditions impact the genetic architecture of female and male traits, and how might this influence adaptive potential in changing environments?

We address these questions through a combination of new theory development and lab and field experimental work on Drosophila populations from eastern Australia, which span tropical climates in the north to highly seasonal temperate climates in the south. Representative publications can be found below.

The successful candidate will contribute to this collaboration. Specific research plans will be developed with the student, and tailored to match their interests, strengths and goals. Individuals with a background in biology or a related field are invited to apply, and those with strong quantitative skills are particularly encouraged. A deep interest in evolutionary biology is essential.

The successful candidate will be fully funded for 3.5 years (full tuition waiver plus stipend) for full time research and no teaching requirements; funded opportunities to contribute to teaching will, however, be available for candidates who wish to do so. Expenses for research, coursework, and conference attendance will also be covered. Both domestic and international students are welcome to apply.

Monash University is a member of Australia's Group of Eight coalition, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences is home to a collegial and interdisciplinary research environment, with strengths in ecology, genetics and evolutionary biology. The Monash doctoral program includes additional training opportunities beyond the research program that enhance employability post degree. Monash is located in Melbourne, one of the most liveable cities in the world and a cultural and recreational hub. To apply, please send a CV, an academic transcript copy (official or unofficial), and a brief outline of research interests to carla.sgro@monash.edu and tim.connallon@monash.edu. Informal inquiries are also welcome at the same addresses. Applicants must hold a Bachelor's degree with first-class honours (4th-year undergraduate research project) or a master's degree. Review of applications will begin immediately, and continue until the position is filled.

Representative publications:

Lasne C, Van Heerwaarden B, SgrÃÂ$^2$ CM, Connallon T. 2019. Quantifying the relative contributions of the X chromosome, autosomes and mitochondrial genome to local adaptation. Evolution 73:262-277.

Connallon T, SgrÃÂ$^3$ CM. 2018. In search of a general theory of species' range evolution. PLoS Biology 16:e2006735.

Connallon T, Débarre F, Li XY. 2018. Linking local adaptation with the evolution of sex differences. Phil Trans Roy Soc B 373:20170414

Lasne C, Hangartner SB, Connallon T, SgrÃÂ$^2$ CM. 2018. Cross-sex genetic correlations and the evolution of sex-specific local adaptation: insights

— / —

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

---

## NTNU Trondheim ReindeerPaleoGenomics

The NTNU University Museum, Department of Natural History PhD position in reindeer evolution throughout the Pleistocene

See the full job posting here: https://www.jobbnorge.no/en/available-jobs/job/167124/-

phd-position-in-reindeer-evolution-throughout-the-pleistocene About the position The NTNU University Museum is seeking a highly qualified, ambitious and motivated candidate for a PhD-position °Hologenomics of Pleistocene reindeer macroevolution±.

The position will focus on the application of a hologenomic approach to Pleistocene mammal natural history collections. In this context, hologenomics describes -omics studies of all the available genetic information within individual specimens, including its entire community of associated microorganisms. The appointment has a duration of 3 years. The position is available from June 1, 2019, thus master students graduating close to this date can apply.

The project is interdisciplinary, and the work of the PhD candidate will be closely associated with the Holo-Museomics research group at the Department of Natural History (NTNU University Museum). This group is part of the Norwegian Centre of Excellence °Centre for Biodiversity Dynamics± (CBD, NTNU), and will be advised by Associate Prof. Michael D. Martin, Prof. Tom Gilbert, and Prof. Bernt-Erik S©ther. The project will be conducted using the NTNU University Museums computational resources and specialized ancient DNA laboratory facilities.

Job description The successful candidate will conduct his/her research on reconstructing genetic records of population size to test hypotheses about the evolution and population dynamics of European reindeer in response to major climatic fluctuations of the Pleistocene. The project will involve work in the field (specimen sampling) as well as in the laboratory (data generation), and computational analysis of the population-level data. In close association with Dr. Brage Bremset Hansen (CBD, NTNU), these data will be combined with fossil morphometric data, as well as environmental and paleoecological records already available for the region, to draw insights into the genomic and epigenomic consequences of climate change in European cervids.The successful candidate will perform sampling, library preparation, and sequencing of a time series of ancient cervids from European natural history collections, as well as modern and ancient samples from across Eurasia.

Qualification requirements The PhD position's main objective is to qualify for work in research positions. The qualification requirement is completion of a masters degree or second degree (equivalent to 120 credits) with a strong academic background in evolutionary biology, population genetics or closely related fields or equivalent education with a grade of B or better in terms of NTNUs grading scale. Applicants with no letter grades from previous studies must have an equally good academic foundation. Applicants who are unable to meet these criteria may be considered only if they can document that they are particularly suitable candidates for education leading to a PhD degree. The appointment is to be made in accordance with the regulations in force concerning State Employees and Civil Servants and national guidelines for appointment as PhD, postdoctor and research assistant

Other qualifications required Excellent written and verbal communication ability in English

Desirable qualifications It is highly advantageous to have experience in genomic data generation and analysis, specifically NGS laboratory and computational analysis methods related to ancient DNA data, and familiarity with the UNIX command-line. Prior involvement with publication of genetic research is also advantageous.

Mike Martin <sameoldmike@gmail.com>

---

## Paris PlanktonPopulations

A PhD position is available at CEA/Genoscope aimed at

Project title: Omics based modeling of marine plankton populations

Director: Eric Pelletier (CEA / Genoscope ' CNRS Research Federation “Global Ocean System Ecology and Evolution”)

Apply here:

https://www.adum.fr/as/ed/voirproposition.pl?matricule_prop$405&siteÂ'umR#version
Deadline: April 14, 2019

Start date: September to December 2019

Qualification: MS in Biological sciences with demonstrated knowledge in network modeling and skills in computational biology.

Context:

Changes in marine plankton communities driven by environmental variability impact the marine food web and global biogeochemical cycles of carbon and other elements. To predict and assess these community shifts and their consequences, it is essential i) to describe functional relationships driving population assemblages and ii) to quantify their relative contribution in the main functional ecosystem traits and services. In order to predict these features, one could use large scale ocean imaging methods (mainly based on satellites) to predict photosynthetic activity. However, these techniques are limited to oversimplified biological processes but do not apply to more complex features such as vertical carbon fluxes, nitrogen fixation or production of sulfur compounds, all of such having great impacts at the global scale. Omics-based techniques represent a great promise to circumvent these limitations, for instance by providing access to populations composition, functional abilities and activities.

Yet, major caveats remain. In particular, gene-centric based approaches describe complex organisms communities (metagenomics and metatranscriptomics) but does not allow to capture biologically insights at the level of organisms when no closely related reference genomes are available, which represents a major drawback for studying the global ocean. To overcome this shortcoming, bioinformatics methods have already been designed to reconstruct genomic data from environmental sequences for bacteria and archeae (i.e., Metagenome based Assembly of Genomes). However, they poorly perform on eukaryotes, partly because of their large genome size and complexity.

This thesis project proposes to bridge these methodological gaps for plankton eukaryotic systems, in particular thanks to the Tara Ocean dataset. Indeed, the Tara Ocean project (1) revealed the catalog of more than 41 million of bacterial and archeal genes (2), and 116 millions of eukaryote plankton unigenes (cDNA contigs) (3), both with a high proportion of newly described genes without known homologs. Again, the paucity of reference sequences could explain this observation for eukaryotic marine plankton, for which very few references are described (4).

To identify major eukaryotic insights, a canopy clustering (5) approach has been applied to group transcripts with similar abundance variation profiles across the collection of samples, generating MetaGenome based Transcriptomes (MGT), corresponding to organismal transcriptomes (6). With this method, it is then feasible for eukaryotes to move from environmental-based gene-centric dataset to organism-level entities, and then to populations. As a complementary analysis, one advocates herein to build a complementary metabolic network to automatically identify the main phenotypic features. Finally, one will extract from the metabolic model the major traits of interest that will be used in state-of-the-art ocean circulation model. Focusing on phenotypic characteristics of plankton communities, i.e. the so called plankton functional traits, or plankton functional types (PFT) (7) are indeed an effective way to link community structure and composition to ecosystem functioning (8) (9). These have already been used to connect large scale description of the oceans with major biogeochemical cycles. By defining essential gene functions specific to each PFT class, it would be possible to connect meta-omics data and functional models with global models.

This thesis will foster and organize all these resources and methods within a single bioinformatic paradigm, in order to target the following aims:

i) apply metabolism reconstruction approaches to describe the global biological functions of these eukaryotic marine organisms through the analysis of the individual genes functions ii) integrate the individual described metabolisms to describe the sampled populations in the context of the samples environmental parameters, iii) identify eukaryotic genes which can be associated with the different main plankton functional traits, extending already available data (10) and iv) connect at the global scale these quantifiable omics elements with the oceans level biogeochemical models.

Steps i) and ii) will be undergone in collaboration with Damien

— / —

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

## QueenMaryU AnnelidBacterialSymbiosis

*** PhD position available; Queen Mary University of London***

The genomic basis of bacterial symbiosis in deep-sea annelid worms

Background Mutualistic relationships between bacteria and complex organisms have repeatedly evolved and this has allowed host organisms to exploit new environments and foods. One of the most extreme and fascinating cases of symbiosis in the animal kingdom is observed in annelid worms of the genus Riftia and Osedax, which are able to live in particularly extreme environments including deep sea hydrothermal vents and carcases thanks to bacteria from the environment that they acquire as juveniles. This ultimately induces a drastic developmental change where they degenerate their guts and rely entirely on the bacterial symbionts to produce the essential nutrients they require for survival in those hostile environments. Which cellular and genetic mechanisms control this bacterial symbiosis? How did these mechanisms evolve? How did its change contribute to animal evolution?

- In this project you would rigorously answer these questions sequencing and comparing the genome of these symbiotic worms with their closest asymbiotic counterparts. - You would have access to a large genomic database, field collections and in-house live organisms to fuel your investigation. - You would gain experience of molecular techniques (nucleic acid extraction, next generation sequencing), bioinformatics (e.g. genome assembly, RNA-seq analyses, gene family evolution), and statistics. - You will be encouraged to develop your own ideas and hypotheses.

The studentship is fully funded and available to EU and UK citizens. It will cover tuition fees as well as provide an annual tax-free maintenance allowance for 3 years at Research Councils UK rates (£17,009 in 2019-20).

Skills preferred In a multidisciplinary project like this, candidates are unlikely to have a background in all disciplines involved. The most important qualification is motivation, enthusiasm and that the project appeals to you. However, previous computational experience would be a plus. We can envisage strong candidates coming through a variety of routes including:

- practical molecular biology - evolutionary theory and phylogenomics - computational biology

To apply, students should have a first class degree or have received a MSc in a relevant field (i.e. marine biology, evolutionary biology, bioinformatics) or are about to finish their MSc.

For informal requests, do not hesitate to contact me at chema.martin@qmul.ac.uk

***Deadline for application: 05.04.2019***

Apply via: https://www.qmul.ac.uk/sbcs/postgraduate/phd-programmes/projects/display-title-649765-en.html Supervisor Information Dr. Chema Martin Email: chema.martin@qmul.ac.uk Website: https://martinduranlab.com/ Dr. Lee Henry Email: l.henry@qmul.ac.uk Website: https://www.qmul.ac.uk/sbcs/staff/leehenry.html Dr Yannick Wurm Email: y.wurm@qmul.ac.uk Website: http://wurmlab.github.io Related References

Cavanaugh, C. M., Gardiner, S. L., Jones, M. L., Jannasch, H. W. & Waterbury, J. B. (1981) Prokaryotic Cells in the Hydrothermal Vent Tube Worm Riftia pachyptila Jones: Possible Chemoautotrophic Symbionts. Science 213, 340-342.

Rouse, G. W., Goffredi, S. K. & Vrijenhoek, R. C. (2004) Osedax: bone-eating marine worms with dwarf males. Science 305, 668-671.

Thornhill, D. J., Fielman, K. T., Santos, S. R. & Halanych, K. M. (2008) Siboglinid-bacteria endosymbiosis: A model system for studying symbiotic mechanisms. Commun Integr Biol 1, 163-166.

Hilario, A. et al. (2011) New perspectives on the ecology and evolution of siboglinid tubeworms. PLoS One 6, e16309.

Chema Martin <chema.martin@qmul.ac.uk>

---

## Rennes France EvolutionaryBiol

I am posting an announcement for a PhD in Rennes from October 2019 under co-supervision of Johannes Overgaard (Aarhus DK) and myself (Herv Colinet, Rennes FR) The subject is proposed to the competition at the EGAAL Doctoral School with high chances of success. The subjects proposed were pre-selected; hence the chances of success are high (50%). Candidates must however have an exemplary academic background and excellent papers from their masters program (top ranking).

Disciplines : Evolution, Ecology, Physiology Laboratory: ECOSYSTEMS, BIODIVERSITY, EVOLUTION (ECOBIO) Host institution: UNIVERSITE RENNES 1 (France) Doctoral school: Ecology, Geosciences, Agronomy, Food (EGAAL) - ED 600

Application deadline : 31/05/19 Duration : 36 month Start date : 01/10/19

Details on the subject can be found here : https://doctorat.campusfrance.org/en/CF201914656 Contact person : herv Colinet (herve.colinet@univ-rennes1.fr)

*Socio-economic and scientific context : *

The “cost of reproduction” refers to the tradeoff between reproduction and lifespan. This cost has been described in a multitude of species, ranging from flies to humans, but this cost sill debated. This tradeoff and its underlying mechanisms remain to be elucidated and still captivate researchers working in ecology, evolution, physiology but also in medical sciences. The theory posits that when endogenous resources are allocated to reproduction, they are less available for somatic or repair functions that are necessary for stress resistance. As a result, reproductive activity would make the organism more vulnerable to environmental stress, reducing therefore its life expectancy. Reproductive activity should therefore generate increased susceptibility to environmental stress, but this relationship is not yet formally established. These notions defines framework of the PhD project that perfectly fits with the goals of international laboratory LIA PRICES (https://ecobio.univ-rennes1.fr/LIA-PRICES/) starting in 2019 between Ecobio (Rennes) and Zoophysiology (Aarhus) for 5 years.

*Assumptions and questions *

Evidence supports the presumption of a tradeoff between reproduction and stress resistance. For example, in Drosophila flies, oogenesis is blocked when environmental or nutritional conditions become unfavorable. To pass the stress of the winter, Drosophila females enter in reproductive diapause (block of oogenesis). Nutritional restriction often increases longevity and promotes stress tolerance, while reducing fecundity or fully blocking gametogenesis in some cases. Other studies report that virgin females, whose oogenesis is deeply restricted, live significantly longer and are more resistant to stress than gravid females. All these elements support the hypothesis that reduction / block of reproduction may be a key factor of stress tolerance but unerlying mechanisms of such a tradeoff remain to be elucidated.

* The main steps of the thesis and scientific procedure *

The physiological mechanisms underlying the cost of reproduction are unknown and likely complex. To address these issues, the Drosophila model is particularly suitable because its stress tolerance is well described, its longevity can easily be accessible in laboratory and its reproduction can be experimentally manipulated. We will explore and characterize this tradeoff mainly via inhibition / stimulation of the reproduction activity. Oogenesis will be _inhibited_ by multiples approaches 1) pharmacological treatments (supplementation with rapamycin, phloroglucinol), 2) genetics (sterile mutants: Ovo, InR, Chico, Orb), 3) environmental treatments (induction of reproductive diapause and virginity) and 4) nutritional manipulations (protein and essential nutrients deficiencies). In addition, oogenesis will be _stimulated_ via 1) hormonal (juvenile hormone analogs) and 2) nutritional treatments (active yeast supplementation), and that, using various fertile or sterile lines. We will study consequences of all these manipulations on longevity and tolerance to environmental stresses (biotic and abiotic), with a particular focus on thermal stress. Part of the PhD project will take place at Aarhus University as part of the international laboratory LIA PRICES (2019-2023) (the duration of the mobility will be according to the wishes of the candidate).

*Methodological and technical approaches considered *

We will study the ecophysiological mechanisms underlying variations in longevity and tolerance to environmental stresses in flies whose reproduction has been manipulated, via molecular (exploratory or targeted transcriptomic), metabolic (metabolomic profiling) and physiological (water / ionic / energy homeostasis and hormonal balance) approaches.

*Scientific and technical skills required by the candidate*

— / —

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

---

## SorbonneU Paris EvolutionaryGenomics

PhDPosition : Deciphering the code for nuclear control over gene expression in chloroplasts and mitochondria

2019-2022 Institut de Biologie Physico-Chimique , Sorbonne Université, Paris, France.

We are seeking a highly motivated Ph.D. candidate to pursue a thesis on the mechanisms of protein-RNA recognition involved in nuclear control of the gene expression of eukaryotic organelles. In photosynthetic eukaryotes, this control circuitry plays an essential role in the molecular adaptation of the chloroplast to environmental changes. The project is at the interface between comparative genomics and molecular biophysics, and the candidate will be expected to contribute both to studies of co-evolution of regulatory proteins and their mRNA targets as well as to molecular dynamics simulations and free-energy calculations on these same macromolecules. The thesis, carried out at the IBPC, will be co-directed by Ingrid Lafontaine (Laboratory of Chloroplast Biology and the Light Perception in Microalgae, UMR7141 CNRS-SU) and by Charles Robert (Laboratory of Theoretical Biochemistry, UPR9080, CNRS).

The candidate should have solid background in physical-chemistry, programming, and statistical analysis and be interested in fundamental mechanisms of genome evolution. This position is financed by the CNRS via a 80|Prime doctoral contract (3 years), and provides a monthly salary of 2135 euros before taxes and charges. The doctoral student must enroll in the Complexité du

Vivant doctoral school at Sorbonne University starting in Autumn 2019.

Candidates should address a detailed CV and university transcripts (Undergraduate and Master's degree), as well as two references, to Ingrid Lafontaine (ingrid.lafontaine@ibpc.fr) and Charles Robert (charles.robert@ibpc.fr) before 25 april 2019.

Ingrid Lafontaine, MaÃtre de Conférences Sorbonne université

Biologie du Chloroplaste et Perception de la Lumière chez les Microalgues Institut de Biologie Physico-Chimique 13 rue Pierre et Marie Curie, 75005 Paris http://www.ibpc.fr/UMR7141/ 01 58 41 50 49

Atelier de Bioinformatique http://wwwabi.snv.jussieu.fr/people/ingridl/ ingrid.lafontaine@sorbonne-universite.fr ingrid.lafontaine@ibpc.fr

Ingrid Lafontaine <ingrid.lafontaine@ibpc.fr>

## StockholmCPG AncientMicrobiomes

PhD Student Position on Ancient Microbiomes

Centre for Palaeogenetics Stockholm University & Swedish Museum of Natural History

PROJECT DESCRIPTION The overall aim of this project is to characterize microbiomes in prehistoric remains from humans and wild megafauna, in order to investigate the interaction between population dynamics and prehistoric diseases. More specifically, the project will investigate to what extent prehistoric contacts between populations lead to spread of diseases, and whether pandemic outbreaks could have caused demographic declines or even extinctions. We will be working on ancient humans that are several thousand years old, as well as several species of the Ice Age Megafauna (e.g. woolly rhino, mammoth, wolf and cave lion). All genetic data for the project has already been generated. The project is part of a "paired PhD student" scheme together with the Department of Mathematics, where a second PhD student will be developing novel tools for the bioinformatic analyses. For this project, good knowledge in bioinformatics and experience of handling genomic data in a Linux environment are important qualifications. The PhD student will join the the new Centre of Palaeogenetics in Stockholm, which is a joint venture between Stockholm University (SU) and the Swedish Museum of Natural History (SMNH). For further details, see www.palaeogenetics.com . ENVIRONMENT The PhD student will be employed by Stockholm University, and will be based at the new Centre for Palaeogenetics (CPG). The centre is located on the Stockholm University campus, and will house several research groups working on ancient DNA analyses. Stockholm is by many regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes as well as the National Genomics Infrastructure at the Science for Life Laboratory. The project will be supervised by Prof. Love Dalen and Prof. Anders Götherström, both based at CPG, as well as Dr. Lars Arvestad (Department of Mathematics, SU).

QUALIFICATIONS In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere. In order to meet the specific entry requirements, the general syllabus for doctoral studies in the field of Systematics and Evolution stipulates that applicants must have completed a research degree (e.g. Master's), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level ("examensarbete") within Systematics and Evolution, Ecology, Population Genetics, Bioinformatics or a similar subject. Applicants who have in principle acquired the corresponding competence in Sweden, or abroad, are also qualified. The qualification requirements must be met by the deadline for applications.

CONTACT For more information, please contact Professor Love Dalén, +46 8 5195 4281, love.dalen@nrm.se or Professor Anders Götherström, anders.gotherstrom@arklab.su.se.

HOW TO APPLY Applications should be done using Stockholm University's online application system. Please follow the link below to obtain further information about how to write your application and how to access the online application system: https://www.su.se/english/about/working-at-su/phd?rmpage=job&rmjob“95&rmlang=UK Closing date: 23 April 2019 Reference number: SU FV-0887-19

Love Dalén <Love.Dalen@nrm.se>

CV, degree certificates and a letter of motivation.

"Anisimova Maria (anis)" <anis@zhaw.ch>

## Switzerland ComputationalPhylogenetic

PhD /postdoc in Computational Phylogenetics

ZHAW Wädenswil, Switzerland

With the advent of new generation sequencing (NGS) bioinformatic methods must keep pace to provide robust scalable solutions to analyse large sets of molecular sequences. The evolutionary history of molecules is described by a tree structure called phylogeny, which is inferred from genomic sequences. Phylogenies are used for testing biological hypotheses with applications ranging from medicine to ecology. Phylogeny inference usually relies on an inferred alignment of homologous sequences, which ' in turn ' relies on a guide-tree reflecting their ancestral relationships. The goal is to address this apparent circularity so to improve the reliability of phylogenetic analyses. Ideally alignment and tree should be inferred jointly. For example, please see our recent article: Maiolo M, Zhang X, Gil M, Anisimova M. "Progressive multiple sequence alignment with indel evolution" BMC Bioinformatics. 2018 Sep 21;19(1):331. doi: 10.1186/s12859-018-2357-1.

In the context of the project funded by Swiss National Science Foundation, we are looking for a suitable candidate for a PhD or a postdoc position, depending on previous background and qualifications.

The successful candidate will work as part of Applied Computational Genomics Team lead by Maria Anisimova at the Institute of Applied Simulations, Zurich University of Applied Sciences (ZHAW Wädenswil) and will have a second affiliation to the University of Zurich.

The group is also part of Swiss Institute of Bioinformatics, which provides additional training and networking opportunities.

Group official ZHAW website: https://www.zhaw.ch/de/lsfm/institute-zentren/ias/forschung/computational-genomics/ Profile requirements: Strong background in computational science, algorithms, statistics, stochastic modeling or similar; Working knowledge of C++ ; Some knowledge of phylogenetics and molecular evolution is an advantage

To apply please send an email with the title JATI2 to maria.anisimova@zhaw.ch

Your application should be in one pdf file including your

## Sydney ForestAdaptation

URBAN FOREST: TESTING TREE PERFORMANCE TO FUTURE HOTTER AND DRIER CONDITIONS Hawkesbury Institute for the Environment, Western Sydney University PhD scholarship http://bit.ly/2tDgvr8 We are looking for a highly motivated and qualified candidate for a 3-year PhD program of research at the Hawkesbury Institute for the Environment, Western Sydney University, commencing in 2019. This studentship is part of an exciting research programme established under Hort Innovations Green Cities initiative (Which Plant Where project www.whichplantwhere.com.au), investigating the performance of urban trees under climate change.

This project aims to test fundamental ecological principles to inform the selection of trees in urban areas across Australia. The studentship will explore questions relating to whether trees are adapted to their climate-of-origin and the extent to which climate and traits are good predictors of tree performance in different urban contexts. The PhD research program will focus on a large Urban Forest Experiment established with a wide range of tree species in the hot and dry conditions in Western Sydney (Richmond NSW) a future climate scenario for much of metropolitan Sydney. The inclusion of a watering treatment will allow evaluation of the extent to which irrigation can alleviate drought and heat stress under field conditions. The applied outcome of the Urban Forest Experiment will be a robust field test of climate suitability for Sydney future urban forest.

Applications are open to international candidates as well as Australian or New Zealand citizens or permanent residents of Australia. The position is based at the Hawkesbury campus of Western Sydney University, Richmond, NSW and is in collaboration with the Department of Biological Sciences at Macquarie University. Candidates will work with Western Sydney University partners and the horticulture industry to achieve key applied outcomes in plant and soil science.

Applicants should discuss their eligibility and interests with Dr Paul Rymer (p.rymer@westernsydney.edu.au), Professor Sally Power (s.power@westernsydney.edu.au) or Professor

Mark Tjoelker (m.tjoelker@westernsydeny.edu.au)

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

Please submit an application form, CV, names and contact information of two referees, and a one-page document stating how your research interests align with the projects aims.

Closing date: 31 March 2019

Paul Rymer Senior Lecturer in Plant Ecological Genetics Hawkesbury Institute for the Environment Western Sydney University https://www.westernsydney.edu.au/-hie p.rymer@westernsydney.edu.au office 0245701094 mobile 0415963139

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

---

## Sydney NationalTreeGenomics

Dear all

We have two PhD positions in Australia on i) evolutionary genomics and ii) computer science. It is open to international applicants with at least one 9 month research project under their belt (e.g. Honours, M. Res, MPhil, MSc with 50% research, work experience etc).

The National Tree Genomics Project (Western Sydney University, University of Adelaide, University of Queensland, Queensland University of Technology, Queensland Department of Agriculture and Fisheries QDAF, Jain Irrigation in India) is integrating new genomic, physiology, and molecular biology approaches for key model species (avocado, almonds, citrus, macadamia, mango) to breed the next generation of fruit and nut trees. To complement our team, we are seeking to support exceptional PhD students to lead projects within our portfolio.

The first project will use comparative genomic analysis of assembled genomes, in the context of our molecular breeding program, to determine what gene set makes a 'good' fruit tree crop, developing new approaches for analysing (allelic) gene expression x genotype interactions, or investigating how environments can influence the development of complex tree traits.

The second project will use cutting-edge machine learning approaches to discover how complex biological traits evolve, develop, and respond to a changing environment. The aim is to generate fundamental knowledge on fruit tree development (such as flowering, branching, pathogen and drought resistance) by integrating diverse data types (genetic, physiological, ecological) in a mathematical framework of the student's design.

For both projects, the student will be mainly based at Western Sydney and co-supervised by the Hawkesbury Institute for the Environment, Centre for Research Mathematics (Western Sydney University) and University of Queensland (Brisbane).

It is a two stage application starting with a short EOI, deadline 12th of April.

You can find more details here:

Evolutionary genomics: https://-cloudstor.aarnet.edu.au/plus/s/HHbgZEVucDjbIUh
Machine learning and computer science: https://-cloudstor.aarnet.edu.au/plus/s/8bLRe5WXps991Xd
many thanks, alexie

–

Dr. Alexie Papanicolaou https://stressedfruitfly.com Senior Lecturer / Assistant Professor in Bioinformatics Hawkesbury Institute for the Environment

P: +61(0) 2 4570 1385 | M: +61 (0) 46 85 81 247 A:Hawkesbury Campus, L3.G07, Richmond 2753 M: Locked Bag 1797, Penrith, NSW 2751, Australia Virtual Office: https://-uws.zoom.us/my/alpapan PGP-key fingerprint: 35410C52CEE74AC2A405BDF92EBE0615C21F009A

Associate Editor for - Publish your nextConcepts & SynthesispaperinScience of Nature(formerly Naturwissenschaften EST'D 1913; Springer) - Publish your next genomics work at Genomics (Elsevier) - Make your research accessible at PLoS ONE

On collaboration: - One can only do so much, but together one can do so much more

On the rise of AI - It's already here

On supervising - PhD students: Work with someone to explore a phenomenon that fascinates them using your methods - Post-docs: Work with someone to explore a phenomenon that fascinates you using their methods - Nights & weekends: Work with family/cat to let you explore a phenomenon that fascinates you using your methods

Alexie Papanicolaou <A.Papanicolaou@westernsydney.edu.au>

## UAberdeen MicrobialEvolution

Funded PhD studentship in microbial evolution at the University of Aberdeen (Scotland, UK): ?Experimental evolution of Thaumarchaeota?

The fundamental aim of this project is to determine the process of adaptive diversification and associated trade-offs in fitness, by studying microbial evolution experimentally.

A 4-year PhD studentship in microbial evolution, starting in Sept 2019, is now open for application at the University of Aberdeen, Scotland, UK. The deadline for applications is April 16th 2019 and this studentship is available to UK and EU students. The PhD project is funded by the Royal Society and will target key evolutionary questions with a special focus on Thaumarchaeota to align with the research thematic of the University of Aberdeen Nitrification Group.

Using microbes to test theory in evolutionary biology has led to major scientific advances. In particular, microbial experimental evolution has allowed analysis of both microbial adaptation (genomic and phenotypic changes) and diversification (phenotypic evolution and lineage-splitting) using controlled environments, through increased understanding of the nature and frequency of genomic substitutions, their effects on microbial fitness and the mechanisms by which diversity is created and maintained in microbial populations. These concepts were established from studies of bacteria, fungi, viruses and phage, focussing mainly on a few bacterial model organisms (1, 2). However, an entire domain of life, the Archaea (3), has largely been ignored by evolutionary biologists, despite their widespread distribution in natural environments, high abundance and essential contribution to global ecosystem functioning that sustains the planet. A priori, no clear reasons for different evolutionary processes between archaea and bacteria can be advanced, but their ancient evolutionary divergence (despite the existence of lateral gene transfer between domains) suggests that the relevance of established microbial models of adaptation and diversification should be tested on these organisms if they are to be considered universal. Indeed, despite the global importance and diversity of archaea, our understanding of the ecological and evolutionary processes generating their high diversity is scarce compared to that of eukaryotes and, to a lesser extent, bacteria.

This project will focus on members of a key microbial phylum, the Thaumarchaeota (4, 5), which are abundant and ubiquitous and perform a critical ecosystem function, ammonia oxidation. The distribution of natural microbial communities is influenced by environmental characteristics, and pH is the major abiotic factor influencing extant thaumarchaeotal niche specialisation (4), and has also influenced their diversification and patterns of lineage formation through deep evolutionary time (5).

This project will involve cultivation of Thaumarchaeota (6) followed by the analysis of their mutation rate under different environmental conditions and in relation with DNA repair mechanisms. The project will be complemented by studying the evolution of these microbes experimentally by imposing environmental changes under controlled conditions, and the evolutionary mechanisms of adaptation and diversification as well as the existence of trade-offs will be determined using genomic and fitness changes over time. The project offers opportunities for innovative ideas and the student will be expected to contribute to the development of the project, including on scientific testable hypotheses and subsequent experimental design to apply.

The PhD student will join a dynamic team of researchers led by Dr C?cile Gubry-Rangin (https://-www.abdn.ac.uk/ibes/profiles/c.rangin) and will benefit from the presence of strong groups in the department working on related topics as well as being embedded in a strong network of international collaborations. The University of Aberdeen provides an excellent scientific environment, state-of-the-art technological support facilities and diverse training opportunities for all aspects of research and for transferable academic and generic skills.

Candidate should have (or expected to achieve) a minimum of 2:1 Honours degree, ideally (but not required) an MSc in evolution, ecology or related, strong theoretical skills and enthusiasm for learning and developing microbial experimental evolution.

Application Process: Formal application should be made as described on https://www.findaphd.com/phds/-project/experimental-evolution-of-thaumarchaeota/-?p107781 but informal enquiries could be addressed to C?cile Gubry-Rangin (c.rangin@abdn.ac.uk).

References: 1. Barrick JE, Yu DS, Yoon SH, Jeong H, Oh TK, Schneider D, Lenski RE, Kim JF. (2009) Genome evolution and adaptation in a long-term

— / —

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

## UAdelaide AncientMarineDNA

Study opportunities in marine sedimentary ancient DNA (aDNA), available now.

Supervisor: Dr Linda Armbrecht, Australian Centre for Ancient DNA (ACAD) at the University of Adelaide, Australia

Marine phytoplankton are globally important microorganisms that live in the ocean's surface. When these tiny organisms die, they sink to the seafloor and over time build up complex layers in the ocean sediments. By extracting ancient DNA from such sediments, past phytoplankton communities can be reconstructed, providing information on past environmental conditions and climate. This novel knowledge about past marine community adaptation to previous regional and global warming periods helps inform predictions of future marine ecosystem resilience guiding management efforts of marine ecosystems during present-day climate change.

Study opportunities on all levels (Internships, Honours, Masters, PhD) are available with regard to the reconstruction of Antarctic phytoplankton communities and their responses to variations in climate. Sediment cores used for this research were collected off East and West Antarctica, and are dated to the Last Glacial Maximum (~20-25 kyr). This research is highly interdisciplinary, spanning across marine science, biological/palaeoceanography, and palaeo-genomics, and a good understanding in at least one of these disciplines is required. Study activities include, for example, marine field-work (topic-dependent), laboratory tasks, bioinformatics and data analysis.

International students should note that they must meet the English Language Proficiency (ELP) < https://www.adelaide.edu.au/graduatecentre/handbook/03-considerations-in-applying/02-entry-requirements/03-english-language/ > requirements, and must apply for an International Scholarship < https://www.adelaide.edu.au/graduatecentre/scholarships/research-international/ >). These scholarships are highly competitive and based on an excellent academic record. Please ensure you meet the eligibility criteria for admission (in relation to PhD or MSc study) prior to contacting us.

If you are interested to commence a degree or conduct an internship in this research area please contact linda.armbrecht@adelaide.edu.au, outlining your motivation and relevant research experience, including your CV, and, if applicable, your current transcript. Please also visit the Australian Centre for Ancient DNA (ACAD) < https://www.adelaide.edu.au/acad/study/ > website for further information about our research centre.

Linda Armbrecht <linda.armbrecht@adelaide.edu.au>

## UBath EvolutionIntelligence

Modelling Brain-Like Intelligence in an evolutionary context for AI applications

https://www.findaphd.com/phds/project/modelling-brain-like-intelligence-in-an-evolutionary-context-for-ai-applications/?p107744 A challenge for AI research is to operate autonomously in natural environments. Although many organisms can respond adaptively to the natural world in milliseconds, the computational complexity in interpreting natural images is an on-going fundamental problem. One suggested solution is to pursue research on Brain-Like Intelligence (Sendhoff, Koerner & Sporns, 2009) as a means of creating biologically-inspired solutions that might provide a generalised approach to the computational demands of multiple sensory inputs and potential motor outputs. The promising perspective to develop Brain-Like AI has been hampered by the mistaken view that intelligence is a hallmark of 'highly evolved creatures'; instead, the pluralistic view that all creatures have evolved adaptive sensory and motor capabilities for different environments might better endow autonomous robots with the flexibility necessary to use different computational approaches attuned to the environment.

This project is associated with the UKRI CDT in Accountable, Responsible and Transparent AI (ART-AI), which is looking for its first cohort of at least 10 students to start in September 2019. Students will be fully funded for 4 years (stipend, UK/EU tuition fees and research support budget). Further details can be found here: http://www.bath.ac.uk/research-centres/ukri-centre-for-doctoral-training-in-accountable-responsible-and-transparent-ai/ .

The approach will be multisensory and task-based, to understand the best biological approaches (e.g., seeing or hearing?) to solve natural computational problems (e.g., how to find food). The supervision for this project will be interdisciplinary and thus provide training and theory from the perspectives of (psychology, primary supervisor Dr Michael Proulx), evolutionary neuroscience (Dr Alexandra de Sousa), and computer science (Prof Eamonn O'Neill).

Desirable qualities in candidates include intellectual curiosity, a strong background in maths and programming experience. Applicants should hold, or expect to receive, the equivalent of a UK First Class or good Upper Second Class Honours degree in a relevant field. A master's level qualification would also be advantageous.

Informal enquiries about the project should be directed to Dr Michael Proulx m.j.proulx@bath.ac.uk .

Enquiries about the application process should be sent to art-ai-applications@bath.ac.uk .

Formal applications should be made via the University of Bath's online application form for a PhD in Computer Science: https://samis.bath.ac.uk/urd/sits.urd/run/-siw_ipp_lgn.login?process=siw_ipp_app&code1=-RDUCM-FP01&code2 Start date: 23 September 2019.

Funding Notes:

ART-AI CDT studentships are available on a competition basis for UK and EU students for up to 4 years. Funding will cover UK/EU tuition fees as well as providing maintenance at the UKRI doctoral stipend rate (15,009 per annum for 2019/20) and a training support fee of 1,000 per annum.

– http://sites.google.com/site/alexandraallisonsousa/ Alexandra Allison de Sousa <alexandra.allison.sousa@gmail.com>

---

## UBergen Norway EvolutionaryEcology

PhD position in Evolutionary Ecology

There is a vacancy for a PhD position in evolutionary ecology at the Department of Biological Sciences (BIO, https://www.uib.no/en/bio), with the Evolutionary Ecology (EvoFish) research group (https://-www.uib.no/en/rg/evofish).

The position is part of the project 'Cost of life-history adaptations: Multiple-trait consequences of fisheries-induced evolution', funded by the Research Council of Norway (https://www.uib.no/en/rg/evofish/120408/-cost-life-history-adaptations-guppies). The position is for a fixed-term period of 3 years with the possibility of a 4th year with compulsory other work (e.g. teaching duties at the department).

To apply: https://www.jobbnorge.no/en/available-jobs/job/166510/stipendiat-i-evolusjonaer-oekologi Deadline: Monday, March 25, 2019

About the project/work tasks

The project set up to understand the complex ways in which organisms pay costs of adapting to external stressors, such as elevated mortality from harvesting. The project is taking advantage of the guppy lines that have been subjected to different types of size-dependent harvesting. The project involves both experiments with live fish and molecular analyses of experimental animals to characterize their trait variation at both macroscopic and microscopic levels, supported by advanced methods for data analyses. The work involves collaboration with partners in Norway, Scotland, Canada, and USA. The PhD student is expected to contribute to all parts of the project, including planning and execution of experiments and analyses, and reporting and communicating the results.

Qualifications and personal qualities:

Applicants must hold a master's degree or the equivalent in evolutionary biology, ecology, or organismal biology, or must have submitted his/her master's thesis for assessment prior to the application deadline. It is a condition of employment that the master's degree has been awarded. Experience from working with multicellular organisms to study questions in ecology or evolution, or with using molecular methods to study phenotypic adaptation is a requirement. Experience with working with fish behavior and physiology are advantages. The applicant must show a good understanding on principles of evolutionary ecology. Applicants must be able to work independently and in a structured manner, and demonstrate good collaborative skills. Applicants must be proficient in both written and oral English. Personal and relational qualities will be emphasized. Ambitions and potential will also count when evaluating the candidates.

We can offer:

- a good and professionally challenging working environment - salary at pay grade 51 (code 1017/pay range 20, alternative 9) in the state salary scale. This constitutes a gross annual salary of NOK 449 400. Further promotions are made according to length of service in the position. - enrolment in the Norwegian Public Service Pension Fund - a position in an inclusive workplace (IA enterprise) - good welfare benefits

Your application must include:

- a brief account of the applicant's research interests and motivation for applying for the position - a brief proposal for a research plan for the PhD-project (about 1 page). This is important! - the names and contact information for two referees. One of these should be the main advisor for the master's thesis or equivalent thesis - CV - transcripts and diplomas showing completion of the bachelor's and master's degrees, or official confirmation that the master's thesis has been submitted - relevant certificates/references - a list of any works of a scientific nature (publication list)

The application and appendices with certified translations into English or a Scandinavian language must be uploaded at Jobbnorge.

About the PhD position The fellowship will be for a period of 3 years, with the possibility for a 4th year, consisting of 25 % compulsory work (e.g. teaching responsibilities at the department) distributed across the employment period. The 4th year is contingent on the qualifications of the candidate and the teaching needs of the department, and will be decided upon appointment.

The employment period may be reduced if you have previously been employed in a qualifying post (e.g. research fellow, research assistant).

About the research training As a PhD candidate, you must participate in an approved educational programme for a PhD degree within a period of 3 years. A final plan for the implementation of the research training must be approved by the faculty within three months after you have commenced in the position. It

— / —

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

---

## UExeter CaptivityAdaptation AvianConservation

Effects of captive breeding on personality and cognition in the North African houbara bustard - Master by Research

https://www.findaphd.com/phds/project/effects-of-captive-breeding-on-personality-and-cognition-in-the-north-african-houbara-bustard-psychology-masters-by-research-fees-only/?p107393 Project Description The University of Exeter's College of Life and Environmental Sciences, in partnership with Reneco, is inviting applications for a fees-only scholarship to commence in May 2019 or as soon as possible thereafter. For eligible students the studentship will cover UK/EU tuition fees for 2 years full-time, or pro rata for part-time study. The student will be based in the College of Life and Environmental Sciences at the Streatham Campus in Exeter. However, fieldwork will take place in Eastern Morocco (ECWP, Missour). Besides Morocco, the student will also be expected to spend time at the Reneco HQ in Abu Dhabi, UAE, to conduct data analysis under the supervision of Dr Enrico Sorato and present research outcomes.

The endangered North African houbara bustard (Chlamydotis undulata undulata) has been declining drastically throughout its range due to overhunting and habitat degradation. Since the late 90s the species has been the subject of a large-scale captive breeding programme at the Emirates Center for Wildlife Propagation (ECWP), Missour, with currently more than 15 000 birds produced annually for release in the wild. The intention of this rearing and release is to restore wild populations and supplement hunting grounds for regulated falconry (http://www.houbarafund.org). However, potential genetic adaptation to captivity may lead to changes in behaviour and life history traits, which may be detrimental in the wild.

The successful applicant will investigate the effects of captive-breeding on personality traits and cognition, by conducting behavioural tests on captive houbaras throughout ontogeny. By testing individuals with varying known histories of captive breeding, and by using quantitative genetics statistical methods, we will assess the extent of adaptation to captivity and disentangle the relative impact of additive genetic, parental and environmental effects. This study will contribute to understanding how selection shapes variation in personality and cognitive traits, and could help improve breeding protocols to avoid adaptation to captivity. This project offers multidisciplinary academic training in behavioural/cognitive ecology, as well as practical applications for conservation of an endangered species.

In addition to funding fees at the University of Exeter, Reneco is also expected to provide the student with research costs, travel, accommodation and a small stipend for living costs in the field. The scholarship will be awarded on the basis of merit for 2 years of full-time study to commence in May 2019. The collaboration with the named project partner is subject to contract. This award provides annual funding to cover UK/EU tuition fees only. Students who pay international tuition fees are eligible to apply but should note that the award will only provide payment for part of the international tuition fee Informal enquiries about the project can be directed to Dr Enrico Sorato: esorato@reneco-hq.org or to Dr Joah Madden : J.R.Madden@exeter.ac.uk

Enrico Sorato RENECO INTERNATIONAL WILDLIFE CONSULTANTS P.O Box 61741 Abu Dhabi, UAE Phone: +971 (0)2 3071 914 Email: esorato@reneco-hq.org

SORATO Enrico <esorato@reneco-hq.org>

## UExeter SexualSelectionTheoryBacteria

Resending this advert as something broke the links in the email of 2/28/19:

PhD position 'Horizontal Gene Transfer & Sexual Selection Theory in Bacteria' Application Deadline: Thursday March 21, midnight UK time https://bit.ly/2ST4j4s Sexual selection is a powerful evolutionary force in many higher organisms, and arises from differences in mating or fertilization success associated with male-male competition and female mate choice. In contrast to the vast amount of research done on sexual selection in insects, birds and mammals, little work has been done on sexual selection on other organisms. Because bacteria frequently engage in sex (through horizontal gene transfer) with substantial fitness consequences, it raises the question whether there is scope for mate choice of mobile DNA elements or competition over DNA insertion in bacteria. And if so, what consequences will sexual selection have on bacterial adaptation?

To understand these questions, the current PhD project aims to develop evolutionary models of mate choice and mating competition in bacteria (using analytical models and/or computer simulations) in collaboration with Dr Bram Kuijper and Prof David Hosken. Dependent on the students own interests, she/he is also welcome to engage in empirical research on bacteria. Moreover, the theoretical work will be informed by empirical analyses on experimental evolution of sexual selection in bacteria, carried out by a postdoctoral researcher working with Dr Edze Westra and Prof Angus Buckling.

Funding and location: The PhD studentship is fully-funded by the Leverhulme Trust and will commence in May 2019 or as soon as possible thereafter. For eligible students the studentship will cover UK/EU tuition fees plus an annual tax-free stipend of at least £14,777 for 3.5 years full-time, or pro rata for part-time study. The student would be based in Centre for Ecology and Conservation in the College of Life and Environmental Sciences at the Penryn Campus in Cornwall, one of the hotbeds of research in ecology and evolution in the United Kingdom.

Entry requirements: Applicants for this studentship must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in an appropriate area of science or technology. Applicants with Masters degree are also encouraged to apply. An interest in learning quantitative skills (e.g., programming, statistical analyses, mathematics) would be highly desirable.

Application deadline: The closing date for applications is midnight on March 21 2019. Interviews will be held on the University of Exeters Penryn Campus the week commencing April 22 2019.

More information and application form: https://bit.ly/-2ST4j4s Bram Kuijper, a.l.w.kuijper@exeter.ac.uk

Bram Kuijper Leverhulme Trust Early Career Fellow University of Exeter Penryn Campus Penryn, Cornwall TR10 9FE United Kingdom

"Kuijper, Abraham" <A.L.W.Kuijper@exeter.ac.uk>

## UGeneva EvolutionaryBiol

The PhD School of Life Sciences at the University of Geneva is pleased to announce the Summer Call 2019 for PhD applications, deadline April 23rd 2019.

The newly created school strives to educate tomorrow's innovative, independent scientists. The PhD School offers the opportunity to perform research in one of the most innovative universities in the world.

Students will join a multidisciplinary environment, uniting over 130 research groups in 6 competitive programs:

Ecology and Evolution

Biomedical Sciences

Molecular Biosciences

Pharmaceutical Sciences

Physics of Biology

Genomics and Digital Health

Students benefit from core training in their home program and any other training of their choice, including training opportunities offered at the partner universities in Lausanne, Fribourg, Neuchâtel, and Berne. The School encourages scientific and social exchange among students in all programs through annual PhD retreats and the PhD Forum.

The PhD School invites applications from motivated candidates all over the world. Applicants should hold or expect to obtain shortly a Master's degree or equivalent from a university in a field of Life Sciences.

Geneva rates among the top ten cities for quality of life, and offers many cultural and sportive opportunities outside PhD life. Students in the research groups of the School are guaranteed a stipend commensurate with the cost of living in Geneva.

Website: lifesciencesphd@unige.ch Email contact: phd-lifesciences-sciences@unige.ch Application link: https://apply.lifesciencesphd.unige.ch/login Claudine Neyen <Claudine.Neyen@unige.ch>

---

## UGreifswald Biomathematics

Job announcement: PhD position available

There is a biomathematics PhD position available in my group as of the 1st of July 2019.

This position is part of a larger project aiming at digitalizing ecological data, but the subproject concerning this PhD position is about graph theory and graph symmetry/balance. Ideally, graph balance measures can be used to interpret root data of plants (which graph theoretically can be modelled by rooted trees or sometimes by networks; and the other subprojects will digitalize suitable underground photographs of roots), but the development of new balance indices is a purely mathematical problem. Thus, this project offers ideal perspectives for a mathematically oriented PhD student to develop new mathematical models for ecology.

For the position, mathematical pre-knowledge, particularly in the area of graph theory, is essential. It is beneficial if the candidate is also fluent in at least one programming language. Ecological and biological pre-knowledge is also beneficial, but not mandatory. However, willingness to cooperate interdisciplinarily is essential. Knowledge of the German language is not essential in this project.

The application deadline is the 14th of April 2019. Applications should be sent as one single PDF file to mareike.fischer@uni-greifswald.de with the job number 19/Sa14 in the subject line.

The official position description (unfortunately in German) is to be found here: https://www.uni-greifswald.de/universitaet/information/stellenausschreibungen/oeffentliche-stellenausschreibungen/wissenschaftliches-personal/institut-fuer-mathematik-und-informatik-19sa14/ Greifswald is located in northeastern Germany directly at the Baltic Sea. It is a beautiful holiday region with a high quality of life. Greifswald is a small town with roughly 55,000 inhabitants. It is renowned for its academic flair, as besides the university, it also hosts a Max Planck Institute and the Friedrich-Loeffler Institute.

Should you have any questions about this PhD position, please do not hesitate to contact me.

Kind regards, Mareike Fischer

Prof. Dr. Mareike Fischer

Biomathematics and Stochastics

Institute for Mathematics & Computer Science Greifswald University Walther-Rathenau-Str. 47 Office 3.15 17487 Greifswald GERMANY

+49 (0) 3834 420 46 43

mareike.fischer@uni-greifswald.de

Mareike Fischer <email@mareikefischer.de>

---

## UIceland EvolutionCodMovement

Movement patterns and environmental preferences of migratory and resident Atlantic cod juveniles

The University of Iceland (hi.is) seeks bright, hardworking individuals for two graduate positions associated with the research project "Movement patterns and environmental preferences of migratory and resident Atlantic cod juveniles ", funded by the Icelandic Center for Research (RANNIS). The research project involves collaboration between Dr GuÃÂºbjÃÂÃ sta Ã'lafsdottir at the University of Iceland, the Research Centre of the Westfjords, Prof. Steven Campana and Prof. SnÃÂbjÃÂPÃÂlsson at the University of Iceland, Faculty of Life and Environmental Sciences, Prof. Einar Eg Nielsen at the Danish Technical University and Prof.

StefÃÂn Ã’li Steingrimsson at Holar University College.

The aim of the project is to test if juvenile Atlantic cod of different migratory genotypes differ in behavior, environmental preferences, habitat use and distribution. We will ask if juveniles of the migratory cod genotype share some of the same traits as adult cod of the same type, that is, forage more broadly, move more quickly, show bolder behavior and have preferences for cooler, high salinity waters. We then ask if juvenile behavior, environmental and habitat preferences diverge across ontogeny, that is, whether the migratory genotypes become more similar to their adult counterparts, and less similar to juveniles with resident genotypes, as they age. Finally, we intend to test if the correlation of migratory genotypes and migratory phenotypes is plastic.

The work will involve field work, behavioral and environmental preference tests in a laboratory setting, acoustic telemetry in natural habitats and SNP genotyping. The positions offered are for one PhD candidate and one MSc candidates. A second PhD candidate has been hired. The students should start no later than August 2019.

The PhD candidate will be enrolled at the Faculty of Life and Environmental Sciences at the University of Iceland, but based at the University of Iceland’s Research Centre of the Westfjords. Applicants should have an MSc degree in biology, aquatic ecology, or similar, have a strong academic background, the ability to independently solve technical problems in the laboratory and field and be able to work independently in demanding situations. Prior experience in fish ecology is preferred and prior experience in aquatic telemetry and/or fish husbandry is an advantage. The PhD candidate will be funded for 3 years with the possibility of an extension.

The MSc candidate will be enrolled at the Faculty of Life and Environmental Sciences at the University of Iceland, but based at the University of Iceland’s Research Centre of the Westfjords and the Danish Technical University. Applicants should hold a BSc degree in biology or a related disciplinary, have a strong academic record, be capable of working under demanding conditions in the field and SNP genotyping in the laboratory. The MSc candidate will receive partial funding for 24 months.

Applicants should contact Dr GuÃÂºbjÃÂÃ sta Ã’lafsdÃÂ³ttir for inquiries (gaol@hi.is). Applications should include a recent CV, a short statement of research interest, names and contact information for two references, and academic transcripts. The application deadline is 1 May 2019 or until appropriate candidates have been recruited.

GuÃÂºbjÃÂÃ sta Ã’lafsdÃÂ³ttir, PhD RannsÃÂ³knasetur HÃÂskÃÂ³la ÃÂslands ÃÂ VestfjÃÂPr ÃÂºum University of Iceland’s Research Centre of the Westfjords

Hafnargata 9b 415 Bolungarvik Iceland

gaol@hi.is + 354 898 9037 https://notendur.hi.is/gaol/ https://www.westfjordresearch.com/ GuÃÂºbjÃÂÃ sta Ã’lafsdÃÂ³ttir <gaol@hi.is>

---

## UIdaho EcologicalGenomicsModeling

3 PhD STUDENT POSITIONS IN LANDSCAPE GENOMICS, ECOLOGICAL GENOMICS AND MODELING OF AQUATIC AND TERRESTRIAL SYSTEMS UNIVERSITY OF IDAHO NSF-EPSCoR GEM3

We seek highly motivated students for 3 Ph.D. positions at the University of Idaho in the recently funded NSF-EPSCoR GEM3 program (https://www.idahogem3.org). The program seeks to understand how genetic diversity and phenotypic plasticity affect species response to environmental change, shaping both population response and adaptive capacity. The program is focused primarily on two taxa: redband trout, a subspecies of rainbow trout, and sagebrush. These taxa are integral to aquatic and terrestrial ecosystems across the American West and are central to land-use management decisions that drive the economy of the region. Two of the PhD positions will focus on these taxa, and the third will focus on landscape genomics and adaptive interactions of terrestrial wildlife species reliant on sagebrush systems such as southern Idaho ground squirrels, pygmy rabbits and sage grouse.

These Ph.D. students will join an interdisciplinary cohort of postdoctoral researchers and students working at scales from genomic characterization of physiological traits in trout and sagebrush, to mapping and modeling of complex ecological, evolutionary, and social-economic systems. Students will have the opportunity to gain skills such as molecular population genomics, landscape genetics analysis, and agent-based and systems modeling.

The possible start dates for these positions are August 2019 or January 2020. Students will be co-advised by Lisette Waits (Fish & Wildlife Sciences) and Paul Hohenlohe (Biological Sciences). Students in the GEM3 program may choose from several degree programs at UI, including Natural Resources, Bioinformatics and

Computational Biology, Environmental Science, or Biology.

To apply, please submit a letter of interest, curriculum vitae, GRE scores, and contact information for three references to Paul Hohenlohe (hohenlohe@uidaho.edu). In your letter of interest please indicate your which of the 3 positions you would like to be considered for as well as your top choice. Review of applications will begin immediately; for full consideration please apply before April 19.

hohenlohe@uidaho.edu

---

## ULisboa QueensU EvolutionaryBiology

PhD opportunity in Evolutionary Biology at the Universidade de Lisboa, Portugal and Queens University, Ontario, Canada

We are seeking one PhD candidate to apply to the 2019 Doctoral Program of the Portuguese Science and Technology Foundation (Fundação para a Ciência e Tecnologia) to conduct research on Population Genomics and Evolution of a highly endangered seabird species complex. The project has recently been funded by FCT, Portugal.

Project:

The NE Atlantic gadfly petrels (genus Pterodroma) are three closely related Macaronesian seabirds: Zino's petrel (P. madeira) breeds on Madeira island, Deserta petrel (P. deserta) in the nearby Bugio islet (Desertas group), and Gon-gon P. feae breeds in Cape Verde. The three taxa are asynchronous breeders. Their taxonomy, evolutionary history and ecological specialization are still a matter of debate. The project will address the following questions:

1) What is the evolutionary history of the North Atlantic Gadfly species?

2) Is there evidence for a genomic basis of breeding time in Madeira's Pterodroma species?

3) What is the demographic history of Pterodroma feae in the Cape Verde archipelago? What are the drivers of population divergence?

Supervision:

Research will be co-supervised by Dr. Mónica Silva, Research Associate at the research center cE3c, University of Lisbon (http://ce3c.ciencias.ulisboa.pt/member/moacutenica-c-silva) and Prof. Vicki Friesen, Queens University, Canada (https://biology.queensu.ca/people/department/professors/vicki-friesen/).

Application:

Applicants must have a good scholar record and hold a Masters degree in a relevant field (Evolutionary Biology, Biology, Bioinformatics). They should also demonstrate strong research and analytical skills, including interpretation of population genomic analyses. The candidate should be fluent in written and spoken English. At least one publication(s) significantly increases the competitiveness of the applicant.

The applicant will apply to a PhD scholarship by Fundação para a Ciência e a Tecnologia which will cover both fees and living expenses (more info here: https://www.fct.pt/apoios/bolsas/concursos/individuais2019.phtml.en). The call will be open until 28 March (17H00 local time). FCT offers a contract of up to four years with a monthly salary and tuition fees. Applications will be submitted in English. The candidate will write and submit a grant proposal working closely with both supervisors.

Candidates should send their CV and a detailed motivation letter demonstrating the fit for the position to Monica Silva, mssilva@fc.ul.pt no later than the 15th March.

Please feel free to contact me directly regarding this opportunity.

Best regards,

Mónica Silva

Monica Silva <mssilva@fc.ul.pt>

---

## UmeaU LandscapeGenomics

Project description This project integrates genomic methods and ecological modeling to assess the effect of landscapes on evolutionary processes. We use recent conceptual and methodological advances in genetics and spatial ecology to study patterns in gene flow and how this is influenced by landscape structure and obstruction of dispersal pathways by land-use activities. The project will use genetic markers to infer how dispersal of riverine plants has been affected by dams in regulated rivers. We will also evaluate the distribution of genetic diversity along the river course in selected plant species. We test (1) whether dams are barriers to plant dispersal, resulting in isolated populations with higher genetic differentiation between sites separated by dams than between populations in the same impoundment or among sites in free-flowing rivers, and (2) whether the downstream increase in genetic diversity of riverine plants documented in many species is absent or less pronounced in rivers fragmented by dams. The results of the project will help manage regulated rivers with the aim to conserve riverine plant communities.

Qualifications We seek a candidate with relevant academic background (genetics, ecology, or equivalent subject) with interest in using genetic methods to understand landscape ecological processes. Experience with genetic analyses and laboratory work using genetic methods are required.

Experience of population genetic analyses, high throughput genotyping methods and knowledge of bioinformatics are meriting. The candidate should be creative, show initiative, independence and good social skills, and have a very good command in both oral and written English. Evaluation will be based on the individual letter, quality and relevance of master thesis and other publications, the interview, and the candidate's performance in a literature essay given after the interview.

The recruitment procedure for the position is in accordance with the Higher Education Ordinance. Prerequisites for PhD studies include a degree on Master level, or 240 ECTS credits of higher education studies of which 60 should be on an advanced level (Master level), or an equivalent qualification. This position specifically requires 120 ECTS credits in a subject relevant for ecology.

Terms for the employment The employment is expected to result in a doctoral degree and the main assignment for the doctoral student is thus to be part of the research education, which includes participation in the described research project but also to take relevant courses. Teaching and other departmental work (up to a maximum of 20%) can be included. The employment is limited to four years at full time or up to five years if teaching and other departmental work is performed. The salary is fixed according to the established salary level for doctoral students.

Application You apply through our recruitment system no later than April 15th, 2019. The application may be written in Swedish or English, and should include:

* A short letter (max 2 pages) describing your research interests and why you are interested in the position * CV, including academic achievements * Digital copies of Bachelor/Master thesis * List of publications * Certificates from higher education and other documentation that supports your application * Contact information of three reference persons.

Contact If you have questions regarding the position, please contact Roland Jansson, tel +4690-786 9573, e-mail roland.jansson@umu.se, or Xiao-Ru Wang, tel+4690-786 9955, e-mail xiao-ru.wang@umu.se.

The Department of Ecology and Environment Sciences, Umeå University, performs research and research education in ecology, environmental science and physical geography. The department has 150 employees of which 30 are PhD students. For more information, visit http://www.umu.se/en/department-of-ecology-and-environmental-science/ Umeå University wants to offer an equal environment where open dialogue between people with different backgrounds and perspectives lay the foundation for learning, creativity and development. We welcome people with different backgrounds and experiences to apply for the current employment.

To apply, visit the website: https://umu.mynetworkglobal.com/se/what:job/jobID:254914/ Roland Jansson <roland.jansson@umu.se>

---

## UNeuchatel MicrobialInteractions

PhD position on Microbial Interactions

I am looking to recruit a PhD student to study microbial interactions, in particular, bacteria dispersal through fungal hyphae networks, and bacteria-fungi interactions under different nutritional conditions, in University of Neuchâtel, Switzerland. The student will be co-supervised by Prof. Pilar Junier and/or Prof. Redouan Bshary.

In soils bacterial dispersal is highly limited because the discontinuity of water paths. Recently, it has been found that bacteria can disperse in the liquid layer on the surface of fungal hyphae. Fungal hyphae networks are like a 3D highway system that connects vast areas in the soil, providing potentially a very efficient way for bacteria to disperse. However, unlike the highways we are familiar with, fungal highways are generated by living organisms and likely the fungus providing a dispersal path interacts with bacteria in complex ways. In this PhD project we will find out how bacteria spread through fungal hyphae networks, and whether the interactions between fungi and bacteria promote or impede the dispersal. In addition, we will study how nutrients influence the interactions between fungi and bacteria. Our pilot experiments have already shown that the nature of interactions between fungi and bacteria can change in function of nutrient availability. Understanding the effects of nutrients can help finding ways to manipulate fungi-bacteria interactions and their effect on soil functioning.

The successful applicant should have a strong background in microbiology lab work and data analysis, and have completed a Master's degree before September 2019. Experience in mathematical modelling and knowledge of a programming language is an advantage. The candidate needs to be fluent in English.

To apply, please send an email to < li@evolbio.mpg.de >. Please include in your email a statement including 1) a brief overview of your previous academic and research experiences, and explain how your background fits with the project, 2) a CV or resume, and 3) a list of 2 to 3 academic references with their names and email addresses.

The position is funded by the Swiss National Science Foundation with a competitive salary for 4 years. The starting time should be September 2019 or earlier. Applications will be reviewed continuously until the position is filled.

Xiang-Yi Li (Dr. rer. nat.) Institute of Biology University of Neuchâtel Rue Emile-Argand 11 CH-2000 Neuchâtel Switzerland

http://web.evolbio.mpg.de/ ˜ li/ Xiang-Yi Li <li@evolbio.mpg.de>

---

## UPadova SturgeonConservation

A PhD position in Evolutionary Biology will be available ad the Department of Biology of the University of Padova, Italy, under the supervision of Prof. Leonardo Congiu.

The project is part of a larger project conducted by 4 Italian Universities with a big effort of massive sequencing (University of Florence), bioinformatics (University of Trieste) population genomics analyses (University of Ferrara), and in vivo (University of Padua) experiments, aimed at applying a Genomic approach to the conservation of five Italian endemic species (a mammal, a reptile, an amphibian, a fish, and an insect).

The doctoral project will specifically focus on one of the above species, the Adriatic sturgeon (Acipenser naccarii), a critically endangered sturgeon Endemic to Italy, and will include both field and laboratory activities.

The PhD project has the following goals: a) assess the degree of accumulation of potentially deleterious mutations in the small residual population of the Adriatic sturgeon; b) evaluate the effect of inbreeding on the fitness of 6 inbred and 6 outbred groups of fingerlings, generated by controlled reproduction, by estimating behavioural and physiological variables; c) identify a panel of ˜4,000 SNPs with alleles predicted to be deleterious will be typed in larvae from each cross to infer the pattern of load segregation and the association with the fitness estimates and the crosses (inbred vs. outbred). d) evaluate the effects of different rearing conditions on the expected survival of released individuals.

The selected candidate is expected be fully involved in the organization, conduction and data analyses of the in vivo experiments that will last the entire first year of activity, supported by post-doctoral fellows and by undergraduate students. In the following years the candidate will be also responsible for the genotyping and related data analyses and will have a primary role in many other planned activities. Finally, the candidate will be in continuous interaction with the other research groups in charge of generating and analyzing genomic data.

Potential candidates are strongly encouraged to contact me (leonardo.congiu@unipd.it) to get additional details about the project.

Opening of the official announcement: April 8th 2019

Application deadline: May 17th 2019

Starting: Oct 1st, 2018

For more information:

University of Padova http://www.unipd.it/en/ Department of Biology https://www.biologia.unipd.it/en/ PhD School in Biosciences https://dottorato.biologia.unipd.it/ Leonardo Congiu Dipartimento di Biologia Università di Padova Via Ugo Bassi 58/b 35121 Padova

tel.: +39 49 8276218 fax:+39 49 8276209

Leonardo Congiu <leonardo.congiu@unipd.it>

## UPorto EvolutionaryBiology

PhD Students Proposals Call for PhD candidates to apply for the FCT 2019 PhD Program competition - Portugal.

https://www.fct.pt/apoios/bolsas/concursos/individuais2019.phtml.en The position is contingent on FCT approval.

Applicants: Primarily Portuguese citizens or citizens of the EU member states. Citizens of other countries may also apply, as long as they have legal resident status in Portugal at the time of the application.

Requirements: The FCT criteria for scholarship selectivity gives a weight of 40% to the individual merit of the applicant (Individual evaluation). Therefore, only candidates with a very competitive curriculum are likely of being selected.

Preference for candidates with demonstrable experience in the area(s) of genetics, genomics, molecular evolution, bioinformatics and biotechnology.

Candidates should possess a Master's degree and English proficiency. Applicants should be Portuguese citizens or citizens of EU member states. Citizens of other countries may also apply, as long as they have legal resident status in Portugal at the time of the application. For further details about application requirements for this scholarship consult the evaluation guide: hhttps://www.fct.pt/apoios/bolsas/concursos/docs/Bolsas_2019_GuiaoAvaliacao_EN.pdf Research project and laboratory: The PhD candidate will develop the awarded project in CIIMAR, Porto (Matosinhos), Portugal, under the Evolutionary Genomics and Bioinformatics group Head by Prof. Agostinho Antunes (http://orcid.org/0000-0002-1328-1732 and https://www.scopus.com/authid/detail.uri?authorIdq02537544) in collaboration with several international institutions. Topic of research could range from Adaptive evolution (e.g. venom diversification, sensory, immunity, reproduction, development, etc), comparative genomics, selection signatures, symbiotic associations (e.g. animals-microorganisms symbioses, microbiomes, etc), bioinformatics, etc.

Candidates should send the CV and copies of their graduation and Master Ì s degrees (including final grades) to Prof. Agostinho Antunes (aantunes@ciimar.up.pt) before 18th March 2019 (first come first served chance).

Prof. Agostinho Antunes, Ph.D. Head of the Evolutionary Genomics and Bioinformatics Group CIIMAR, University of Porto Terminal de Cruzeiros do Porto de LeixÃµes, Av. General Norton de Matos, s/n 4450-208 Porto, Portugal Tel: (351) 22 3401 813 Fax: (351) 22 3390 608 & Department of Biology, Faculty of Sciences, University of Porto Rua do Campo Alegre s/n Porto, Portugal

Agostinho Antunes <aantunes777@gmail.com>

## UPotsdam EvolutionaryRescue

PhD student position at the University of Potsdam: Evolutionary Rescue in Complex Communities

A PhD student position is available in the Ecology and Ecosystem Modelling group headed by Prof. Ursula Gaedke at the University of Potsdam. This project will be under the supervision of Dr. Ellen van Velzen, in collaboration with Dr. Christian Guill.

Project description: Environmental change may drive species extinct; but evolutionary rescue (ER) of a species may occur if it can adapt rapidly enough to the new conditions. ER has been extensively studied in single-species contexts; however, very little is known on ER when species are embedded in a larger community such as a food web, and is interacting with prey, predators and competitors. In this project we will develop new theory on ER in such complex communities, comprising the incidence of, mechanisms for, and effects of ER in food webs ranging in size from small (4 species) to large (20-50 species). This new theory will be based on well-established theory of eco-evolutionary feedbacks, where rapid trait changes affect ecological dynamics in real time, and vice versa. The focus will here be on traits mediating predator-prey interactions: defensive traits in prey and offensive traits in predators. Such traits directly affect community dynamics, and therefore provide a rich potential for aiding ER that has gone essentially unexplored by existing theory.

The location: The Ecology and Ecosystem Modelling Group is an established centre for both theoretical and experimental study on eco-evolutionary dynamics. It is located in the middle of beautiful Park Sanssouci in Potsdam, a Cultural World Heritage site centrally located in Potsdam, and about 30 minutes away from Berlin. Further information on current group research can be found at https://www.uni-potsdam.de/en/ibb-ecology/ To apply: For this project we are looking for candidates with a MSc degree in ecology, evolutionary biology, or physics. Applicants should have a strong theoretical background, not be scared by mathematical modelling, and have some experience with models using differential equations. Experience with modelling population dynamics is particularly welcome. Knowledge of German is not required.

Interested applicants should send one PDF containing the following: - CV - letter of motivation - contact details of 2 references to Ellen van Velzen (velzen@uni-potsdam.de). Applications will be reviewed starting March 18, and reviewing will continue until the position is filled.

–

Dr. Ellen van Velzen Ã kologie & Ã kosystemmodellierung / Dept. Ecology & Ecosystem Modeling UniversitÃÂt Potsdam / University of Potsdam Institut fÃÂ¼r Biochemie und Biologie / Institute of Biochemistry and Biology

Maulbeerallee 2 (postal address: Am Neuen Palais 10) D-14469 Potsdam, Germany Tel. + 49 (0)331-977-1907

velzen@uni-potsdam.de

---

## UppsalaU ComputationalGenetics

PhD Student position in Computational Genetics, Uppsala University

The Carlborg research group at the Department of Medical Biochemistry and Microbiology, Uppsala University, are looking for PhD student candidates for admission during the fall semester of 2019.

The research group focus on studying the genetics of complex traits with a particular emphasis on non-additive genetic inheritance in polygenic genetic architectures. An interdisciplinary, interspecies approach is used, where new genetic models, statistical methods, and bioinformatics approaches are developed to explore experimental data from a range of species ’ from yeast to plants and domestic animals. Powerful experimental datasets are obtained from a variety of sources, including public repositories, collaborators or own experimental work. Researchers and PhD-students in the group are all involved in both methods development and experimental data analyses. You can find more information about the research group at https://www.imbim.uu.se/research-groups/genetics-and-genomics/carlborg–rjan/ . In the fall semester of 2019, we will be able to offer up to two candidates funding for performing their PhD studies with us. This funding is in the form of a full time four-year employment at Uppsala University. The position comes with salary and full benefits of being a Swedish University employee. During the studies, the PhD candidate will have full access to state of art computing resources and training programs provided by SciLife & Uppsala University. Limited travel funding for attending conference and summer schools are available within the program. Up to 20% teaching can be requested annually, in which case the position will be prolonged to five years. The PhD program includes a total of 30 credits (20 weeks) of courses, a few obligatory and most optional, the rest of the program is own research. More information on the PhD program can be found at http://www.imbim.uu.se/Education/-Postgraduate+education/information-and-documents/ .The starting date is flexible, but the initial plan is for admission during the fall semester of 2019. Review of applications will start immediately and will continue until suitable candidates have been found.

The first half (2 years) of the PhD projects will include work with the Virginia lines ’ a chicken population developed during a long-term (60 year) bi-directional, single-trait selection experiment. This is an excellent model to study the genetic basis of long-term selection response on an adaptive trait that is highly polygenic. Earlier work has shown that selection has acted on a complex genetic architecture including loci with either tightly linked adaptive variants, multiple segregating haplotypes and/or interactions between loci. By working with this experimental data, the PhD students will get training and hands-on experience with standard sequencing bioinformatics methods and tools, as well as state of the art statistical, population and quantitative genetics analyses. A valuable resource to the project is a dataset including approximately 4000 phenotyped, pedigreed and individually low-coverage sequenced individuals from a 19 generation deep advanced intercross line between the divergently selected lines. The later half (2 years) of the project will be decided depending on the interest and competence of the admitted PhD student, and could therefore involve, for example, detailed explorations of specific genetic mechanisms via analyses of data from other species or data simulations, or more focus on development of new models and methods for trait mapping or modeling of genotype-to-phenotype mappings.

Qualifications

MSc in Bioinformatics, Statistics, Computational biology, Quantitative/Population/Evolutionary genetics or similar qualifications is a requirement. If the degree is not already completed, it should be indicated when it is estimated to be obtained.

Given the analytical content of the project, it is a merit to have good knowledge and experience of both genetics and informatics. This can be shown through earlier research experience in the field. Programming is an important tool in the project and therefore you should have experience in programming in e.g. R, C++, Fortran, Perl, Python or Java. You should have excellent English abilities, both orally and in writing. If you are a mathematician/statistician/computer scientist, complementary knowledge in genetics or genomics is meriting. Knowledge in mathematics/statistics/computer science is in the same way meriting if your exam is in biology.

If you are interested in this PhD student, send us a letter of interest (including a description of formal qualifications, research interests and

— / —

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

## UTartu HumanPopGenomics

PhD position in human population genomics (Institute of Genomics, Estonian Biocentre; Institute of Cell and Molecular Biology), University of Tartu, Estonia

Supervisors Dr. Mayukh Mondal, University of Tartu (Estonia)

Dr Francois-X Ricaut, University of Toulouse (France)

Prof. Richard Villems, University of Tartu (Estonia)

Deadline May 31 st 2019

The Institute

T he Institute of Genomics of the University of Tartu was formed in 2018 through a merger of the Estonian Genome Center and the Estonian Biocentre, bringing together world class expertise in medical, population and evolutionary genomics. We host the Estonian Biobank (www.geenivaramu.ee) which has 150,000 participants and is connected to national health registries for phenotypic information. In May 2018, we opened a new ancient DNA laboratory, in which we have a core facility for DNA/RNA sequencing and genotyping and access to a High-Performance Computing Cluster (www.hpc.ut.ee). We publish widely in top journals and pride ourselves in our vibrant and international research community of 70 researchers and students.

The Institute's web page : [ https://www.genomics.ut.ee/en | https://www.genomics.ut.ee/en ]

and for the Estonian Biocentre: [ https://www.geenivaramu.ee/en/about-us/estonian-biocentre | https://www.geenivaramu.ee/en/about-us/estonian-biocentre ]

Project title

“New Guinea, a hotspot for human evolution: settlement history and adaptation in northern Sahul”

Background/Knowledge gap: Papuans are the oldest continuous human population found outside Africa. Recent advances in human genetics have highlighted the unique genomic characteristics of these populations. Isolated from the rest of the world for most of the last 50ky, they have undergone an independent genetic and cultural evolution and diversificatio n that is largely unexplored. Today Papuans harbor the highest proportion of genetic introgression (5%) and genomic traces ( <2%) from an archaic human, Denisova , vestiges of a possible early extinct expansion of modern humans out of Africa. Since their arrival into t he Sahul (ancient landmass composed of Australia and New Guinea), they have been shaped by a wide variety of environments (coast, swamp, high altitude), strong geographical barriers (high mountains, isolated valleys), exceptional cultural diversity (900 languages), and the independent development of agriculture in the highland (9000BCE). The biological patrimony of these human groups is inherited from a complex history involving: (1) the initial settlers (50kya), (2) admixture with extinct hominins; and (3) with the mid-Holocene Asians. Distinguish ing and isolating these three layers will help to answer some of the highly debated questions in human genetic history.

Aim/innovation: The PhD students will analyse new Papuan genomes, combining existing and recently developed software, and develop new research approaches/tools to: (1) better characterize the genetic ancestries inherited from extinct hominins; (2) reconstruct demographic processes during the last 50ky (population genetic model); and (3) identify specific selection signals from local adaptation or adaptive introgression (Asian or Denisova) related to environmental pressure s (high altitude, pathogen, diet). These results are crucial to understand out-of-Africa models and human adaptation to environmental pressures. We combine the reliability of previously developed analytical tools and the cost-effective usage of already generated and unpublished whole genome sequences associated to phenotypic and environmental data. Innovations rely on the largest dataset of high quality genomes analyzed for this under-explored region and the integration of several layers of biological diversity (genome and phenotype).

Collaborative research

The position will be part of a collaborative research network involving Prof Murray P Cox (Univ. of Massey, New Zealand), Dr Matthew Leavesley (Univ. of Papua New Guinea, PNG), Irene Gallego-Romero (Univ. of Melbourne, Australia), Dr Lounes Chikhi (Instituto Gulbenkian de Ciência, Portugal), Dr Nicolas Brucato (Univ. of Toulouse, France), Dr Robert Attenborough (Univ. of Cambridge, UK).

Duties and responsibilities

The PhD student will carry out his research activity in the field of modern human population genomics, including but not limited to the generation of DNA data from samples to the genomic library stage, the analysis of whole genome data and writing publications. He/she will have the opportunity to undertake fieldwork in Papua New Guinea, and would have to be capable of interacting and contributing to a research team

— / —

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

---

## UTechnologySydney RealTimePhylogenetics

Project description: We are looking for a talented PhD student to develop methods for real-time analysis of bacterial and viral outbreaks. The project will be part of a larger effort with international collaborators in the UK and USA that aims to develop methods that efficiently and accurately analyse data streams being generated by laboratories around the world. The project will provide the student experience in statistical modeling, programming, bioinformatics, and evolutionary biology.

Requirements: Undergraduate or postgraduate degree in bioinformatics, computer science, statistics, engineering or a related quantitative field.

Knowledge and skills to be developed: Bayesian statistics Phylogenetics and evolutionary biology Software development in R, Python, Java, C or C++ Production software engineering Linux command-line, HPC and cloud computing Excellent written and oral communication skills

Project supervisors: Professor Aaron Darling and Dr. Mathieu Fourment

Research environment: This role is within the ithree institute in the Faculty of Science, one of the largest faculties at UTS, which is Australia's top ranked young university, with a particular focus on research translation. The ithree institute brings together a team of scientists with diverse skill sets who collectively address key challenges in the understanding and control of infectious diseases in humans and animals.

Commencement date: Domestic applicants would be expected to commence studies in the Spring 2019 or Autumn 2020 terms (Closing dates April 30 2019 and September 30 2019). International applicants would be expected to commence studies in the Autumn 2020 terms (Closing date June 30 2019).

Contact: Informal enquiries can be sent to aaron.darling@uts.edu.au or mathieu.fourment@uts.edu.au –

Dr. Mathieu Fourment ithree institute University of Technology Sydney mathieu.fourment@uts.edu.au

Mathieu Fourment <Mathieu.Fourment@uts.edu.au>

## UVictoria PhytoplanktonBiodiversity

M.Sc. Student Position on Marine Phytoplankton Biodiversity

Biodiversity of Phytoplankton fron the North Pacific and Arctic Oceans: Using Molecular Tools to Understand Biological Oceanography

Department of Biology, University of Victoria, Victoria, Canada

We are looking for a highly motivated candidate for a 2-year M.Sc. research project in the Department of Biology at the University of Victoria (https://www.uvic.ca/science/biology/), commencing in September 2019 or as soon as possible thereafter. This position is part of an exciting project: ???Oceans of Biodiversity??? (https://www.foodfromthought.ca/oceans-of-biodiversity/), which aims to characterize the distribution and diversity of marine organisms through high-throughput DNA barcoding and other molecular genetic approaches.

The genetic diversity of marine phytoplankton is vastly under-characterized. This project will develop methods and undertake metabarcoding of mixed-species assemblages of phytoplankton from the subarctic North Pacific Ocean and the Pacific Arctic region (Bering and Chukchi Seas). Through the use of state-of-the-art molecular sequencing techniques, microscopy and computation, the student will analyze samples collected during oceanographic cruises to provide detailed information of the composition of phytoplankton assemblages. In parallel, the student will focus the attention to those diatom taxa responsible for harmful effects on fin- and shellfish fisheries and aquaculture, and on natural fish and avian populations through the production of domoic acid.

This project is ideal for a student with a strong background in cell and molecular biology and knowledge of marine biology, interested in the application of these techniques to environmental science. The student will be co-supervised by Dr. Ryan Gawryluk (Department of Biology) and Dr. Diana Varela (Department of Biology, and School of Earth and Ocean Sciences), and will have opportunities to interact with other researchers at the University of Victoria and across Canada through their participation in the ???Oceans of Biodiversity??? and ???Food from Thought??? projects.

Preference will be given to a student with an excellent academic standing (GPA > 7/9 in the UVic scale or 3.3/4), and appropriate background. Applications are open to international candidates as well as Canadian citizens or permanent residents of Canada.

Applicants should submit a resume highlighting their previous research experience, copies of university transcripts (undergraduate and graduate as appropriate ??? unofficial copies are adequate at this stage) and a brief statement of scientific and academic interests to both: Drs. Ryan Gawryluk (ryangawryluk@uvic.ca) and Diana Varela (dvarela@uvic.ca).

Ryan Gawryluk <ryangawryluk@uvic.ca>

---

## UWyoming SalmonidEvolutionAlpineLakes

***MSc position - University of Wyoming - salmonid evolution in alpine lakes***

An MSc position is available to work on a funded collaborative, interdisciplinary project examining fish evolutionary responses to introduction in alpine lakes of the Wind River Range, Wyoming. The position is jointly in the labs of Catherine Wagner (cewagnerlab.com) and Amy Krist (http://www.uwyo.edu/krist/), with additional collaboration with Annika Walters (http://wyocoopunit.org/labs/walters-lab/people) and Bryan Shuman (https://sites.google.com/site/shumanlab/Home).

This MSc project is a component of a larger project examining ecological and evolutionary responses to fish introduction in alpine lakes of the Wind River Range, a stunning and little-studied mountain range in western Wyoming. The project is studying three key components of change associated with fish introduction into alpine lakes: 1) the response of contemporary zooplankton communities to fish; 2) lake ecosystem change associated with fish introduction through the study of lake sediment cores, and 3) fish evolution in response to their introduction into these lakes by humans ~50-100 years ago. The MSc project advertised here will focus on this third component, and will involve collection an analysis of fish and zooplankton communities, measurement and analysis of fish phenotypes, and genetic work. The MSc student will work integratively with other MSc students focused on analysis of zooplankton communities and analysis of ecosystem change in sediment cores.

Candidates should have a strong background and interest in ecology and evolution, and motivation for highly collaborative team-based fieldwork in the high alpine for several weeks each summer. Previous experience working with fish would be useful but is not required. Study sites are difficult to access and require extended backcountry travel; field teams make use of stock animals during extended trips to carry supplies and samples. The starting date for this position is summer 2019 with the goal of obtaining samples during this field season prior to starting as an MSc student in fall semester 2019.

Please send a letter of interest, CV, and contact information for three references to Dr. Catherine Wagner: catherine.wagner@uwyo.edu. Position will remain open until filled, but applicants are encouraged to submit applications by April 5, 2019.

"Catherine E. Wagner" <Catherine.Wagner@uwyo.edu>

---

## ZFMK Bonn InvertebrateMetabarcoding

PhD studentship: Metabarcoding of invertebrates

(TV-L E13, 65%)

The Zoological Research Museum Alexander Koenig in Bonn (ZFMK) invites applications for a 3-year PhD position starting no later than May 1st, 2019.

The position is part of the project "Integrative Analysis of the influence of pesticides and land use on biodiversity in Germany" (INPEDIV). The interdisciplinary joint research of seven partner institutes is led by the Zoological Research Museum Koenig and funded for 3 years by the Leibniz Competition. The aim of this study is to investigate consequences of organic and conventional farming for biodiversity in protected areas. By use of traditional methods and new technologies, we will examine agricultural land use effects on a broad range of plant and animal taxa at study sites in the Rhineland and in Brandenburg.

We seek an enthusiastic and highly motivated candidate for field sampling and metabarcoding of invertebrates in the Center for Molecular Biodiversity Research at the ZFMK in Bonn. The main task of the PhD student is to analyze insect and soil fauna samples using novel metabarcoding bioinformatic pipelines and the GBOL reference database.

The project will involve the analysis of metabarcoding sequence data from thousands of samples and their integration with data from soil pesticide and nutrient content, land-use patterns and vegetation characteristics, as well as with the occurrence of insectivorous vertebrate species. The PhD student will be supervised by a multi-disciplinary team led by Dr Sarah Bourlat (metabarcoding) and Dr Livia Schäffler (biodiversity assessments) and closely cooperate with researchers at partner institutes (vegetation, invertebrate and vertebrate ecologists, ecotoxicologists).

The PhD candidate should be highly motivated, with excellent bioinformatic skills and with a strong enthusiasm for environmental molecular biodiversity, as well as field experience and a decent background in biodiversity and ecology. Desirable skills are experience in handling large sequencing datasets, python or perl scripting skills, knowledge in statistical analyses with R and in data visualization. Students are expected to acquire and develop new skills but candidates with prior expertise in analysis of high throughput data (Illumina Mi-Seq) and using tools such as Qiime or R will be given preference. The candidate should have a Master's degree, or be close to completing a Master's degree in bioinformatics, biology or a related discipline. Fluent spoken and written English is essential.

The Zoological Research Museum Alexander Koenig (ZFMK) is one of three natural history research museums in the Leibniz Association and a lead institute in the documentation, research, and interpretation of animal biodiversity. The combination of classical museum work and various cutting-edge approaches with a modern molecular laboratory at the Center for Molecular Biodiversity Research and a state-of-the-art high-performance computing cluster offers a highly motivating and stimulating research environment. For more information about the museum see http://www.zfmk.de . Applications should include:

(1) Letter of motivation (relevant skills, experience and research interests)

(2) Curriculum vitae

(3) Official BSc and/ or MSc certificates

(4) Contact details of two (ideally academic) references

Please submit your application electronically as a single PDF file until March 17th, 2019 to Mrs. Heike Lenz: h.lenz@leibniz-zfmk.de

Questions concerning the project may be directed to Dr Livia Schäffler (l.schaeffler@leibniz-zfmk.de), those on metabarcoding to Dr Sarah Bourlat (s.bourlat@leibniz-zfmk.de).

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

Dr. Sarah J. Bourlat, Assoc. Prof. Metabarcoding section Centre for Molecular Biodiversity Research Zoological Research Museum Alexander Koenig (ZFMK) Adenauerallee 160, 53113 Bonn, Germany s.bourlat@leibniz-zfmk.de

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

Bourlat Sarah <S.Bourlat@leibniz-zfmk.de>

# Jobs

Barcelona TransmittingScience CourseCoordinator 62
DukeU LabManager EvolutionaryBiomechanics . . . . 63
Duke Univ LabTechEvolutionaryGenetics . . . . . . . . . 63
GulbenkianInst Portugal 1-3yr Bioinformatics . . . . . 63
LosAngeles NHM IchthyologyManager . . . . . . . . . . . . 64
MacquarieU Sydney EvolutionaryGenomics . . . . . . . . 65
Montana LabTech eDNA . . . . . . . . . . . . . . . . . . . . . . . . . 66
MountainLakeBiological Interim FieldStationManager 67
PrincetonU Tech EvolutionBehaviorGenomicsNeuro 67
SouthAfrica FieldManager StripedMouseProject . . . 68
StAndrews UK AquacultureGenetics . . . . . . . . . . . . . . 69
StonyBrookU DirectorLauferCenter . . . . . . . . . . . . . . . 70
UAE ConservationGenomicsResearcher . . . . . . . . . . . 71
UArkansas LabTech NeuroEvoDevo . . . . . . . . . . . . . . . 71
UBergen EvolutionMarineAnimals . . . . . . . . . . . . . . . . . 72
UGlasgow 1-2month Bioinformatician . . . . . . . . . . . . . 73
UGuam Genomics . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 74
UIowa TeachingEvolution . . . . . . . . . . . . . . . . . . . . . . . . . 74
UKansas ResAsst DrosophilaComplexTraits . . . . . . . 75
UmeaU Sweden Evolution . . . . . . . . . . . . . . . . . . . . . . . . . 76
UMontana LabTech InvasiveSpecies . . . . . . . . . . . . . . . 76
UNebraska LabTech GeneFunction . . . . . . . . . . . . . . . . 76
UNorthTexas BioinforamticsStaff . . . . . . . . . . . . . . . . . . 77
ZFMK Bonn Metabarcoding . . . . . . . . . . . . . . . . . . . . . . 77

## Barcelona TransmittingScience CourseCoordinator

Dear colleagues,

Transmitting Science is looking for a person to work as course coordinator full-time for 6 months, with the possibility of extending it afterward. That person has to have a background in research, and be willing to move out of academia to develop other activities related to science and evolution.

Main responsibilities of a course coordinator

* Answering daily emails related to the courses. * Being with the group of students during the course. * Being in charge of the logistics needed to run the course. * Helping with the advertising of the course.

Requirements

* Degree in Biology, Anthropology, Archaeology or other scientific disciplines. * Experience in research (Master, PhD or any other experience in Academia). * Good level of written and spoken English. * Good level of written and spoken Spanish and/or Catalan. * To own

a car. * Being based in Barcelona province.

We also appreciate the following:

* Good level of R, Python and/or Pearl. * Background on genomics or ecology. * Previous experience organizing conferences and courses. * Extrovert personality. * Ability to work both independently and in a team. * Very well organized.

Application deadline: 10th of March 2019

Applicants should send a2 pages CV and a Motivation Letter before March 11th to info@transmittingscience.org

Selected applicants will be contacted after that date with more information and to set up an interview.

Best wishes Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org Soledad De Esteban Trvigno <soledad.esteban@transmittingscience.org>

## DukeU LabManager EvolutionaryBiomechanics

Lab manager position in comparative, evolutionary biomechanics research

The Patek Lab in the Biology department at Duke University has an open position for a full-time lab manager/research associate position, starting early summer 2019. This position is approximately 50% aquarium animal care and administrative support, and 50% research in areas including biomechanics, evolutionary analysis, engineering, and mechanics. This position is suitable for recently-graduated undergraduates who need an extra year of research experience before applying to graduate school. It is not suitable for gap year pre-medical students, given that this position is geared toward research apprenticeships for future basic research scientists or engineers.

If you are interested in applying, please upload a cover letter detailing your interest in the position, the Patek Lab research program, and any relevance to your career goals/interests. Please also include your CV/resume, unofficial transcript and the names/contact info for three references. Submit materials to Academic Jobs Online: https://academicjobsonline.org/ajo?joblist—3-12934 The salary will be approximately $17-18/hour or ~$37,000/year.

Job applications are reviewed continuously. There is not a set deadline for job applications, so it is best to submit as soon as possible.

Inquiries about the position should be sent to Prof. S. Patek, snp2@duke.edu

Sheila Patek <snp2@duke.edu>

## Duke Univ LabTechEvolutionaryGenetics

Lab Technician ("Associate In Research") position available in Mohamed Noor lab at Duke University in Durham, North Carolina, USA. Duties will be to aid in project studying abundance of lethal alleles in natural Drosophila fruit fly populations. Anticipated start date June 1, 2019.

For general information and to apply, please use this site: https://academicjobsonline.org/ajo/jobs/13493 Please DO NOT send applications via e-mail.

noor@duke.edu

## GulbenkianInst Portugal 1-3yr Bioinformatics

The Evolutionary Biology Lab at the Instituto Gulbenkian de Ciọncia (IGC) is recruiting a collaborator in Bioinformatics and/or Computational Biology.

We are seeking a highly motivated person with experience in analysis of genomics data of prokaryotes to work at IGC, in the context of a collaborative project between Isabel Gordo (Principal investigator of the Evolutionary Biology Lab) and Michael Lassig (Principal investigator of the Statistical Physics and Quantitative Biology Lab at the University of Cologne).

The ideal candidate should have a PhD in the field of Bioinformatics or Computational Biology, research experience in NGS data analysis or modelling of microbial evolution. Candidates with a Ms degree will also be considered if they have experience in this field.

The successful applicant will be fully integrated in the team working in Gordos Lab, actively participating in lab meetings, seminars and training. S/he will also interact closely with members of Lassigs Lab and collaborators of the Collaborative Research Centre (SFB) 1310 Predictability in Evolution. To fulfil this role, s/he will be given a high degree of responsibility and freedom.

S/he will be encouraged to undertake periodic visits to the University of Cologne to strengthen the international collaborations that have been established in Gordos Lab. Fluency in English (written and spoken) is required.

The fellowship will have the duration of 12 months with possibility of extension at the end of this period, for a maximum of 3 years. The successful candidate will be contracted on the basis of exclusivity as regulated by the directives of the Instituto Gulbenkian de Cio̲ncia ( www.igc.gulbenkian.pt).

Applications should be sent by email to igordo@igc.gulbenkian.pt <vmartins@igc.gulbenkian.pt> with the subject: Bioinformatician IGC-Cologne. The application should consist of one PDF file including a motivation letter, CV and the contact of two previous supervisors (mentors or teachers in the case of a Ms holder). Potential candidates will be pre-selected on the basis of CV and motivation letter, and selected candidates will be called for interview.

Ricardo Ramiro <ramiroricardo@gmail.com>

---

## LosAngeles NHM IchthyologyManager

Job posting: Collections Manager of Ichthyology, Natural History Museum of LA County

The Natural History Museum of LA County (NHMLA) seeks a Collections Manager of Ichthyology. NHMLA's fish collection consists of approximately 190,000 lots (about 3 million specimens) of wet specimens and skeletal material, with related collections including frozen tissues, otoliths, eggs and larvae, cleared and stained specimens, photographs, radiographs, and field notes.

Under the direct supervision of the Curator of Ichthyology, the Collections Manager will oversee the day-to-day operations of the fish collection, including processing incoming and outgoing loans and accessions, maintaining the collection's records in NHMLA's EMu database, maintaining and organizing specimens, improving and enhancing the collection through physical improvements and digitization projects, facilitating use of the collection by researchers, and supporting the needs of other NHMLA departments including Exhibitions, Education and Programming, and Marketing and Communications.

NHMLA is especially interested in candidates whose background and experience have prepared them to contribute to our commitment to engage and include culturally diverse audiences in museums and in science.

RESPONSIBILITIES:

-

- Cares for the Ichthyology collection on a day-to-day basis, including organizing, storing, securing and conserving. Plans and oversees consolidation, rehousing, and movement of the collection as necessary and/or directed by the Curator or VP Research & Collections. Assists with the development and implementation of plans for collection growth and improvement. Works cooperatively with other collection management and conservation staff to achieve the highest level of collection care and productivity across organizational units.
-

- Provides documentation for the collection, including cataloging, entering/updating database records, inventorying, enhancing documentation through digitization, and researching specimen and/or material information.
-

- Processes all incoming and outgoing specimens and/or materials including purchases, donations, exchanges and loans. Maintains extensive knowledge concerning the organisms and specimens in the Ichthyology collection. Serves as liaison to donors and lenders between Ichthyology and the Registrar's Office. -

- Supports the Curator and/or VP Research & Collections in the acquisition of new specimens and/or materials for the collection through purchase, donation, exchange, and field collection. -

- Facilitates visits by researchers using the collection. -

- Supports the planning, installation and maintenance of temporary and permanent exhibits.

Expedites the use of collection materials for display. -

- Participates in education and other public program activities of the Museum including but not

limited to tours for the public and Museum members, and training of Museum Docents and Gallery Interpreters. Handles inquiries from the public and researchers. Conducts collection and lab tours as requested.

-

- Stays current with the research field related to the collection including trends and techniques in collections management, collection-based research, conservation, digitization, biodiversity informatics, and documentation. -

- May lead or participate in ongoing or original research related to the collection. -

- Initiates and/or assists with identifying potential funding sources and writing proposals seeking

grant funding for the collection. -

- Trains, supervises, and manages collections personnel, including students and volunteers. - Advocates for natural history collections and effectively communicates their importance to - members of the public and the scientific community.

REQUIRED QUALIFICATIONS:

-

- Master's degree with specialization in ichthyology, museum studies, or a related field and at least two years of technical experience in the collection, organization, care and/or conservation of natural history specimens/collections; or a bachelor's degree in an applicable field and 5 years collection experience; or an equivalent combination of education and experience. -

- Working knowledge of fish taxonomy and the organization and management of ichthyological collections. -

- Database and Informatics Experience: Experience with database software typically used in natural history collections; working knowledge of common principles of biodiversity informatics and external data repositories such as VertNet, GBIF, and iDigBio. -

- Communication: Demonstrated excellence in oral and written communication. -

- Writing Skills: Ability to write reports, grants, professional correspondence, and procedure

manuals. -

— / —

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

---

## MacquarieU Sydney EvolutionaryGenomics

Lecturer or Senior Lecturer in Evolutionary Genomics

Job no: 505380 Work type: Full Time Vacancy type: Internal Vacancy, External Vacancy Categories: Academic - Teaching and Research

Salary Package: Lecturer (Level B) from $103,914 to $122,947 p.a., or Senior Lecturer (Level C) from $126,879 to $145,912 p.a., plus 17% employer's superannuation and annual leave loading

Appointment Type: Full-time, continuing

Macquarie University (North Ryde) location

The Role

We are seeking to appoint a dynamic and enthusiastic individual wishing to develop a distinguished academic career in the field of evolutionary genomics. This position is an exciting opportunity to develop a world-class research program in evolutionary genomics, including for example comparative or functional genomics, that draws strength from the department's excellence in integrative biology.

The successful applicant will be expected to develop, teach and convene units in the Bachelor of Medical Sciences, Bachelor of Science and Master of Research programs and to take a leading role in development of curricula within the Bachelor of Medical Science. In addition, they will develop and lead an active research group, including supervision of Higher Degree Research students. They will also be expected to make an active contribution to the administration and function of the Department, Faculty and University and support the Department's values of collegiality, sustainability, inclusion and respect.

About Us

The Department of Biological Sciences at Macquarie University is a leading research and teaching department and conducts research at all levels of biological organisation as well as across a diversity of taxa. Genomics is central to biology and the ability to link genomics with form and function is now the most important feature of the world's most successful biology departments. The Department has strong research and teaching partnerships within the Faculty of Science and Engineering and across the Faculty of Human Sciences and the Faculty of Medical and Health Sciences. Our priority is to create a safe, supportive and inclusive culture for all staff and students. For more information please visit http://bio.mq.edu.au/ Macquarie is a university engaged with the real and often complex problems and opportunities that define our lives. Since our foundation 54 years ago, we have aspired to be a different type of university. Over the years, we've grown to become the centre of a vibrant local and global community. Connect with us today < https://www.mq.edu.au/ >.

To Apply

Macquarie University has selected this position as a trial for Anonymised Recruitment < https://secure.dc2.pageuppeople.com/apply/TransferRichTextFile.ashx?sData=UFUtVjMto6VjLYT_WiszVYml7kw_8D9iEMwed7tLTbuUwvlxPuNSGpW8_tSAMqcQfmntcbZdluFr63CPDyzf7gGvt64RJJMYgHsRtL6Q5qFxoZ4Oe6BV_Z2YT_gEtKxve4TtRpzdwn-JtfhZ0HFzUOvEr7cg%7e%7e >. To be considered for this position, please apply online by submitting your cv and completing the application screen questions. Please note that although you will be asked to provide personal details and your cv during the application process we will be assessing and selecting applicants for interview based on responses to the questions in the application screen. Applicants invited to an interview will be assessed against the selection criteria below:

Essential Selection Criteria for appointment at Level B relative to opportunity:

* A PhD in a relevant discipline * Demonstrated output of high-quality research in evolutionary genomics * Demonstrated capacity to attract external research funds * Demonstrated success in developing and delivering teaching material, including the ability to develop scholarly and innovative approaches to teaching and learning, particularly in an online environment * Demonstrated ability to supervise higher degree research students * Excellent written and verbal communication skills * An interest in building collaborations within and outside the department * A commitment to support and contribute to the Department's values

Additional selection criteria for appointment at Level C relative to opportunity:

* Proven track record of research excellence in evolutionary genomics * Proven track record in attracting external funds * Proven track record in curriculum development

Specific Role Enquiries: Professor Michelle Leishman, Head of Department of Biological Sciences michelle.leishman@mq.edu.au

General Enquiries: Anne Kumanan, HR Officer at anne.kumanan@mq.edu.au

— / —

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

---

## Montana LabTech eDNA

Job announcement/advertisement

LAB TECHNICIAN FOR ENVIROMENTAL DNA (eDNA) RESEARCH & MONITORING

Project: Detecting invasive species using qPCR & novel water sampling methods

Principal Investigators: Gordon Luikart, Steve Amish, & Brian Hand, Flathead Lake Biological Station and Montana Conservation Genomics Laboratory, Division of Biological Sciences, The University of Montana. gordon.luikart@umontana.edu; Steve.Amish@umontana.edu (406-872-4517).

Start Date & Duration: May 2019; 1 year with likely extension

Project Description/Summary: Aquatic Invasive Species (AIS) such as rainbow trout, bass, and zebra mussels are spreading across North America causing massive economic and ecological problems. To help prevent spread, new environmental DNA (eDNA) sampling and laboratory qPCR tests are now available for early detection and monitoring AIS. This lab position will involve optimizing real time qPCR assays applying them to track spread of AIS. Much of the work will involve testing water samples from Montana, Idaho, and adjacent states. The successful applicant could help collect water eDNA samples in national parks and wilderness areas across Montana. Sampling would include use of a mobile qPCR on lakes (from a speed boat), and the use of autonomous sampling instruments that collect multiple samples daily (automatically, with no human on site) from streams. We are especially concerned about stopping the spread of zebra mussels which were discovered in Montana in 2016 (Fig. 1). The successful applicant will also test for invasive rainbow trout, brook trout, and bass (Fig. 2). Skills required: The applicant should have experience applying qPCR assays (e.g. TaqMan) to eDNA samples or difficult/ancient DNA samples. The successful applicant would ideally also have a Master's degree or equivalent experience in writing reports or publications, working as a team, and collaborating successfully with natural resource agency field biologists. The applicant will participate in planning and publishing model projections of AIS spread. Experience with metabarcoding and next generation sequence data analysis would be helpful.

Applications: Send a brief letter ( < 1 page) describing your motivation and background, your CV, and the names and contact information for three references. Review of applications will start immediately (February) and remain open until a suitable candidate is hired.

Salary: will depend on your experience and CV.

Key references: see our web pages, this eDNA video at: https://flbs.umt.edu/giving/default.aspx?id=1 and click on the video (arrow) on the right side; and contact us. See also Gingera et al. 2017 DOI: https://doi.org/10.3391/mbi.2017.8.3.03 . Fig. 1 Invasive (a) zebra & quagga mussels, (b) encrusted research equipment, (c) a crayfish encrusted with zebra mussels.

Fig. 2 Invasive (a) rainbow & (b) brook trout that threatening native trout.

gordon.luikart@mso.umt.edu

## MountainLakeBiological Interim FieldStationManager

Mountain Lake Biological Station (MLBS.org) is searching for a temporary, leave replacement, Station Manager to run field station office and manage operations, July - November 2019.

Link to this notice: mlbs.org/MLBS-Interim-Manager-2019

Direct link to full job description and UVA HR application posting: https://uva.wd1.myworkdayjobs.com/en-US/UVAJobs/job/Other-Locations/Interim-Station-Manager–Wage-_R0002603 Or alternatively, follow this HR path: Go to: https://uva.wd1.myworkdayjobs.com/UVAJobs Search for: R0002603

Questions about the position? Contact Associate Director Eric Nagy. enagy@virginia.edu +1-434-243-4989

esn8n@virginia.edu

## PrincetonU Tech EvolutionBehaviorGenomicsNeuro

The McBride Lab at Princeton University (http://mcbridelab.princeton.edu) is looking for a lab technician to support research on the molecular, neural, and evolutionary basis of preference for human odor in mosquitoes. The technician will devote ~75% of his/her time to a specific research project and the remaining ~25% time to general maintenance and lab support. The technician will be welcomed as a full lab member and expected to attend journal clubs and lab meetings and to contribute to a dynamic and interactive lab atmosphere. This is an opportunity to become deeply involved in exciting research at the interface of evolution, genetics, and neuroscience and is well-suited for a recent college graduate looking for more experience/focus before graduate school.

Responsibilities

Research project activities may include Â Mosquito behavioral experiments and breeding Â Generation of transgenic strains using CRISPR/Cas9 Â Odor collection and analysis using GC-Mass Spec Â Molecular biology studies including DNA/RNA extraction, PCR, cloning Â Preparation of high throughput sequencing libraries. Â General maintenance and lab support.

Qualifications

The interested candidate should have a bachelor's degree in biology or related field and previous experience in a research laboratory (beyond lab classes). Previous experience rearing insects, studying behavior, and/or carrying out molecular biology protocols in a research setting is strongly preferred. A demonstrated interest in evolution, neuroscience, genetics and/or behavior is also preferred. It is absolutely essential that candidates be highly organized, detail-oriented, and demonstrate enthusiasm for working and communicating with others in a collaborative lab setting.

Princeton University is an Equal Opportunity/Affirmative Action Employer and all qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity or expression, national origin, disability status, protected veteran status, or any other characteristic protected by law. EEO IS THE LAW

Applications will be reviewed starting March 15th and continue on a rolling basis. Contact Lindy McBride at csm7@princeton.edu with questions. TO APPLY visit https://research-princeton.icims.com/jobs/9987/research-specialist-i/job?hub&mobileÃo̲lse&width00&heightP0&bga=-true&needsRedirectÃo̲lse&jan1offset=-300&jun1offset=-240 csm7@princeton.edu

---

## SouthAfrica FieldManager StripedMouseProject

1 position as station manager at the striped mouse project in South Africa,

starting July (latest October) 2019 for 1.5 - 3 years

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project in July 2019 or latest October for a maximum of 3 years as station manager. This position is suitable for somebody who would like to gain experience in field work and scientific management. Managers get free accommodation at the station and a compensation of R4700-5400/month to cover their daily costs. Travel costs can be refunded by up to an additional R 15 000 / year. As such, the position compensates for all arising costs but does not represent a legal employment.

The station manager will work closely together with the research manager and both managers will share responsibilities. Each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained).

Our present station manager will leave the project end of October. The new station manager will be instructed by the present station manager and both will overlap for 3 months.

Great opportunity: This is a great opportunity to spend 1.5-3 years in Africa, acquiring important skills in field biology and project management, while improving your CV. These skills will become valuable whether you later continue with a PhD or other jobs. It will be very hard and demanding, but also a once in a life time experience!

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You should love to live at a remote place in nature, without regular internet and cell-phone reception. You must have a drivers licence. Most importantly, you are fascinated by nature and science! The station manager must also have technical skills (respirometry laboratory) and be able to do some maintenance work at the research station (handy man skills).

Shared duties

We want to know at all time all striped mice present at the field site and their social tactic!

- Trapping
- Observing
- Radio-tracking, putting radio-collars on
- Blood sampling
- Collect data for specific research projects (to be determined. Examples would be collecting urine samples, data on basking, cognitive testing .)

Primary duties station manager / secondary duties research manager

- Technical support research station:
- Water system incl. sewage system
- Solar system
- Gas bottles replacement
- House and furniture
- Running of the respirometry laboratory
- Management of the captive colony
- Management of the research station car
- Management of bank account and cash box
- Management of research station supplies

Primary duties research manager / secondary duties station manager

- Data:
- Weekly data entry
- Weekly data check
- Monthly data backup
- Monthly data report
- Training and supervision of field assistants
- Training of students and postdocs
- Support for students and postdocs
- Management of transmitters
- Management of field and laboratory supplies

Job description: Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included are four weeks of holiday for 12 months, which has to be taken outside the main breeding season (August to November) during periods when other students are present at the research station.

Compensation:

- Free accommodation.

- A monthly compensation of R 4700, which is sufficient to pay all costs of living (approx. 4000/month). The compensation can gradually raise up to R5400/month. - For travel costs, R15 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after 12 months and can be in Rand or in Euro. - You can become a honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. - Scientific co-authorship will be possible if the manager contributes to the success of projects by not only collecting the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

- The manager has to cover the costs to get to the station, including travel costs and visa fees. For this, a refund can be paid (see above).

- The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to the stations. The costs for this qualify for travel compensation.

Place and project: Succulent Karoo Research Station in the Goegap Nature Reserve near Springbok in the Northern Cape of South Africa. The research projects are on the socio-ecology of small mammals, studying ecological and

— / —

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

---

## StAndrews UK AquacultureGenetics

Scientific Officer in Aquaculture Genetics Xelect Ltd. Scotland, UK

Job Type: Full-time

Salary: £28,000.00 to £30,000.00 /year

Xelect Ltd, the leading UK aquaculture genetics service company is seeking to appoint a highly motivated candidate for a permanent position on its scientific staff. The successful candidate will have a BSc in a relevant biological science and a PhD in molecular biology or genetics. Practical experience with customised DNA library construction and next-generation sequencing is essential and previous work experience is highly desirable. The ability to work to high standards of accuracy with large volumes of samples is of critical importance whilst some knowledge of programming in R would be an advantage. The company operates an internal training programme and offers a pleasant, stimulating and varied working environment with the benefits of a competitive salary (starting range £28-30K) and a defined benefit pension scheme. Applicants should send a cover letter, curriculum vitae and the names and contact details of three referees. The closing date for applications is 5pm Monday 1st April 2019.

About Xelect

Xelect Ltd is a privately-owned aquaculture genetics company founded in 2012 following a spin-out from the University of St Andrews, one of the United Kingdoms leading research Universities. The company provides a complete service for the genetic management of breeding programmes employing a team of aquaculture specialists, bioinformaticians, quantitative geneticists, molecular biologists and fish physiologists. Xelect has modern genetics laboratories and offices in the historic heart of the coastal town of St Andrews around 80 km north of the Edinburgh, Scotlands capital city. The company has invested heavily in state-of-the-art genotyping and DNA sequencing platforms and maintains an active research and development programme in collaboration with leading academic institutions across Europe. It is one of the few companies able to provide custom genetics tools, in house genotyping and advanced quantitative genetics support in a single package. A dedicated breeding programme manager and deputy provide practical hatchery support for each customer. Xelect currently manages breeding programme genetics for customers in North and South America, Europe, SE Asia, and Oceania covering sea bream, striped bass, sea bass, Barramundi, Eurasian perch, rainbow trout, Atlantic salmon, Chinook salmon and several prawn species. Further information about the company can be found on our web site at www.xelect.co.uk . Experience:

Next generation sequencing and library preparation: 1 year (Preferred)

Education:

PhD (Required)

Marie Smedley <marie.smedley@xelect.co.uk>

---

## StonyBrookU DirectorLauferCenter

This ad for a Senior Endowed Position at Stony Brook. I an Chair of the search committee. An evolutionary biologist could be considered.

Walt

Endowed Full Professor Laufer Center for Physical & Quantitative Biology Stony Brook University

Responsibilities & Requirements: We seek an outstanding senior scientist for a tenured endowed full professor position. We want a bold innovator working at the interface between the life sciences and physical sciences. We seek expertise in the physical biology of cell actions – principles, mechanisms, adaptation/evolution. Examples include – but are not limited to – cellular networks, single-cell experiments, fitness landscapes and stochastic dynamics. We focus on basic research, but are cognizant of the impacts on challenges such as aging, amyloid diseases, cancer, or drug resistance. We prefer an experimentalist, but we welcome applications from theorists.

This is a basic-research position, with minimal teaching. It has attractive resources, including a Laufer Endowed chair that provides some annual research support. The successful individual will have considerable freedom to choose his or her departmental affiliation. Preference will be given to a candidate with leadership skills who can help guide the Center's future.

The Laufer Center is an exciting collaborative cross-disciplinary place for physical and quantitative biology at Stony Brook University, just minutes from Stony Brook Medicine, comprising the Renaissance School of Medicine and the Stony Brook Cancer Center. We have researchers from Biomedical Engineering, Chemistry, Physics, Applied Mathematics and Statistics, Computer Science, Pharmacology, Molecular Genetics and Microbiology, and Ecology and Evolution, and close ties to our neighbors at Cold Spring Harbor Laboratory and Brookhaven National Laboratory. Stony Brook is in a beautiful mid-Long-Island location on the LI Sound with outstanding local schools, 70 miles from New York City.

This is a basic-research position, with minimal teaching.

Required Qualifications: PhD and a strong record of research productivity in relevant field.

Special Notes: This is a tenure track position. FLSA Exempt position, not eligible for the overtime provisions of the FLSA. Internal and external search to occur simultaneously. Eligibility for tenure will be based upon applicants' qualifications and experience. To qualify for tenure and/or a senior faculty appointment, the candidate must meet the criteria established by Stony Brook University. Anticipated Start Date: Spring 2020.

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 Governors Office of Employee Relations at (518) 474-6988 or via email at info@goer.ny.gov.

Stony Brook University is 100% tobacco-free as of January 1, 2016. See our policy and learn more at stonybrook.edu/tobaccofree.

The selected candidate must successfully clear a background investigation.

Application Procedure: Those interested in this position should submit a State Employment Application , cover letter, resume/CV, a two- to three-page description of research plans, and arrange to have at least three letters of reference uploaded to AJO by clicking Apply. Alternately, you may submit your application package to the departmental address below. Please also fill out an online Applicant Information Survey . Do not submit this survey to the department. Applications should be sent to: https://academicjobsonline.org/ajo/jobs/-13401 Campus Description: Stony Brook University, home to many highly ranked graduate research programs, is located 60 miles from New York City on Long Island's scenic North Shore. Our 1,040-acre campus is home to 24,600 undergraduate, graduate, and doctoral students and more than 13,500 faculty and staff, including those employed at Stony Brook Medicine, Suffolk County's only academic medical center and tertiary care provider. The University is a member of the prestigious Association of American Universities and co-manager of nearby Brookhaven National Laboratory (BNL), a multidisciplinary research laboratory supporting world class scientific programs utilizing state-of-the-art facilities such as the Relativistic Heavy Ion Collider, the National Synchrotron Light Source, and the Center for Functional Nanomaterials, and the New York Blue IBM BG/L+P supercomputer, owned by Stony Brook and managed by BNL. Stony Brook is a partner in managing the Laboratory for the Department of Energy, and is the

— / —

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

## UAE ConservationGenomicsResearcher

Researcher in Conservation Genomics

We are looking for a highly motivated researcher to integrate our Conservation Genetics team, with a focus on Conservation Genomics. Our genetic research interests are genetic management of conservation programs (both in- and ex-situ), population genetic structure, sexual selection, aging, migration behaviour.

The successful candidate must have proven academic background in Conservation Genomics or Population Genomics. She / He will participate to ongoing research projects in Conservation Genomics in order to support RENECO's diverse conservation efforts; and will report to the Genetic research coordinator.

Duties will include:

Molecular laboratory techniques (e.g., DNA extraction, PCR, genotyping),

Bioinformatic analyses of non-model species whole-genomes sequencing data (i.e. de-novo assembly, annotation, SNP identification, etc.)

Share management of the genetic laboratory, including supervision of staff (including students), equipment and budgets

Mentoring undergraduate and graduate students

Genetic data management and analyses

Contribute to publication in peer-reviewed scientific journal.

Participate in sampling collection in the field

Essential qualifications/skills include:

PhD in Conservation genomics or related subjects

Experience in conducting population genomics studies in non- model species

Experience in molecular biology

Solid data analysis skills and bioinformatics background are required.

Demonstrated ability to work independently, and as part of a team

Demonstrated ability to work on multiple assignments with overlapping deadlines

Demonstrated record of research productivity and publications

This is a full-time permanent position (40 hours per week) located in Abu Dhabi (United Arab Emirates) but willingness to travel in different countries is essential.

Interested candidate can apply/inquire at hrsourcing@reneco-hq.org. Application materials include a cover letter describing your interest in the position and qualifications, a CV, and the names and contact information for at least two references.

Further information on RENECO research activities can be found at: https://www.researchgate.net/institution/Reneco_International_Wildlife_Consultants LESOBRE Loïc <llesobre@reneco-hq.org>

## UArkansas LabTech NeuroEvoDevo

Research associate in cnidarian neural development and evolution, University of Arkansas, Fayetteville

The Nakanishi lab at the Department of Biological Sciences, University of Arkansas, seeks a research associate to assist in studying cnidarian neural development and evolution. The laboratorys research uses the sea anemone Nematostella vectensis and the moon jellyfish Aurelia sp.1 as experimental models to investigate conserved and divergent mechanisms of neural development at the molecular and cellular levels. The research associate will be responsible for providing technical support for research activities in the laboratory, which may involve nucleic acid extraction, PCR, cloning, sequencing, immunohistochemistry, in situ hybridization, microinjection, microdissection, transgenesis, genome editing via CRISPR/Cas9, and confocal microscopy. In addition, this person will facilitate research in the laboratory by ordering and maintaining lab equipment and supplies, ensuring EH&S compliance in the laboratory, and maintaining live marine invertebrate animals at the aquarium facility.

Requirements: Bachelors or Masters degree in biology or related field. The applicant must possess excellent written and oral communication skills, and extensive experience in molecular biology techniques. Experience with cnidarians or other marine invertebrates is desired but not required. This is a full time, 40 hour per week position, and includes benefits. Starting date can be immediately. Initial appointment will be for one year, with the possibility to extend to future years contingent upon the availability of funding.

Salary: Commensurate with experience

Application: For a complete position announcement and information regarding how to apply, visit http://-jobs.uark.edu/postings/32091. Applicants must submit by a letter of interest, CV, and contact information for two professional references.

For inquiries, please contact Nagayasu Nakanishi at nnakanis@uark.edu

The University of Arkansas is an equal opportunity, affirmative action institution. The university welcomes applications without regard to age, race/color, gender (including pregnancy), national origin, disability, religion, marital or parental status, protected veteran status, military service, genetic information, sexual orientation or gender identity. Persons must have proof of legal authority to work in the United States on the first day of employment. All applicant information is subject to public disclosure under the Arkansas Freedom of Information Act.

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

---

## UBergen EvolutionMarineAnimals

Group Leader Positions (Researcher I, code 1110) - 6 year contracts

University of Bergen

Sars International Centre for Marine Molecular Biology

The University of Bergen (UiB) is an internationally recognized research university with more than 14,000 students and close to 3,500 employees at seven faculties. The university is located in the heart of Bergen. Our main contribution to society is excellent basic research and education across a wide range of disciplines.

Sars International Centre for Marine Molecular Biology (E.M.B.L. partner)

The Sars International Centre performs basic research on the development and evolution of marine animals, using advanced methods of molecular/cell/computational biology. It is a partner of E.M.B.L. (European Molecular Biology Laboratory) and is located in the Bergen High Technology Centre together with several departments of the University of Bergen.

Group Leader Positions (Researcher I, code 1110) - 6 year contracts

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

Qualifications and personal qualities:

The applicant must:

* hold a PhD considered equivalent to the Norwegian PhD degree * be able to train and lead junior scientists and technical staff towards a common goal defined in the group leader proposal * be able to develop collaborations with other research groups located in and out of the institution

We offer:

A good and professionally challenging working environment, in modern research facilities

Starting salary at pay grade 79, code 1110 (currently NOK 778.700) upon appointment

Enrolment in the Norwegian Public Service Pension Fund

A position in an inclusive workplace (IA enterprise)

Good welfare benefits

Your application in English must include:

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

Application Deadline is 01 April 2019. All shortlisted candidates must be available for a seminar and interview by the Sars Centre Scientific Advisory Committee held in Bergen on 23-24 May 2019.

The application and appendices must be uploaded on the JobbNorge website. It is the applicants responsibility to ensure that all relevant attachments are submitted by the deadline.

Applications or documents sent by e-mail only will not be considered.

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

General information:

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

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

The University of Bergen applies the principle of public access to information when recruiting staff for academic positions. Information about applicants may be made public even if the applicant has asked not to be named on the list of persons who have applied. The applicant must be notified if the request to be omitted is not met.

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

Dr Pawel Burkhardt Group Leader Sars Centre for Marine Molecular Biology

University of Bergen Thormohlensgate 55 5020 Bergen, Norway

Tel: +47 55 58 43 57 E-Mail: Pawel.Burkhardt@uib.no <mailto:pawbur@mba.ac.uk> Webpage: https://www.uib.no/en/sarssenteret/114773/burkhardt-group Twitter: https://twitter.com/Pawel_Burkhardt Pawel Burkhardt <Pawel.Burkhardt@uib.no>

---

## UGlasgow 1-2month Bioinformatician

Greetings,

We're advertising a short-term bioinformatics opportunity and looking for someone who can begin ASAP.

*TECH/POSTDOC JOB OPPORTUNITY* - The cocoa lab group at University of Glasgow and Durham University is seeking a technician or short-term postdoc to perform bioinformatics analyses for 1-2 months on our project entitled 'Bird and bat diet metabarcoding can benefit African Cacao Farmers and Rainforest Biodiversity'. More information is available about the position and how to apply, here: http://biodiversityinitiative.org/?page_id'6 . The candidate with work with two PIs: geneticist Dr. Andreanna Welch and ecologist Dr. Luke L. Powell. The work will entail updating the Unix/Linux-based bioinformatics pipeline used to perform quality control, clustering, and taxonomic assignment of DNA sequences from the diets of insectivorous and frugivorous African birds and bats. The candidate will work to install programs onto a high performance computing cluster, write scripts to more fully automate the pipeline, and also update Python scripts to handle recent changes in the online reference database. Depending on the expertise, interest and involvement of the candidate, there exists the possibility of *co-authorship *on this project (probably several publications) as well as on several other related projects. We would like the successful candidate to start as soon as possible. Working remotely is not a problem. Pay is 2000-5000 pounds depending on experience and number of months worked.

Cheers,

Luke L. Powell, PhD Research Fellow, Durham University Associate Staff, University of Glasgow Director, BiodiversityInitiative.org

Luke Powell <luke.l.powell@gmail.com>

## UGuam Genomics

The University of Guam Marine Laboratory is recruiting an assistant professor with expertise in marine mollusks and reef-coral genomics.

The full job announcement can be found here: https://www.uog.edu/administration/administration-finance/human-resources/049-19_Assistant-Professor-Marine-Mollusk-and-Reef-Coral-Genomics-03.21.19.pdf For more information about the Marine Laboratory and the University of Guam visit https://www.uog.edu/ml/ Bastian Bentlage, PhD

Assistant Professor of Bioinformatics University of Guam Marine Laboratory 303 University Dr. UOG Station Mangilao, GU 96923

Research Coordinator and co-PI, NSF Guam EPSCoR http://www.guamepscor.org

Bastian Bentlage <bastian.bentlage@gmail.com>

## UIowa TeachingEvolution

Instructional Faculty Track Lecturer ' Biology The Department of Biology at the University of Iowa invites applications for a non-tenure, Instructional Faculty track Lecturer position beginning August 2019. The initial appointment is for three years subject to annual review and renewal. While the Instructional Faculty track does not include the possibility of tenure, it otherwise parallels the tenure track having opportunities for promotion with a longer appointment interval. More information about the Instructional Faculty track can be found on the Provost's website at https://provost.uiowa.edu/instructional-faculty-track-appointments. Salary will be commensurate with experience.

The successful applicant will have: 1) a PhD or equivalent in biology, biology education, or a related field; 2) a commitment to excellence in undergraduate biology education; 3) experience teaching introductory biology lecture and/or laboratory courses; 4) a willingness to collaborate with faculty, staff, and students to maintain a cycle of assessment and revision of introductory undergraduate biology curriculum; and 5) excellent communication, organization, and leadership skills. Candidates with experience designing and implementing learner-centered, evidence-based instructional practices and assessment in large lecture courses are encouraged to apply.

This position will primarily contribute to administration and instruction in the introductory biology curriculum for the life sciences, specifically Foundations of Biology, the first course in our two-course series that is followed by Diversity of Form and Function. The curriculum and pedagogy of these courses supports the recommendations of the Vision and Change (2011) report. Foundations of Biology examines the unifying concepts that apply to living things organized into three main conceptual units: Molecules & Cells, Transmission & Molecular Genetics, and Evolutionary Mechanisms & Patterns. Responsibilities of this position include instruction in Foundations of Biology lecture and oversight of the curriculum and pedagogy of the integrated laboratory. The successful candidate will be expected to perform the following roles: define learning objectives and develop engaging lecture content that supports these learning goals; train and supervise Biology undergraduate and graduate student TAs; revise or create lab activities, materials and assessments; develop additional course materials such as syllabi, assessments, lecture slides, digital resources for LMS; and other instructional duties as needed.

Education Requirement Ph.D. or equivalent in biology, biology education, or a related field completed by the start date, August 21, 2019.

Required Qualifications Applicants should have a commitment to excellence in undergraduate biology education; experience teaching introductory biology lecture and/or laboratory coursesÍ¾ a willingness to collaborate with faculty, staff, and students to maintain a cycle of assessment and revision of introductory undergraduate biology curriculumÍ¾ and excellent communication, organization, and leadership skills.

Desirable Qualifications Demonstrated experience with the following will also be used to evaluate candidates: implementation of learner-centered, evidence-based instructional practices and assessment; use of software platforms such as Canvas and TopHat (or equivalent LMS and polling software); lecturing in a large class; applying best-practices in the design and assessment of lecture/lab materials; mentoring and professional development of undergraduate and graduate TAs; implementation of discipline-based education research; and/or postdoctoral research experience.

All applications must be completed online at https://jobs.uiowa.edu, referring to Requisition #73630. Applications must include a CV, a letter of interest, and list the name and contact information for three references. Additional materials that may be included are course syllabi, teaching materials, and a teaching statement. Screening of applicants will begin on May 15, 2019 and will continue until the position is filled.

The Department Biology, and the College of Liberal Arts and Sciences are strongly committed to diversity; the strategic plans of the University, College, reflect this commitment. All qualified applicants are encouraged to apply and will receive consideration for employment free from discrimination on the basis of race, creed, color, national origin, age, sex, pregnancy, sexual orientation, gender identity, genetic information, religion, associational preference, status as a qualified individual with a disability, or status as a protected veteran. The University of Iowa is an equal opportunity/affirmative action employer.

"McAllister, Bryant F" <bryant-mcallister@uiowa.edu>

---

## UKansas ResAsst DrosophilaComplexTraits

A research assistant position is available in my lab at KU to work on the genetic analysis of complex traits in flies. The position will involve both fly work and molecular biology (including approaches using high-throughput sequencing), and might be great for someone interested in gathering more research experience before going to graduate school. Experience with flies would be a plus, but isn't required. The formal announcement, and links to the institutional employment website are provided below. Feel free to email me with any questions. Stuart (sjmac@ku.edu)

A research assistant position is available in the Macdonald lab in the Department of Molecular Biosciences at KU. We explore the genetic basis of complex phenotypic variation using Drosophila as a model system. The successful candidate will help maintain a panel of fly lines, supervise and carry out large-scale phenotyping screens for response to toxic metals (see https://bit.ly/-2H6Lcge), and generate next-generation sequencing libraries for various genomics applications. We are looking for an enthusiastic and organized individual who is willing to learn new skills, and has excellent oral and written communication skills. Previous research assistants in the Macdonald group have undertaken independent research projects and been authors on research publications from the lab. The position is funded through a new multi-year NIH grant and has an anticipated start date of June 1, 2019 (although this is negotiable).

Required qualifications include a Bachelor's degree in biology (or a related field) by the time of appointment, and some experience with laboratory molecular biology techniques. Prior experience with flies and/or next generation sequencing library construction would be a plus.

For a complete announcement and to apply online, go to employment.ku.edu/staff/13828BR

Please direct any questions about the position to Stuart Macdonald (sjmac@ku.edu).

A complete online application includes the following materials: A CV/resume, a cover letter outlining relevant experience, and contact information (phone/email/address) for three referees. Initial review of applications begins 1 April 2019 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university's programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY 9for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

### Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045 ### office: 785-864-5362 email: sjmac@ku.edu ### Google Scholar: https://scholar.google.com/citations?user=-pTXRo_gAAAAJ&hl=en ORCiD: http://orcid.org/-0000-0002-9421-002X ###

"Macdonald, Stuart" <sjmac@ku.edu>

## UmeaU Sweden Evolution

The Department of Ecology and Environmental Science, Umeå University, Sweden, invites applicants for a professor position in Ecology.

Candidates with a research profile on biodiversity, conservation, or evolution are encouraged to apply.

For information and instruction, please visit the site:

https://umu.mynetworkglobal.com/en/what:job/-jobID:257492/ Xiao-Ru Wang Dept. of Ecology & Environmental Science Umeå University S-901 87 Umeå, Sweden

Xiao-Ru Wang <xiao-ru.wang@umu.se>

## UMontana LabTech InvasiveSpecies

Lab Technician/Researcher for eDNA monitoring of invasive species

Project: Preventing spread of invasive fish & mussels using qPCR & novel water surveillance

Principal Investigators: Gordon Luikart, Steve Amish, & Brian Hand, Flathead Lake Biological Station and Montana Conservation Genomics Laboratory, Division of Biological Sciences, The University of Montana. gordon.luikart@umontana.edu; Steve.Amish@umontana.edu (406-872-4517).

Start Date & Duration: May 2019; 1 year with likely extension

Project Description/Summary: Aquatic Invasive Species (AIS) such as rainbow trout, brook trout, and zebra mussels are spreading across North America causing massive economic and ecological problems (Figs. 1, 2). To help prevent spread, new environmental DNA (eDNA) sampling and laboratory qPCR tests are now available for early detection and monitoring of these AIS. This lab position will involve applying real time qPCR assays to track spread of AIS in Montana and adjacent states. The successful applicant could help collect water eDNA samples in national parks and wilderness areas across Montana. Sampling would include use of a mobile qPCR on lakes (from a speed boat), and the use of autonomous sampling instruments that collect multiple samples daily (automatically, with no human on site) from streams. The successful applicant will help publish novel approaches to understand, predict, and prevent evolutionary adaptation and spread of AIS (Fig. 2). Skills required: The applicant should have experience applying qPCR assays (e.g. TaqMan) to eDNA samples or difficult/ancient DNA samples. The successful applicant would ideally also have a Master's degree or equivalent experience in writing reports or publications, working as a team, and collaborating successfully with natural resource agency field biologists. Experience with metabarcoding and next generation sequence data analysis would

Applications: Send a brief letter ( $<1$ page) describing your motivation and background, your CV, and the names and contact information for three references. Review of applications will start immediately and remain open until a suitable candidate is hired.

Salary: will depend on your experience and CV.

Key references: see our web pages, this eDNA video at: https://flbs.umt.edu/giving/default.aspx?id=1 and click on the video (arrow) on the right side; and contact us. See also Gingera et al. 2017 DOI: https://doi.org/-10.3391/mbi.2017.8.3.03 . Fig. 1 Invasive (a) zebra & quagga mussels, (b) encrusted research equipment, (c) a crayfish encrusted with zebra mussels.

Fig. 2 Invasive (a) rainbow & (b) brook trout that threatening native trout.

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

## UNebraska LabTech GeneFunction

The Mower Lab in the Center for Plant Science Innovation at the University of Nebraska-Lincoln is seeking a full-time lab technician position, starting ASAP. This is a six-month temporary position with the option for extension for up to 2.5 additional years, contingent on the availability of grant funds and subject to satisfactory performance.

Duties: The tech will be expected to conduct research on the evolution of gene function via the development and characterization of transgenic plants. The research will include assembly of genetic constructs, genetic transformation of plants, molecular characterization of derived transformants, and maintenance of transgenic plants grown under greenhouse conditions. The tech will also be expected to assist with other projects, as needed, and will be responsible for maintaining the lab, including ordering of supplies and ensuring EHS compliance.

Requirements: A BS degree in the plant sciences is required, a MS degree is preferred. One to two years of lab research experience is required, and prior experience in the area of plant genetic engineering and molecular biology is desired.

Salary: Approximately $16-17/hour or $36,000-$39,000/year, depending on qualifications.

Application: Interested applicants should submit a cover letter, a CV/resume, unofficial transcripts and contact information for two to three references in a single PDF to jpmower@unl.edu. Job applications will be reviewed immediately and continuously until a suitable applicant is identified.

Inquiries about the position should be sent to jpmower@unl.edu.

Jeffrey Mower <jpmower@unl.edu>

---

## UNorthTexas BioinforamticsStaff

Use your knowledge and skills to improve the discipline of forensic genetics. The Budowle lab (https://www.unthsc.edu/graduate-school-of-biomedical-sciences/molecular-and-medical-genetics/laboratory-faculty-and-staff/) at the University of North Texas Health Science Center is a seeking a staff scientist in bioinformatics.

Candidates must be proficient in at least one coding language, preferably one higher level language (e.g., R/Python) and one lower level language (e.g., C/C++). Coursework in computation (e.g., algorithms) is desired, as well as a track record of software development. A working knowledge of statistics and population genetics is also preferred.

Interested candidates should send their CVs and a brief statement of their research interests and goals to August at August.Woerner@unthsc.edu for more information.

Applicants may also apply using the following:

www.unthscjobs.com/applicants/Central?quickFinda505 “Woerner, August” <August.Woerner@unthsc.edu>

---

## ZFMK Bonn Metabarcoding

Job advertisement

Tenure-track researcher position in Metabarcoding

The Center of Molecular Biodiversity Research (https://www.zfmk.de/en/zmb) at the Zoological Research Museum Alexander Koenig (ZFMK) seeks enthusiastic, creative, and productive applicants for a full time tenure track position in the field of metabarcoding. Recent developments in the field of metabarcoding have enabled large-scale applications in biodiversity monitoring and conservation. We seek to expand our metabarcoding section to cover a range of areas such as biomonitoring and next generation biodiversity assessments, the study of food webs, plant-animal and host-parasite interactions, as well as large-scale processing and analysis of metabarcoding data from bulk samples (e.g. insects from malaise traps).

We are particularly interested in candidates using metabarcoding in their research and/or candidates developing analytical tools for metabarcoding. We seek an innovative and accomplished scientist whose research program will complement and diversify existing departmental research areas which include integrative taxonomy, phylogenomics, evolutionary biology and biodiversity research on animals.

Assessment Criteria: The ranking of eligible applicants will be based primarily on research expertise. This comprises research merits as well as the applicants potential to contribute to the future development of metagenomics. Special weight will be given to expertise in large-scale metabarcoding studies and biodiversity assessments, as well as to scientific independence and the ability to attract external funding. The planned research of the applicant shall complement on-going research at the Center of Molecular Biodiversity Research. The candidate is expected to establish an internationally competitive research group, to successfully apply for research grants, to publish in internationally recognized journals, and to tightly collaborate with other research groups at the ZFMK.

Required qualifications: It is essential that the applicant has

- a PhD in Biology or a closely related field with strong emphasis on (meta)genomics; - an internationally competitive publication record; - experience in processing amplicon high-throughput sequencing data; - experience in metabarcoding data analysis and visualization; - experience in staff management and student supervision; - motivation to work in a team and take responsibility; - excellent communication skills.

The ZFMK is a Zoological Research Museum of the Leibniz Association cooperating with the University of Bonn, funded by the Federal State of NRW and the federal government. The Center of Molecular Biodiversity Research has been established to foster molecular research spanning from genomics and speciation genetic research to developing high-throughput barcoding applications. We offer a highly motivating environment and ability to work independently. Salary and benefits are according to a public service position in Germany (TV-L E 13). An upgrade of salary and benefits to TV-L E 14 is possible and will be subject of the tenure evaluation. The ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely disabled applicants will be given preference. The contract will start as soon as possible and will initially be restricted to three years. A tenured position will be subject to personal performance reviewed by a commission. Please send your application by e-mail attachment, including a detailed CV, a complete publication record, a research plan, a list of successful grant applications, names of three potential referees and five selected publications, until 08.04.2019 to Mrs. Heike Lenz (e-mail: h.lenz@leibniz-zfmk.de). In case of questions concerning the position please contact Dr. Sarah Bourlat (e-mail: S.Bourlat@leibniz-zfmk.de). For more information about the museum see http://www.leibniz-zfmk.de https://www.zfmk.de/en/zfmk/work-at-zfmk/-job-offerings – Zoologisches Forschungsmuseum Alexander Koenig - Leibniz-Institut fur Biodiversität der Tiere - Adenauerallee 160, 53113 Bonn, Germany www.zfmk.de Stiftung des offentlichen Rechts; Direktor: Prof. J. Wolfgang Wägele Sitz: Bonn

S.Bourlat@leibniz-zfmk.de

# Other

Biodiversity Awards . . . . . 79
EvolutionaryDevelopmentalBiol PadovaU Press . . . . 79
Fellowship Teaching Evolution . . . . . 79
Fisher1918 SymposiumTalkVideos . . . . . 80
Gotland UppsalaU FieldAssist NestboxBirds . . . . . . 80
MolecularEcolPrize Nominations . . . . . 80
NorthDakota REU AvianPhysiologicalEvol . . . . . . . . 81
Omenn PrizeEvolutionaryMedicineArticle Mar31Deadine 81
Software PGT update . . . . . 81
Spain VolFieldAssist PlantEvolEcol JunJul . . . . . . . . 82
SSE THHuxley Award . . . . . 82
Survey PreservingAvianDNA FinalCall . . . . . 83
UCRiverside NSF REU Livebearing Fish Placenta Evolution . . . . . 83
UExeter FieldAssist UKBees . . . . . 84
UMaine REU EvolutionaryBiology . . . . . 84
UMichigan NSF REU EvolutionaryPhysiology . . . . . 85
UMichigan REU RedSquirrelPopulation . . . . . 86
UndergraduateDiversity AtConferences Mar31 . . . . . 87
Vignettes on EvolutionaryApplications . . . . . 87

## Biodiversity Awards

DEADLINES APPROACHING: 2019 GBIF Young Researchers Award

The GBIF Young Researchers Awards is an annual programme aimed at fostering innovative research and discovery in biodiversity informatics by providing two prizes of €5,000 each to two graduate students whose work relies on GBIF-mediated data.

The global deadline for this year's programme is 15 May 2019, but EARLIER LOCAL DEADLINES DO APPLY!

Read the full call for nominations: https://www.gbif.org/news/1FAyeRyxs8A00UyiSmu4oG To be eligible, students must be either a) citizens of a country participating in GBIF or b) students at an institution located in a GBIF participant country. View the full list of GBIF member countries: https://www.gbif.org/the-gbif-network Current national deadlines for 2019 GBIF #YoungResearchers Award are as follows:

South Africa 5 April http://bit.ly/yra2019-za Portugal 12 April http://bit.ly/yra2019-pt Colombia 21 April http://bit.ly/yra2019-co Spain 30 April http://bit.ly/yra2019-es

In other cases, eligible candidates should contact relevant national heads of delegation from the list of GBIF member countries: https://www.gbif.org/the-gbif-network A jury organized by GBIF Science Committee will select two award recipients'generally one Master's candidate and one Ph.D candidate'from the pool of nominees whose names are received by the GBIF Secretariat by 15 May 2019. The winners will be announced in the summer of 2019.

Find a list of past winners and general background on the awards here: https://www.gbif.org/article/44SftFORi0A6mwGK4sgAKW Questions? Email us at youngresearchersaward@gbif.org

Thanks, Kyle

Kyle Copas Communications Manager

GBIF Secretariat Universitetsparken 15 DK-2100 Copenhagen Ã Denmark https://www.gbif.org

Kyle Copas <kcopas@gbif.org>

## EvolutionaryDevelopmentalBiol PadovaU Press

Perspectives on Evolutionary and Developmental Biology edited by Giuseppe Fusco Padova University Press 2019

The book is open access and freely downloadable at http://www.padovauniversitypress.it/publications/9788869381409 This essay collection spans a wide range of approaches to the study of development and evolution, especially at their fertile interface, evolutionary developmental biology (or, evo-devo). While being mainly aimed at professional researchers in the field, the book could also provide material for discussion groups in undergraduate and graduate university courses.

giuseppe.fusco@unipd.it

## Fellowship Teaching Evolution

*Science-Corps* *Providing an opportunity for recent PhD graduates, as Science-Corps Fellows, to teach science to underserved students and build science capacity in the developing world*

Interested in taking a six month break from the research/academic track to work in a different part of the world and share your expertise where it is needed? Science-Corps has launched a new fellowship, which provides STEM PhD graduates the opportunity to teach science, design curriculum, and build scientific capacity abroad.

Science-Corps is recruiting STEM PhD students near degree completion and up to four years post completion. Application submission deadlines are June 30, 2019 and Dec 30th, 2019. Fellowships begin approximately six months after acceptance. Placement start times can in most cases be negotiated.

If interested, visit http://www.science-corps.org/ Science Corps <fellows@science-corps.org>

## Fisher1918 SymposiumTalkVideos

In October of last year the Fisher Memorial Trust held a one-day symposium to celebrate the publication of RA Fishers seminal 1918 paper. The symposium featured talks by a range of excellent speakers across the fields of quantitative and population genetics. The talks are now available on The Fisher Memorial Trust Youtude channel:

Nick Barton V The infinitesimal model - https://youtu.be/dz3YzaV4ZIA Sharon Browning V Identity by Descent and the Correlation Between Distant Relatives - https://youtu.be/w2BaxmaWTTo Ed Buckler V How to get to plant breeding 4.0, given that Fisher was right? - https://youtu.be/gE8ddyf7lrA Heather Cordell V Regional IBD analysis (RIA): linkage analysis in extended pedigrees using genome-wide SNP data. - https://youtu.be/Y4REO1nCdCQ Josselin Clo V How does selfing affect the genetic variance of quantitative traits? An updated meta-analysis on empirical results in angiosperm species - https://youtu.be/N0Mu6XA1s8I Daniel Crouch V The genetics of the human face. https://youtu.be/7bDU8Zr_Ci8 Michael Goddard V The Fisher Memorial lecture - Genetic architecture of complex traits. Quantitative genetics 100 years after Fisher (1918) - https://youtu.be/obaFcjXqZYI Jarrod Hadfield V Hamiltons rule in multiple dimensions - https://www.youtube.com/watch?v=r5tXxdduaIs&ts Chandana Basu Mallick V Making sense of GWAS:understanding the genetic basis of human hair shape using mouse models V https://youtu.be/R3n-7r9MaFs Richard Mott V Structural variants as quantitative traits - https://youtu.be/2SW9NNy3-Zs Josephine Pemberton V Quantitative genetics of free-living populations: successes and challenges - https://youtu.be/d11U2Gv3dhs Himani Sachdeva V Introgression under the infinitesimal model with linkage - https://youtu.be/w0dZ32aEU50 Adam Eyre-Walker

Professor Adam Eyre-Walker Treasurer, Fisher Memorial Trust School of Life Sciences University of Sussex Brighton BN1 9QG a.c.eyre-walker@sussex.ac.uk

Adam Eyre-Walker <a.c.eyre-walker@sussex.ac.uk>

## Gotland UppsalaU FieldAssist NestboxBirds

We offer expenses-paid field assistant positions in a long-term project conducted in the wild collared flycatcher population on the Baltic island of Gotland (Sweden). Assistants will have their accommodation and other expenses covered, we also offer a smaller salary add-on depending on experience and declared period of work in the project. Lodging will be provided in a large house rented for the period of the field season.

Basic duties: performing nest-boxes checks and monitoring of breeding pairs; ringing of nestlings; capture of adult individuals, ringing and basic morphological measurements. Prior experience with wild birds handling and a valid driving license will be an advantage. The work is not extremely exhausting but sometimes requires long hours in the woods, in diverse weather conditions.

Period of work: ~10th of May until approx. end of June/first days of July, or a shorter period within this time window.

For more information and to apply - please contact Prof. Lars Gustafsson (lars.gustafsson@ebc.uu.se) or Dr Szymon Drobniak (szymek.drobniak@uj.edu.pl).

Szymek Drobniak <szymek.drobniak@uj.edu.pl>

## MolecularEcolPrize Nominations

Second Call for Nominations for Molecular Ecology Prize We are soliciting nominations for the annual Molecular Ecology Prize.

The field of molecular ecology is young and inherently interdisciplinary. As a consequence, research in molecular ecology is not currently represented by a single scientific society, so there is no body that actively promotes the discipline or recognizes its pioneers. The editorial board of the journal Molecular Ecology therefore created the Molecular Ecology Prize in order to fill this void, and recognize significant contributions to this area of research. The prize selection committee is independent of the journal and its editorial board.

The prize will go to an outstanding scientist who has made significant contributions to Molecular Ecology. These contributions would mostly be scientific, but the door is open for other kinds of contributions that were crucial to the development of the field. The previous winners are: Godfrey Hewitt, John Avise, Pierre Taberlet, Harry Smith, Terry Burke, Josephine Pemberton, Deborah Charlesworth, Craig Moritz, Laurent Excoffier, Johanna Schmitt, Fred Allendorf , Louis Bernatchez, Nancy Moran, and Robin Waples.

Please send your nomination with a short supporting statement (no more than 250 words; longer submissions will not be accepted) directly to Robin Waples (robinw3@uw.edu) by Tuesday, April 2, 2019. Organized campaigns to submit multiple nominations for the same person are not necessary and can be counterproductive. Also, note that nominations from previous years do not roll over.

With thanks on behalf of the Molecular Ecology Prize Selection Committee

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

## NorthDakota REU AvianPhysiologicalEvol

Ever wondered about how stress affects the body or why some individuals are more resilient than others?

If so, join our research team and learn more about it!

The Heidinger lab in the Department of Biological Sciences at North Dakota State University (NDSU) in Fargo, ND, is seeking undergraduate students to participate in a project examining the long-term consequences of stress exposure in a local population of house sparrows. There is one full time National Science Foundation-funded Research Experience for Undergraduates (REU) position and several volunteer positions. Duties will include manipulating stress exposure, monitoring parental behavior, checking nests, and measuring offspring growth. Successful applicants must be enthusiastic and motivated. They must work well independently and as part of a research team. If interested please email 1) a cover letter describing your interest in the project and previous research experience, 2) a resume, and 3) the names of two references to Rebecca Young (rebecca.c.young@ndsu.edu) by April 1, 2018. Positions will run May-August. Salary $500/week and housing will be provided.

rebecca.c.young@ndsu.edu

## Omenn PrizeEvolutionaryMedicineArticle Mar31Deadine

The International Society for Evolution, Medicine & Public Health invites nominations for the Omenn Prize of $5000 for the best article published in the previous calendar year in any scientific journal on a topic related to evolution in the context of medicine and public health. The prize, provided by the generosity of Gilbert S. Omenn, will be awarded to the first author of the winning article. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome. The submission deadline is March 31, 2019. Full information at https://isemph.org/Omenn-Prize . The Winner also receives expenses to present a talk at the 2019 meeting of the International Society for Evolution Medicine and Public Health in Zurich August 14-16, 2019 https://isemph.org/2019-Meeting Randolph Nesse <nesse@asu.edu>

## Software PGT update

Dear All,

I have just uploaded a new version of PGT software for generating geophylogenies (phylogenetic tree mapped onto a high resolution map). PGT is extremely easy to use. It takes only eight mouse-clicks from installation to generating a high-resolution geophylogeny.

The main updates are:

1) Added geophylogeny that "stands on" maps with vertical lines scaled to branch lengths. Here is the link to the new geophylogeny: http://dambe.bio.uottawa.ca/PGT/PGT_BranchLen.PNG 2) The slow google satellite map is replaced by google terrain map (which is fast and also more relevant to biogeographic studies)

3) The PGT paper has been accepted by Global Ecology & Biogeography, so now you can cite:

Xia, X. 2019. PGT: Phylogeographic Tree for Mapping a Phylogeny onto Geographic Regions. Global Ecology

& Biogeography (in press)

PGT is available at http://dambe.bio.uottawa.ca/PGT/PGT.aspx for Windows, Macintosh and Linux.

Best Xuhua http://dambe.bio.uottawa.ca http://science.uottawa.ca/biology/people/xia-xuhua https://scholar.google.ca/citations?hl=en&user=fbAS_FcAAAAJ&view_op=list_works Xuhua.Xia@uottawa.ca

---

## Spain VolFieldAssist PlantEvolEcol JunJul

Nick Barton's group at the Institute of Science and Technology (IST) Austria is recruiting volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (June-July).

The project: We are studying the evolutionary dynamics underlying population divergence in wild Antirrhinum majus (snapdragons). We focus on natural hybrid zones between two subspecies with different flower colours. Most of the field work is contributing to a long-term pedigree project aimed at establishing a direct link from genotype to phenotype to fitness. With tens of thousands of samples collected over ten years so far, this provides an exciting and powerful system to examine many outstanding questions about adaptation and quantitative genetics in wild populations. We are seeking volunteers to assist with the field work, which involves working in teams mapping the location of individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits, phenotyping them for flower pigmentation and processing material for later DNA extraction. There may also be opportunities to be involved in other projects we are doing on plant-insect interactions. Most of the work is outdoors, however we do spend some time indoors processing samples. The work is highly team orientated, typically in groups of 2-3 in the field and larger groups processing samples back at the research station. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-insect interactions.

The field site is located near Ripoll in a beautiful part of the Pyrenees in Catalonia in northeastern Spain. We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (within Europe) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and enthusiastic biology students/graduates with a strong interest in working outdoors with plants. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require assistance between June 1 and July 31. Depending on the year and the plants, we may extend our time into August. Length of stay is flexible but a minimum stay of 3 weeks is required.

Please send any questions and your application to carina.baskett@ist.ac.at. To apply, send your CV or resume, with a few sentences about your background and why you are interested. Please include the length of time you would be available. Please get in touch by March 18 if youre interested, even if you are still figuring out availability.

Carina BASKETT <carina.baskett@ist.ac.at>

---

## SSE THHuxley Award

The Society for the Study of Evolution (SSE) Education Committee is pleased to announce the T. H. Huxley award, named in honor of Darwin's very public supporter, which recognizes and promotes the development of high quality evolution education resources. If you have an interesting project or educational activity to share, consider applying for this award. Information on previous awards is available here: http://bit.ly/2kP2pPM. Graduate students and postdoctoral fellows are encouraged to apply. This award provides funding for an SSE member to present evolution education resources at the National Association of Biology Teachers (http://nabt.org/) annual conference. This year's NABT conference will be held Nov. 14-17, 2019 in Chicago, IL. The deadline for applying for the Huxley award is April 7th, 2019. Apply here: https://bit.ly/2RzKnyh . Questions? Contact Phil Gibson (jpgibson 'at' ou.edu) or Gaby Hamerlinck (ghamerlinck 'at' ufl.edu).

– Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608) 622.9394

*Summer Workshop 2019* Save the date! July 14-19, 2019 Check here for more information: https://

qubeshub.org/community/groups/summer2019 Kristin Jenkins <Kristin.Jenkins@bioquest.org>

---

## Survey PreservingAvianDNA FinalCall

Do you work with avian blood?

Please, share your experience by filling our survey 'Preserving avian DNA from the wild: your experience of blood sampling, DNA extraction and storage'.

https://www.surveymonkey.com/r/avian_blood_storage It is addressed to biologists and molecular ecologists handling blood samples collected from birds in the field and managing the long-term storage of blood and DNA extracts. We would like you to share with us your past and current experiences, along with the adversities you faced, both in the field and in the lab.

Sincerely,

Irene Di Lecce, Joanna Sudyka, David F. Westneat and Marta Szulkin (University of Warsaw and University of Kentucky)

Joanna Sudyka <joanna.sudyka@cent.uw.edu.pl>

---

## UCRiverside NSF REU Livebearing Fish Placenta Evolution

National Science Foundation Research Experiences for Undergraduates (NSF REU) Position in Livebearing Fish Evolution & Reproductive Behavior Research

Overview: A 10-week NSF REU position is available in David Reznick's lab at the University of California, Riverside for June-August 2019 (June 17 preferred start date). The REU Student will participate in research on the evolution of placentation in livebearing fishes (poeciliids). Poeciliids have the unique attribute of having evolved the functional equivalent of a mammalian placenta at least nine times. There are at least three clusters of species that contain close relatives with and without placentas. This raw material gives us the opportunity to address questions about why and how placentas evolved that cannot be addressed in mammals because all placental mammals trace their common ancestry to a single origin of the placenta that happened 100-200 million years ago. We are studying aspects of reproductive behavior, development, and genomics with experiments involving crosses between females from different populations of several placental and non-placental species. These crosses are performed to assay female and offspring fitness based on the genetic distance between the female and male's populations. Furthermore, we, in collaboration with another lab, use genetic techniques to determine the paternity of offspring produced in experimental crosses in which females are artificially inseminated with sperm from multiple males. The goal is to determine if there is differential success among males siring offspring and differential provisioning of offspring during development.

Duties: The REU Student will be working with a PhD student to choose a project and collect/analyze data. Duties will include helping to maintain experimental fish (e.g. feeding, water changes and tank cleaning) and record data throughout the duration of the experiment. Additional duties (i.e. genetics benchwork or specific experimental methods) will depend on the applicant's skills and interests.

Eligibility: All animal care and laboratory training will be provided, and no experience is required. Applicants should be highly motivated, responsible, and have a strong desire to learn about and conduct evolutionary biology research. It is essential that applicants be able to work in a collaborative environment and be able to perform occasionally repetitive, meticulous tasks. NSF requires that applicants be US citizens or permanent residents of the USA or its possessions. Furthermore, students must be current undergraduate students enrolled through Fall 2019. We especially encourage students from under-represented groups and institutions with relatively limited research opportunities (e.g., community colleges and undergraduate-only institutions) to apply.

Travel, Stipend, & Research Expenses: Travel to and from Riverside, CA will be provided (up to $800) as well as a stipend of $500/week ($5000 total) for approx. 40 hours per week. Housing will not be provided.

Application Details: Send a cover letter and CV (see below for contents) in an email with the subject "Reznick REU Position" to Samantha Levell ( sleve004@ucr.edu) by April 20th, 2019 at 5pm PST. All applications will be reviewed after the deadline, and top applicants will be contacted for Skype interviews shortly after. All applicants will be notified by May 6th whether they have received the position or not.

Your cover letter: should be 1-2 pages (single-spaced) and describe why you want this position and how it fits into your career goals. Indicate any experience you have working with fish/live animals. You may also suggest potential independent research projects, which we may be able to accommodate during the REU period.

Your CV must include: relevant coursework and current GPA, any work/volunteer/research positions held, current/past research project descriptions or publications, awards/honors, and contact information for three references.

The Reznick lab strives to maintain a positive environment for all its members. All qualified applicants will receive consideration for this position without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, disability, protected veteran status, or any other characteristic protected by law.

sleve004@ucr.edu

---

## UExeter FieldAssist UKBees

Social Insect Fieldwork Assistants, UK:

We seek two field assistants to work on a study of social behaviour in ground-nesting sweat bees (Halictidae). The start and end dates of the position are somewhat flexible but also will depend on when bees start nesting in Spring. One position will start approximately 1 May and the other from the middle of June, and they will ideally end when the bees have finished nesting for the year (mid August to early September).

The assistants will be working alongside a Postdoctoral researcher and research technician in Gloucestershire, UK. The study species is a small/medium-sized bee that nests in small colonies (with fewer than 10 individuals) in the ground and has an insignificant sting. Work will involve: observing foraging behaviour, handling and marking bees, setting up video cameras/uploading video footage etc. In warm weather, field assistants will work all day in the field; in bad weather there will be tasks to carry out back at the accommodation but also opportunity for time off. Because the work involves recording colour marks on individual bees, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (https://biosciences.exeter.ac.uk/-staff/index.php?web_id=Jeremy_Field).

Experience of working with insects and a Degree (or working towards a Degree) in a Behaviour/Evolution/Ecology-related topic are desired. Flexibility around the start and end dates of the assistant positions is required. The successful applicants must be prepared to work hard and have enthusiasm for fieldwork. They will obtain excellent experience of cutting-edge social insect research.

Shared accommodation is provided, but assistants are required to pay for their own food/personal expenses. Assistants receive an additional £125 per week to help cover personal costs.

Please contact Dr Rebecca Boulton (r.boulton@exeter.ac.uk) and CC Prof. Jeremy Field (j.p.Field@exeter.ac.uk) to discuss these positions further. Please attach a CV and briefly outline your motivation to carry out the work.

Jeremy Field Professor of Evolutionary Biology Centre for Ecology and Conservation University of Exeter Penryn Campus Cornwall TR10 9EZ http://biosciences.exeter.ac.uk/cec/staff/-index.php?web_id=Jeremy_Field "Field, Jeremy" <J.P.Field@exeter.ac.uk>

---

## UMaine REU EvolutionaryBiology

This year, several faculty mentors have projects of potential interest to students studying evolutionary biology, including research into the genetic basis for disease in wild and domestic animals, host-pathogen co-evolution, and adaptation to other environmental stressors?

Other: Paid Undergraduate Summer Research Program in One Health and the Environment

The University of Maine Initiative for One Health and the Environment is excited to announce a new NSF-funded REU program for summer 2019, entitled Accelerating New Environmental Workskills (ANEW). REU ANEW is a 10-week paid summer research internship. Each summer, we will invite 10 motivated undergraduate students to join our faculty and graduate students to conduct cutting-edge research at the intersection of human, animal, and environmental health. REU ANEW students will have the opportunity to work directly with faculty research mentors, as well as Broader Impacts mentors who are working in the field to apply One Health research to real world problems. Through our program, students will develop critical research and thinking skills that are directly relevant to future career success, and build lasting professional relationships with their undergraduate peers, graduate students, and faculty and broader impacts mentors.

This year, several faculty mentors have projects of potential interest to students studying evolutionary biology, including research into the genetic basis for disease in wild and domestic animals, host-pathogen co-evolution, and adaptation to other environmental stressors? For more information about these projects and several others, and to apply, visit https://nsfa.umaine.edu/one-health/REU. Application review will begin on March 20 and all complete applications submitted before this deadline will receive full consideration. Applications received after this date will continue to be reviewed until all positions are filled. Please direct any questions you have about the program or the application process to anne.lichtenwalner@maine.edu and kristina.cammen@maine.edu.

Stipend: All REU participants will receive a generous summer stipend ($5,750) and living expenses, including travel expenses and housing at the University of Maine in Orono.

Eligibility: All REU students must be U.S. citizens, U.S. nationals or permanent residents of the U.S. Students must have completed at least one year of an Associates or Baccalaureate degree program prior to the summer internship, and must plan to continue in their degree program following this summer internship (graduating seniors are not eligible). As part of the National Science Foundations and our commitment to broadening participation, we especially encourage students who self-identify with groups that are under-represented in science, technology, engineering and math (STEM) to apply, as well as students attending institutions with relatively limited research opportunities (e.g., community colleges and some undergraduate-only institutions).

The University of Maine is an EEO/AA employer, and does not discriminate on the grounds of race, color, religion, sex, sexual orientation, transgender status, gender expression, national origin, citizenship status, age, disability, genetic information or veterans status in employment, education, and all other programs and activities. The following person has been designated to handle inquiries regarding non-discrimination policies: Sarah E. Harebo, Director of Equal Opportunity, 101 North Stevens Hall, University of Maine, Orono, ME 04469-5754, 207.581.1226, TTY 711 (Maine Relay System).

Kristina Cammen <kristina.cammen@maine.edu>

---

## UMichigan NSF REU EvolutionaryPhysiology

*National Science Foundation Research Experiences for Undergraduates (NSF REU) Position in Mammalian Behavior & Physiological Ecology*

*Overview: *A 14-week NSF REU position is available in the lab of Ben Dantzer at the University of Michigan ( https://sites.lsa.umich.edu/dantzerlab/) for May-August 2019. The REU Student will participate in research regarding the effects of elevated maternal glucocorticoids (colloquially referred to as 'maternal stress') on the physiology, behavior, and life history traits of the offspring and design and conduct their own independent research project under the general umbrella of understanding how parents shape the development of their offspring. The REU Student will spend 14 weeks in the Kluane region of the Yukon, Canada as a member of the Kluane Red Squirrel Project (KRSP), which is a 30+ year study of individually-marked North American red squirrels ( www.redsquirrel.ca). The REU Student will live and work at our field site and interact with an international team of researchers on the KRSP.

*Duties:*The REU Student will assist in trapping and handling squirrels, conducting behavioral observations, using VHF telemetry to locate squirrels or their nests, and assist in experimental manipulations of maternal hormone levels. Additional duties will be contingent upon the specific research project of the successful applicant. The successful applicant and the PI will jointly design an independent research project.

*Eligibility:*All training will be provided and no experience is required. Applicants should have strong enthusiasm for learning, a desire to conduct their own independent research project, and be highly motivated. Applicants should also have an interest in animal behavior, evolutionary biology, ecology, and field biology. Previous experience with field research, independent research, working with wild animals is a plus. The field camp is remote and low tech, so successful applicants must enjoy the outdoors and be able to remain positive and be a responsible team member under relatively isolated and demanding conditions. The successful applicant must be a collaborative team player as they will be working closely with other researchers. Students should be current undergraduate students. NSF requires that applicants be US citizens or permanent residents of the USA or its possessions. The Dantzer Lab aims to be a welcoming, safe, and inclusive research group and strongly encourages applications from members of underrepresented groups.

*Travel, Stipend, & Research Expenses: *Travel to and from the field site in the Yukon will be provided as will lodging and food during the duration of the position. The successful applicant will also receive a stipend of $400/week ($5600 total) and an additional $400 will be available to help pay for some of the costs associated with the research project.

*Application Procedure: *Send a cover letter and CV (with contact info for three references) in an email with the subject 'REU Position' to Ben Dantzer (dantzer@umich.edu) by April 5. The cover letter should describe why you want this position, how it fits into your career goals, any record of overcoming challenges, ideas for possible independent research projects, and an overview of your past experiences with independent research, field research, animal handling, and living/working in a remote area. Applications will be considered as they are received.

*Ben Dantzer, Ph.D.* Assistant Professor Dept Psychology Dept Ecology & Evolutionary Biology University of Michigan Ann Arbor, MI 48109

Email: dantzer@umich.edu Phone: 734-615-2352 Follow me < https://twitter.com/ben_dantzer?ref_src=twsrc%5Egoogle%7Ctwcamp%5Eserp%7Ctwgr%5Eauthor > or the Kluane Red Squirrel Project < https://twitter.com/KluaneSquirrels > on Twitter Visit my website < https://sites.lsa.umich.edu/dantzerlab/ >

dantzer@umich.edu

---

## UMichigan REU RedSquirrelPopulation

*National Science Foundation Research Experiences for Undergraduates (NSF REU) Position in Mammalian Behavior & Physiological Ecology*

*Overview: *A 14-week NSF REU position is available in the lab of Ben Dantzer at the University of Michigan (https://sites.lsa.umich.edu/dantzerlab/) for May-August 2019. The REU Student will participate in research regarding the effects of elevated maternal glucocorticoids (colloquially referred to as 'maternal stress') on the physiology, behavior, and life history traits of the offspring and design and conduct their own independent research project under the general umbrella of understanding how parents shape the development of their offspring. The REU Student will spend 14 weeks in the Kluane region of the Yukon, Canada as a member of the Kluane Red Squirrel Project (KRSP), which is a 30+ year study of individually-marked North American red squirrels ( www.redsquirrel.ca). The REU Student will live and work at our field site and interact with an international team of researchers on the KRSP.

*Duties:*The REU Student will assist in trapping and handling squirrels, conducting behavioral observations, using VHF telemetry to locate squirrels or their nests, and assist in experimental manipulations of maternal hormone levels. Additional duties will be contingent upon the specific research project of the successful applicant. The successful applicant and the PI will jointly design an independent research project.

*Eligibility:*All training will be provided and no experience is required. Applicants should have strong enthusiasm for learning, a desire to conduct their own independent research project, and be highly motivated. Applicants should also have an interest in animal behavior, evolutionary biology, ecology, and field biology. Previous experience with field research, independent research, working with wild animals is a plus. The field camp is remote and low tech, so successful applicants must enjoy the outdoors and be able to remain positive and be a responsible team member under relatively isolated and demanding conditions. The successful applicant must be a collaborative team player as they will be working closely with other researchers. *Applicants must be current undergraduate students and enrolled in an undergraduate program in Fall 2019. NSF requires that applicants be US citizens or permanent residents of the USA or its possessions.* The Dantzer Lab aims to be a welcoming, safe, and inclusive research group and strongly encourages applications from members of underrepresented groups.

*Travel, Stipend, & Research Expenses: *Travel to and from the field site in the Yukon will be provided as will lodging and food during the duration of the position. The successful applicant will also receive a stipend of $400/week ($5600 total) and an additional $400 will be available to help pay for some of the costs associated with the research project.

*Application Procedure: *Send a cover letter and CV (with contact info for three references) in an email with the subject 'REU Position' to Ben Dantzer (dantzer@umich.edu) by April 5. The cover letter should describe why you want this position, how it fits into your career goals, any record of overcoming challenges, ideas for possible independent research projects, and an overview of your past experiences with independent research, field research, animal handling, and living/working in a remote area. Applications will be considered as they are received.

*Ben Dantzer, Ph.D.* Assistant Professor Dept Psychology Dept Ecology & Evolutionary Biology University of Michigan Ann Arbor, MI 48109

Email: dantzer@umich.edu Phone: 734-615-2352 Follow me < https://twitter.com/ben_dantzer?ref_src=twsrc%5Egoogle%7Ctwcamp%5Eserp%7Ctwgr%5Eauthor > or the Kluane Red Squirrel Project < https://twitter.com/KluaneSquirrels > on Twitter Visit my website < https://sites.lsa.umich.edu/dantzerlab/ >

Ben Dantzer <bendantzer@gmail.com>

---

## UndergraduateDiversity AtConferences Mar31

The Undergraduate Diversity at Evolution (UDE) program sends undergraduate students to the annual Evolution meeting < https://www.evolutionmeetings.org/ >, the joint meeting of the Society for the Study of Evolution < http://www.evolutionsociety.org/ > (SSE), the Society of Systematic Biologists < http://www.systbio.org/ > (SSB), and the American Society of Naturalists < http://www.amnat.org/home.html > (ASN). At the meeting, students will (i) present a poster, (ii) receive mentoring from graduate students, postdocs, and faculty, and (iii) participate in a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. Awardees receive: Conference registration, round-trip airfare, dorm accommodations, a $200 meal stipend, ticket to the super social.

The application deadline is Sunday , March 31st, and decisions will be announced by Sunday, April 7th. Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students.

APPLY HERE: https://goo.gl/T8vJdi

Louise S. Mead, PhD Education Director BEACON Center for the Study of Evolution in Action 567 Wilson Rd Michigan State University East Lansing, MI 48824

"Mead, Louise" <lsmead@msu.edu>

---

## Vignettes on EvolutionaryApplications

Dear EvolDir,

We are seeking your help in developing two-page vignettes on Applications of Evolution to topics that impact our world in a variety of ways. The concept is to identify primary research papers that have exciting applications of evolution to areas of impact on environment (climate change, conservation, biotic assembly, etc.), medicine (infectious disease, genomics, human phenotypic variation, etc.), and Society (agriculture, law, computation, language, etc.). Then develop a lay summary (2 page, 2 figure/table) of the research topic for use in teaching efforts at high school, college, and political levels. We envision graduate seminars and/or lab groups focused on developing such vignettes and submitting for peer review via EasyChair https://easychair.org/cfp/EvolApps2019. We are developing a distinguished Program Committee to review vignettes and welcome additions to the Program Committee as well. The top 50 vignettes will be published in a volume by Oxford University Press with up to four articles winning a cash prize. We hope faculty and graduate students will organize around the world and produce exciting vignettes for submission by our May 31, 2019 deadline. You can find more information and some example vignettes here https://www.evolutionapps.org/. Please let me know if you have any questions or need any guidance as your are developing your Evolutionary Applications!

Sincerely,

Keith Crandall kcrandall@gwu.edu

"Prof. Keith A. Crandall" <kcrandall@gwu.edu>

# PostDocs

AarhusU ComputationalPhylogenetics . . . . . 88
AarhusU PrimatePopulationGenomics . . . . . 89
Albuquerque NewMexico ConservationGenomics . . . 90
ArizonaStateU BiodiversityDataScience . . . . . 90
ArizonaStateU PrimateGenomics SexChromosomes 91
AuburnU EvolutionaryGenomics . . . . . 91
Brest France DeepSea SpeciesGenetics . . . . . 92
Caltech MicrobesSocialParasiteBeetles . . . . . 93
CarnegieMNH Pittsburgh AmphReptiles . . . . . 94
CornellU TeachingEvolution . . . . . 95
Eawag Switzerland AquaticEvolution . . . . . 96
Houston SexChromosomeSexDetermination . . . . . 96
Italy PDF PhD ConservationGenomics . . . . . 97
Lausanne PlantEvolution . . . . . 97
Lisbon EvolutionaryEcol . . . . . 98
LosAlamosNatlLab Bioinformatics . . . . . 98
Lyon HorizontalGeneTransfer . . . . . 99
MaxPlanck Ploen ModelingAntibioticResistance . . 100
MichiganStateU EvolutionPlantResilience . . . . . 101
MichiganStateU GlacialLakeEvolutionaryEcol . . . . 102
NHM LosAngeles DinosaurMacroevolution . . . . . 103
QMUL London EvolutionEthiopianCropResiliance 103
Switzerland ComputationalPhylogenetics . . . . . 104
Switzerland Modeling Microbial Interactions . . . . . 104
Switzerland PhD PDF ComputPhylogenetics . . . . . 105
TexasTechU Phylogenomics . . . . . 106
Tours France Metabarcoding . . . . . 106
TU Madrid MicrobialEvolution . . . . . 107
UArkansas NeuroEvoDevo . . . . . 108
UBielefeld ShellfishPopGenomics . . . . . 108
UCalgary MedicalPlantEvolution . . . . . 109
UCalifornia Irvine EvolutionaryGenomics . . . . . 110
UExeter SocialBees . . . . . 110
UGeorgia EvolutionaryGenomicsAbioticStress . . . . 111
UGuelph FishEvolGenetics . . . . . 111
UInnsbruck AquaticEvolutionaryEcol . . . . . 112
UJohannesburg AdaptiveGenomics . . . . . 112
UKansas DrosophilaComplexTraits . . . . . 113
UMontana EvolutionInvasiveSpecies . . . . . 114
UNewBrunswick EvolutionFloralScent . . . . . 114
UNorthTexas PopulationGenomics . . . . . 115
UOtago ConservationGenomics . . . . . 115
UOxford EvolutionSenescence . . . . . 116
UPittsburgh EvolutionaryBiology . . . . . 116
UQueensland CoralReefEvolutionaryGenomics . . . 117
URochester EvolutionaryGenetics . . . . . 118
USouthFlorida-Tampa HumanPopulationGenetics 118
UTexas Austin BumblebeeCognition . . . . . 119
UToyko EvolutionaryAnthropology . . . . . 119
UTromso Norway AncientDNA . . . . . 120
UWisconsin Madison Evolution . . . . . 120
UWisconsin Madison EvolutionaryGenomics . . . . . 121
UWisconsinMadison MutationEvolutionaryGenetics 122
UWisconsin Milwaukee Bioinformatics . . . . . 122
UWisconsin StevensPoint WhitefishGenomics . . . . 123
UZurich 2 EvolutionaryBiol . . . . . 123

## AarhusU ComputationalPhylogenetics

The department of Bioscience, Aarhus University, Denmark invites applications for a 2-year postdoc position in plant phylogenetics and macroevolution.

Read more and apply here: http://international.au.dk/about/profile/vacant-positions/job/postdoc-in-computational-phylogenetics-and-macroevolution/
Deadline: 15 April 2019

Job description: This postdoc is part of PhyloSynth, an international collaboration aiming to make the plant Tree of Life more comprehensive, useful, and up-to-date. You will contribute to the development of a bioinformatics pipeline that gathers all publicly available phylogenetically informative data for plants, builds phylogenetic trees using state-of-the-art methods, and disseminates them to a variety of audiences. You will have the opportunity to use the resulting trees in e.g. macroevolutionary analyses of plant diversification. You will be expected to develop well-documented software packages and publish your work in high-impact scientific journals. Although PhyloSynth is focusing on plants, we expect most of the methods developed to be applicable to other taxa and thus of broader interest and impact. For more information on the aims of PhyloSynth, see: https://doi.org/10.1002/ajb2.1041. The exact focus of your work within the overall scope of PhyloSynth is flexible de pending on your skills and interests.

Your profile: You have a PhD degree (or submitted your PhD thesis for assessment before the application deadline) in biology, bioinformatics, computer science or similar. Computers are among your most important research tools - the bigger the better. You would rather write a well-documented script than risk having to do something twice. You have written programs in more than one language, but have your favourite. However, you do not just want to develop code, you want to solve scientific problems. Ideally, you have an interest in (and experience with) tree thinking and phylogenetic analysis. You enjoy working in a highly collaborative environment including many other computer-minded biologists who will discuss a biological hypothesis and a computational challenge with equal enthusiasm.

International applicants who do not have English as their first language must prove strong English language writing skills and fluency.

Supervisor: Associate Professor Dr Wolf Eiserhardt (wolf.eiserhardt@bios.au.dk, +45 8715 6136).

Collaboration: You will have plenty of opportunity to interact with, and receive support from, other members of the PhyloSynth network. In particular, you will develop your work in close collaboration with Dr Stephen Smith and his group at the University of Michigan, USA (http://blackrim.org/). This includes the possibility of spending time in Michigan.

Place of employment: You will be part of the Section of Ecoinformatics & Biodiversity (ECOINF), Department of Bioscience, Aarhus University, Ny Munkegade 114, DK-8000 Aarhus C, Denmark. ECOINF is an ambitious, collaborative and highly international research group. Postdocs and PhD students are encouraged to collaborate within the group, across departments and with other universities. More information about the people and research activities of the group can be found at http://bit.ly/ecoinfAU . Wolf.Eiserhardt@gmx.net

---

## AarhusU PrimatePopulationGenomics

Post doc in primate population genomics

A 2-year postdoc position in population genomics is available in the research group of Mikkel H. Schierup at the Bioinformatics Research Centre, Aarhus University.

The position is available starting May 1, 2019 or as soon as possible hereafter.

The postdoc will develop and apply approaches to study the evolutionary processes affecting sex chromosome evolution with specific focus on human population data sets and new data sets of great apes genomes. The goal is to elucidate the mechanisms underlying the very strong natural selection affecting the X chromosome and its involvement with speciation processes as well as in male fertility. Specific speciation processes among great apes including archaic humans can also be investigated. Depending on your interests, focus can be on population genetics methods development, large scale analysis, or both. Available new data will include comparative single cell RNA data from testis and sperm samples in multiple individuals of both humans and other great apes.

Qualifications We are looking for a highly motivated person trained in population genetics and with some prior experience with analysis of large population genomics data sets.

The candidate must hold a Ph.D. degree (or equivalent) in biology, bioinformatics, statistics or computer science with some experience in population genetics.

It will be an advantage, if the candidate has

* direct experience with statistical analysis of high throughput data such as population genomics data and/or single cell expression data. * programming skills in R and/or Python * publications as main author within genomics and/or population genetics * excellent communication skills in English

About Bioinformatics Research Centre (BiRC). BiRC (www.birc.au.dk) provides a young, interdisciplinary environment, presently with ~45 professors, postdocs and PhD-students. There are strong links to Department of Computer Science, Mathematics/statistics and Biology as well as to the Faculty of Health. Within population genomics and evolution, BiRC hosts the integrated research groups of Kasper Munch (recombination, selection in primates, X and Y chromosome evolution), Thomas Bataillon (evolutionary theory, experimental evolution), Asger Hobolth (coalescent methods) and Mikkel H. Schierup (primate population genomics, X and Y).

The place of work is C.F. Møllers Allé 8, DK-8000 Aarhus C, Denmark.

Further information For further information and discussions of specific ideas, please do not hesitate to contact Professor Mikkel Heide Schierup, Phone: +4527782889, email: mheide@birc.au.dk

Application procedure Shortlisting is used. This means that after the deadline for applications ' and with the assistance from the assessment committee chairman, and the appointment committee if necessary, ' the head of department selects the candidates to be evaluated. All applicants will be notified whether or not their applications have been sent to an expert assessment committee for evaluation. The selected applicants will be informed about the composition of the committee, and each applicant is given the opportunity to comment on the part of the assessment that concerns him/her self. Once the recruitment process is completed a final letter of rejection is sent to the deselected applicants, including the main considerations emphasized during the selection process.

Application deadline March 15, 2019. Starting date as soon as possible after May 1, 2019

Mikkel H. Schierup Bioinformatics Research Centre, Aarhus University, CF Mollers Alle Building 1110, 8000 Aarhus C Denmark Ph: +45 8715 6535 Email: mheide@birc.au.dk http://www.birc.au.dk/˜mheide Mikkel Heide Schierup <mheide@birc.au.dk>

## Albuquerque NewMexico ConservationGenomics

*Post-doctoral position- Conservation Genomics*

We are currently seeking applications for a post-doctoral researcher to be involved in several new research projects in the Biology Department at the University of New Mexico (Albuquerque, USA). These projects will develop high throughput markers for a number of endangered freshwater fishes found in the Southwestern United States. Successful applicant be responsible for (i) analysis of next-gen sequencing data (ii) development SNP arrays for ongoing genetic monitoring/evolutionary ecology projects and (iii) development of sex specific markers for Rio Grande silvery minnow. Funding is available for 2 years. The candidate selected for the position will primarily be involved in the bioinformatics portion of the projects but there will also be opportunities for engagement in field and laboratory work. The successful applicant will have a background in population/conservation genetics and strong analytical skills particularly in genomics/bioinformatics and a willingness to engage with all members of the research team (including undergraduates and graduate students). A PhD is required. Our lab also works closely with state and federal agencies so a willingness to engage with the broader community is also important.

For enquiries about this position please contact:

Megan Osborne (mosborne@unm.edu; 1 505 2773234)

https://biology.unm.edu/ http://www.unm.edu/ *Minimum Qualifications:*

PhD in discipline by the start date of appointment

*Preferred Qualifications–*

Background in population/conservation genetics

Strong analytical skills particularly in genomics/bioinformatics

Laboratory experience with next-gen sequencing methods, e.g. SNP development and GTseq

Excellent written and oral communication skills

A demonstrated commitment to diversity, equity, inclusion, and student success, as well as working with broadly diverse communities.

Applications due: March 31st 2019, will remain open until filled.

Applications: https://unm.csod.com/ats/careersite/-JobDetails.aspx?id=7816&site – Megan Osborne

Department of Biology University of New Mexico Albuquerque New Mexico

megansbrn@gmail.com

## ArizonaStateU BiodiversityDataScience

The Biodiversity Knowledge Integration Center (BioKIC) at Arizona State University (ASU) invites applications for a postdoctoral research scholar position in biodiversity data science. The position is part of a new Biodiversity Data Science Initiative launched at ASU and led by Beckett Sterner and Nico Franz. The initiative will focus on building an innovative web platform that leverages theoretical advancements and prototype software for taxonomic intelligence (https://doi.org/10.1093/sysbio/syw023), with the goal of demonstrating high-value use cases for conservation biology, ecology, and science publishing. The platform will accelerate the growth of high-quality, reproducible biological data to address emerging data science challenges for monitoring and predicting biodiversity loss.

Position ad: https://sols.asu.edu/sites/default/files/job_12643.pdf This postdoctoral position will focus on connecting the taxonomic intelligence platform to users through quantifying the value of taxonomic intelligence for applied use cases. The position will also involve building a broader network of researchers working on taxonomic intelligence in order to validate and inform the underlying platform design. The successful candidate will therefore have a strong record of achievement in biodiversity informatics, including building data aggregation and analysis pipelines, applying visualization tools, using machine learning models, and designing front-end systems. Experience working with NGOs, digital curation of biological data, and the economic, social and ethical dimensions of data infrastructure are also preferred. Mentoring of students and co-/authorship of peer-reviewed publications, presentations, and of research proposals, will be strongly encouraged.

Exploratory e-mail inquiries are strongly encouraged. Interested applicants should send a one-page research statement, clearly indicating their qualifications and motivation to join the project, Curriculum Vitae, and contact information for three references to nico.franz@asu.edu and bsterne1@asu.edu. The review of applications is rolling until the search is closed, and the position is open for an immediate start date.

Salary is commensurate with experience, with a range of $55,000 to 75,000 annually, plus ASU benefits, for exceptionally well qualified applicants. Reasonable relocation funds are available.

bsterne1@asu.edu

---

## ArizonaStateU PrimateGenomics SexChromosomes

Join the Pfeifer (http://spfeiferlab.org/) and Wilson Labs (http://www.sexchrlab.org/) at Arizona State University (ASU) as a Center for Evolution & Medicine (CEM) Research Scholar to study the evolutionary and selective forces that have shaped sex chromosomes in non-human primates.

Scholars will receive a salary of $60,000 and will have access to funding of up to $10,000 per annum to support their research ($1,500 may be allocated for moving expenses). The initial closing date for receipt of complete applications is March 15, 2019; applications will be reviewed weekly thereafter until the search is closed. The earliest anticipated start date is July 1, 2019; the latest is January 1, 2020.

More information can be found at https://evmed.asu.edu/news/open-position-evolution-medicine-postdoctoral-research-scholar Research topics are open to discussion and mutual interest thus contact us for additional details.

Susanne P. Pfeifer Assistant Professor Arizona State University School of Life Sciences http://spfeiferlab.org spfeife1@asu.edu

---

## AuburnU EvolutionaryGenomics

Postdoctoral Research Associate in Evolutionary Genomics 2019 I am looking for a postdoc with research interests at the intersection of evolutionary, quantitative, and functional genomics. My lab is in the Biological Sciences Department at Auburn University and our research interests are centered on evolutionary and functional genomics of sexual dimorphism.

This position is funded by an NSF CAREER award and I envision responsibility for projects related to this award as part of the position. However, trainees will have support for pursuing their own independent research interests and projects.

Our current research is focused on the role of hormone signaling in sex-differential gene expression, sexual conflict and sexual dimorphism of complex traits. Current students have projects focused on the innate immune response, stress, and the response to endocrine disruptors. My lab group uses Drosophila as a model system to investigate our questions. I also have ongoing collaborations on projects using the brown anole to investigate dimorphism in aging (https://www.schwartzlab-ecoevolutionarygenomics.org/), in comparative genomics of the innate immune response in acorn worms (http://metazoan.auburn.edu/halanych/lab/), and in the role of stress in variation in recombination (https://sites.google.com/site/lstevison/home).

My lab group also has a strong interest in teaching and outreach focused on diversity and inclusion in STEM, and we would love to bring someone in who is also interested in this aspect of our work. We participate in two summer REUs (Computational Biology and Collaborative Approaches among Scientists and Engineers) and sponsor summer research for high school students from regional underserved schools.

A strong background in evolutionary genomics, functional genomics, and/or quantitative genetics and science communication, organizational, and management skills are desired. The applicant should have a strong work ethic, and is expected to develop new ideas that promote current research and their own future independence. The post-doc will be expected to assist with training graduate and undergraduate students in the lab, develop synergistic projects, write grants, produce first authored papers, and contribute to co-authored papers. I hope that the post-doc will also have enthusiasm for participating in development of new teaching approaches (integrating our research into education at Auburn), our ongoing outreach and/or novel outreach projects.

Applicants will have: - Strong written and oral communication skills - A record of being a productive and creative member of a research team - Have come proficiency or a strong interest in bioinformatics (we can provide training!) - Produce high quality research (as evidenced by first authored publications) - Work effectively and collegially with others - Be respectful and supportive of students and peers

Other traits not required, but ideal: - Ability to code in at least one programming language - Experience with *nix and using an HPC - Experience with best practices for analyzing RNA-seq data - Some familiarity with statistical or quantitative genetics - Molecular biology lab skills (e.g. RNA extraction and library preps)

Full support is available for one year, with up to two additional years possible pending satisfactory performance and available funds. Selected applicants will also benefit from funds to travel to national meetings annually, opportunities for mentoring experience and career development. Additional lab funds for independent projects are available with written proposals. Anticipated start date is August 2019.

The selected applicant would be joining a strong research community in the Southeastern US. Nearby universities/research facilities (within 2 hours) include UGA, Georgia Tech, Emory, Hudson Alpha, and UAB. The wider SE Community also includes UF, Clemson, UNC, and Duke with local area meetings annually to network within this community. Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Those from groups that are underrepresented in STEM are strongly encouraged to apply.

This announcement is informal in nature and candidates of interest will be asked to submit a formal application for complete consideration after initial screening. If interested, please send a cover letter/statement of interest with a list of relevant skills, a CV, including a list of peer-reviewed publications, and contact information for two references by email to Rita Graze at rmgraze (at) auburn (dot) edu References will not

— / —

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

---

## Brest France DeepSea SpeciesGenetics

POST-DOCTORAL CONTRACT IN THE DEEP-SEA LAB AT IFREMER (BREST, FRANCE)

Supervisors : Florence Pradillon & Marjolaine Matabos

Collaborateurs : Didier Jollivet (CNRS/Station biologique de Roscoff) & Sophie Arnaud (Ifremer, Sète)

A 12 month post-doctoral fellowship is available in the Ifremer deep-sea lab (Brest, France) to study the genetic connectivity of several vents species along the Mid-Atlantic ridge using RADseq genomic approaches. This project is part of the Abyss Ifremer national project.

There will be a possible opportunity of extension with Dr. Didier Jollivet at the CNRS/Marine Biological station of Roscoff (in collaboration with our team) working on bathymodiolin mussels connectivity at the same sites using similar approaches as part of the H2020 European project iAtlantic.

DEADLINE OF APPLICATION: MAY 31, 2019

START: OCTOBER 1, 2019

To apply send a Curriculum Vitae and a letter of application to Florence.Pradillon@ifremer.fr or Marjolaine.Matabos@ifremer.fr

TITLE: Demographic history and population connectivity of hydrothermal vent species along the mid-Atlantic Ridge using a ddRDAseq approach

ABSTRACT: Dispersal and colonization in hydrothermal vent species are essential to support local populations over short time scales, as well as in demographic history of species and speciation over longer time scales. This project is based on the development of genomic scan approaches (RAD seq and possibly RNA seq) to estimate past and contemporary connectivity among Mid-Atlantic Ridge vent species. The shrimps _Rimicaris_ spp., as well as the gastropod species _Peltospira smaragdina_ and _Lepetodrilus atlanticus_ are major species in animal communities, especially at vent work sites that have been visited repeatedly by our laboratory, including those within a mining exploration license (AIFM) and part of a deep-sea observatory (EMSO-Azores). We propose to conduct a comparative approach on those species with contrasting life-history traits in order to 1) describe the distribution of genetic diversity, to infer past and contemporary connectivity patterns, and, 2) examine possible links between genetic connectivity and species life cycle (reproduction and larval life), geographic barriers, or ecological gradients (depth, chemical signature of vent fluids). To this end, first an exploratory approach will be undertaken on different species and one or two will be selected for a more thorough analysis. This project falls within the scope of the Ifremer ABYSS project on deep-sea genomics, and will contribute fundamental data to help define possible strategies to ensure sustainable human activities in this threatened ecosystem.

[1] http://www.deepseaspy.com mmatabos <Marjolaine.Matabos@ifremer.fr>

---

## Caltech MicrobesSocialParasiteBeetles

Postdoctoral position in microbial interactions between ants and social parasite beetles (Parker Lab)

Research focus: A postdoctoral position is available to study the impact of endosymbiont microbes on animal-animal symbiotic relationships in the lab of Joe Parker at the California Institute of Technology.

Work in the Parker lab is focused on social and symbiotic relationships between animals. We use a unique system to explore these phenomena: the convergent evolution of social parasitism of ant colonies by rove beetles (family Staphylinidae). Rove beetles comprise the largest metazoan family (64,000 species), and include multiple lineages that have evolved to infiltrate ant societies, employing behavioral, anatomical and chemical adaptations. The Parker lab studies these adaptations at the molecular and neurobiological levels. We are now seeking a postdoctoral researcher to probe the endosymbiotic microbiota of rove beetles and their host ants, to address how communities of microbes and multicellular organisms influence each others evolution and function.

The successful candidate will spearhead community metabarcoding and metagenomics of ants and social parasite rove beetles to uncover microbial interactions within and between these animal species. The focal system is a model ant-beetle symbiosis that has evolved in the South Western US, in which multiple rove beetle lineages have convergently evolved to infiltrate colonies of a single ant genus. This project involves fieldwork at local sites near Caltech, as well as in Southern Arizona. To better understand how microbes influence social and symbiotic interactions between these species, experimental laboratory manipulations of beetle and ant microbiomes will be pursued, together with phenotypic analysis of behavior and chemical ecology. Inferences about how the evolution of animal interactions impacts the microbiome will be pursued by comparative studies of the microbiota of parasitic and related, free-living beetles. There is substantial opportunity to collaborate with other microbiology labs at both Caltech and the University of Southern California, as well as collaboration with theoretical biologists to develop empirically-based models of multilevel, microbe-animal networks.

The following papers illustrate the rove beetle-ant symbiosis:

Maruyama, M., and Parker, J. (2017) Deep-Time Convergence in Rove Beetle Symbionts of Army Ants. Current Biology, 27, 920V926 PMID: 28285995

Yamamoto, S., Maruyama, M. and Parker, J. (2016) Evidence for Social Parasitism of Early Insect Societies by Cretaceous Rove Beetles. Nature Communications, 7: 13658 PMID: 27929066

Parker, J., Eldredge, K.T., Thomas, I.M., Davis, S., Coleman, R.T. (2018) Hox-Logic of Preadaptations for Social Insect Symbiosis in Rove Beetles. bioRxiv, 198945

Applications are encouraged from talented and motivated individuals who have a Ph.D. or are nearing completion of their Ph.D. with experience in microbial ecology, microbiome sequencing, bioinformatics and metagenomics. Interest or experience in insect biology, behavioral analysis and chemical ecology is desirable but not essential. Top candidates will have a strong track record of research productivity, excellent communication skills, enthusiasm for basic research and a collegial approach to science. Candidates should provide a cover letter, a detailed CV, and names and contact details for three references. For more information, or to apply, please contact joep@caltech.edu

Start Date and Project Duration: The start date is flexible and depends on the candidate. Preference is for candidates who can start in Fall 2019. The position is funded for two years at least and potentially longer depending on progress. The California Institute of Technology Caltech is consistently ranked among the top research universities in the world and hosts a diverse and collaborative scientific community. Caltech is located in Pasadena, California, a vibrant city 10 miles northeast of downtown Los Angeles and minutes from the Parker labs fieldwork sites in the San Gabriel mountains. More info about the Parker lab: https://www.beetles.caltech.edu/ We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, or national origin, disability status, protected veteran status, or any other characteristic protected by law.

– Joe Parker, Ph.D. California Institute of Technology Division of Biology and Biological Engineering 1200 E. California Blvd. MC 216-76 Pasadena, CA 91125

Tel: +1 626 395 8729 https://www.beetles.caltech.edu/
"Parker, Joseph" <joep@caltech.edu>

---

## CarnegieMNH Pittsburgh AmphReptiles

Post-Doctoral Researcher Carnegie Museum of Natural History Pittsburgh, PA

Carnegie Museums of Natural History, one of the four Carnegie Museums of Pittsburgh, is among the top natural history museums in the country. It maintains, preserves, and interprets an extraordinary collection of artifacts, objects, and scientific specimens used to broaden understanding of evolution, conservation, and biodiversity. Carnegie Museum of Natural History generates new scientific knowledge, advances science literacy, and inspires visitors of all ages to become passionate about science, nature, and world cultures.

To Apply: Visit http://www.carnegiemuseums.org/opportunities. Click on Search Jobs and Click on Apply within this job posting (Req #224). It is encouraged that you upload your CV/resume and cover letter (in one file) - detailing your specific and unique educational and research experiences.

Carnegie Museums of Pittsburgh is interested in candidates who, through their experience and collaborations, will contribute to diversity and excellence of the Carnegie Museums community.

The Carnegie Museum of Natural History's (CMNH) Section of Amphibians and Reptiles invites proposals for a POST-DOCTORAL RESEARCHER. The successful applicant will work with the Curator, and may incorporate collections-based research, field work in the US or Borneo, remote sensing, molecular work, or some combination thereof. Applicants should refer to the Curator's website (jasheridan.com) for information on possible research directions to develop a proposal that complements ongoing work. Preference will likely be given to proposals that use amphibians and/or reptiles. Possible topics include, but are not limited to: climate change, land use change, trophic cascades, remote sensing terrestrial primary productivity, movement ecology, or evolution. The successful candidate will have opportunities to perform research in world class collections housed at CMNH, Powdermill Nature Reserve (CMNH's research station approximately 1 hour east of Pittsburgh), or in Malaysian Borneo. Other research sites will be considered with strong justification. As this is a museum-based post-doc, development of citizen science programs or other outreach related to the chosen project is strongly encouraged.

EDUCATION AND EXPERIENCE: -PhD in Ecology, Evolutionary Biology, Conservation Biology, or related field -Demonstrable knowledge of amphibian and reptile ecology and/or evolution -Record of peer-reviewed publications, including lead-author papers in research relevant to the position.

KNOWLEDGE, SKILLS, AND ABILITIES: -Demonstrable knowledge of amphibian and reptile ecology and/or evolution -Record of peer-reviewed publications, including lead-author papers in research relevant to the position -Experience with multivariate analyses or ecological modeling a plus

PHYSICAL REQUIREMENTS: Depending on the successful proposal, there is likely to be a combination of office, field, and collections-based work, all of which have different physical requirements.

ESSENTIAL FUNCTIONS AND ACCOUNTABILITIES: Exact functions and accountabilities will be determined by mutual agreement prior to the start of employment, based on the successful applicant's proposed research.

The following PA Act 153 clearances, or proof of application of clearances, are required beginning employment and as a condition of continued employment: *Pennsylvania Child Abuse History Clearance *Pennsylvania State Police Criminal Record Check *FBI Fingerprint Criminal Background Check Obtaining the required clearances is completed as part of the new hire process.

Carnegie Museums is an Equal Opportunity-Affirmative Action Employer - Minorities / Females / Veterans / Individuals with Disabilities / Sexual Orientation / Gender Identity

"Brooks, Glenn" <BrooksG@CarnegieMuseums.Org>

---

## CornellU TeachingEvolution

Teaching Postdoctoral Associate - Organismal Biology (University Title - Instructor) College of Agriculture and Life Sciences Cornell University Ithaca, New York

The Department of Entomology, in collaboration with Cornell's Active Learning Initiative, invites applicants for a full-time Teaching Postdoctoral Associate (University Title - Instructor) with interest in developing skills and experience in Biology Education Research and Evidence-Based Pedagogy in preparation for an academic career. Specifically, the postdoc will play a key role in supporting the transition of three large non-major courses in Entomology (Alien Empire, Honeybee Biology, Plagues and People) from a traditional lecture course format to active learning format, focusing on student participation and group problem solving. This position is part of a Cornell-wide initiative to shift the undergraduate curriculum toward active learning approaches; the wide range of participating departments is summarized here: http://news.cornell.edu/stories/-2019/02/active-learning-initiative-funds-nine-projects Active Learning Initiative funds nine projects | Cornell Chronicle news.cornell.edu Cornell's Active Learning Initiative (ALI) will nearly double in scope and impact with a new round of funding for innovative projects to enhance undergraduate teaching and learning in nine departments. In the first universitywide ALI grant competition, about $5 million has been awarded in substantial new grants ranging from $195,000 to almost $1 million, spread over two to five years.

The Teaching Postdoctoral Associate will be appointed for a one-year period renewable for a second year and a third year contingent upon performance. The successful candidate will collaborate with four Entomology faculty (Caillaud, Danforth, Harrington and Sanderson) towards the following goals: formulate learning goals, develop active learning-based modules that align with the learning goals and are transferable among the three courses, provide feedback on course teaching practices, evaluate and assess learning gains, present/publish the results, act as a consultant for other Faculty members in the department. We expect that successful candidates will devote 30% of their effort to organizing the active learning transition process, 50% effort to developing active learning material and activities pertaining to the goals and content of the courses, and 20% effort to assessment of the implementation of active learning, presentation/publication and consulting.

* Qualifications * Candidates should hold a doctoral degree in Organismal Biology, Ecology/Environmental Sciences /Entomology, Biology Education, or a related field and have excellent organizational, interpersonal communication, team building and collaboration skills. Experience in developing active learning curricula and coaching educators is highly desirable.

* Terms of Appointment * This is a 1-year appointment with the possibility of extension. Salary will be commensurate with experience and qualification. The anticipated start date for the appointment is June 1, 2019 (start date is negotiable).

* Applications * To ensure full consideration, applica-

tions must be received by March 15, 2019. To apply: applicants should submit an application via Academic Jobs Online: https://academicjobsonline.org/ajo/jobs/13306. Applications should include a CV, a statement of teaching philosophy/experience, a statement of research experience, and the names, phone numbers, and email addresses of three individuals who can serve as references. Entomology/CALS, Cornell University < https://academicjobsonline.org/ajo/jobs/13306 > Full service online faculty recruitment site for academic institutions worldwide. We offer unique solutions tailored for academic communities.

Bryan N. Danforth, Professor and Chair Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-2601 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu Lab website: http://www.danforthlab.entomology.cornell.edu/ The Solitary Bees (forthcoming): https://press.princeton.edu/titles/13525.html The Bee Course (2019): https://www.thebeecourse.org/ bnd1@cornell.edu

---

## Eawag Switzerland AquaticEvolution

The yearly call for the prestigious "Eawag-Postdoc", a 2-year postdoctoral fellowship at Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is open:

https://apply.refline.ch/673277/0682/pub/3/index.html Please refer to the advert for details. The call is open for researchers in any field within in the area of aquatic science and technology, including ecologist and evolutionary biologists.

Information on our research in these fields is available via the following links: https://www.eawag.ch/en/department/eco/organisation/ https://www.eawag.ch/en/department/fishec/ https://www.eawag.ch/en/department/umik/ Feel free to contact any of Eawag's group leaders to discuss opportunities.

Christoph Vorburger Eawag, Swiss Federal Institute of Aquatic Science and Technology & Institute of Integrative Biology, ETH Zurich Überlandstrasse 133 8600 Dubendorf Switzerland

Phone: +41 58 765 5196 e-mail: christoph.vorburger@eawag.ch or vorburgc@ethz.ch group homepage: http://homepages.eawag.ch/ ˜ vorburch/ "Vorburger, Christoph" <Christoph.Vorburger@eawag.ch>

---

## Houston SexChromosomeSexDetermination

The Department of Biology & Biochemistry at the University of Houston invites applications for one postdoctoral position in Dr. Richard Meisels group to study the evolution of sex chromosomes and sex determination in flies. Applicants with research interests in evolutionary genetics and genomics are encouraged to apply. The successful applicant will have a background in population genetics, molecular ecology, evolutionary genomics, bioinformatics, or entomology. The position requires a Ph.D. and relevant academic experience. Responsibilities will include contributing to ongoing research in the Meisel lab, developing independent research projects, and mentoring graduate/undergraduate students.

The Department of Biology & Biochemistry has state-of-the-art laboratory space, well-equipped core facilities, and high-performance computing resources. Broad opportunities exist for research collaborations within the University of Houston as well as at nearby institutions. Interested applicants should apply by emailing Richard Meisel (rpmeisel@uh.edu) a curriculum vitae, cover letter, and names and contact information for two references. Applications will be reviewed as they are received and continue until the position is filled.

The University of Houston is an Equal Opportunity/Affirmative Action institution. Minorities, women, veterans and persons with disabilities are encouraged to apply. Additionally, the University prohibits discrimination in employment on the basis of sexual orientation, gender identity or gender expression.

Richard Meisel Assistant Professor Department of Biology and Biochemistry University of Houston

3455 Cullen Blvd Suite 349 Houston, TX 77204-5001

Office: 421C SR2 Lab: 428/433 SR2

rpmeisel@.uh.edu bchs.uh.edu/˜rpmeisel 1-713-743-3607

rpmeisel@Central.UH.EDU

## Italy PDF PhD ConservationGenomics

We are seeking expressions of interest for one Post Doc and one PhD position at the University of Ferrara (Italy) for a project investigating the population genomics patterns in five animal species endemic to Italy. The formal selection process will be announced soon, but we ask to all interested candidates to send their CV and contact details of two references as soon as possible. We expect the postdoc to start about September, while the phd student will be enrolled in November.

This three year project has recently been funded by the Italian Ministry for Education and Research. Using five iconic endangered Italian endemics as model species (a mammal, a reptile, an amphibian, a fish, and an insect), we plan to investigate the dynamics of the accumulation of deleterious mutations in small populations, and their impact on individual fitness. We will estimate the genomic susceptibility to extinction due to mutation load, predict the consequences of genetic rescue, and propose conservation actions. We will also perform two functional assays to corroborate the population genomics analyses.

The project is a collaborative effort among four different Italian Universities (Ferrara, Padova, Trieste, Firenze), coordinated by Giorgio Bertorelle at the University of Ferrara. The postdoc and phd positions offered in this ad will be both based at the University of Ferrara, and will mainly focus on the population genomics analyses. The postdoc will additionally be responsible with the PI for the coordination of the whole project. There will be a regular interaction among students and researchers from all units, sharing and discussing the advancements in every topic relevant to the project. This will contribute to the scientific growth of graduate students and postdocs in many different fields: genomics, population genetics, evolution, conservation biology, bioinformatics, biotechnology.

The salary for the phd student is fixed nationally and will be 1140 Euros per month. The salary for the postdoc is negotiable, but it will vary depending on the previous experience between 1500 and 2200 Euros.

For any question, please contact Giorgio Bertorelle, ggb@unife.it

Giorgio Bertorelle Department of Life Sciences and Biotechnology University of Ferrara

Bertorelle Giorgio <ggb@unife.it>

---

## Lausanne PlantEvolution

Postdoc position, Department of Ecology and Evolution, University of Lausanne, Switzerland

A postdoctoral position in plant evolutionary biology is available in the Department of Ecology and Evolution, University of Lausanne. The postdoc will join a team working on the evolution of plant sexual systems, sexual dimorphism, and the resolution of sexual antagonism in dioecious and hermaphroditic plants. For details, see https://www.unil.ch/dee/pannell-group . Research scope and skills sought

The postdocs research direction and projects can be tailored to her or his interests and expertise. However, apart from having a strong interest (and PhD) in evolutionary biology and/or population genetics, we are ideally seeking someone with a skill set that includes at least one of the following: generation and analysis of genomic and transcriptomic data; evolutionary, population genetic or demographic modelling; experimental design and statistics. Experience and an interest in working with plants could be an advantage, e.g., including managing glasshouse, common garden and/or field experiments. The successful candidate should also have good communication and interpersonal skills, and an ability to work in a team. Although not a requirement, some knowledge of French would be an asset.

Host Department and University

The Department of Ecology and Evolution hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and is close to the Swiss and French Alps.

Contract details

The position is envisaged at 100% for an initial period of one year, with two possible renewals of two years each (up to five years, depending on continued funding). Most of the postdocs time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. The starting date is flexible, but funding is available immediately.

Applications

Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications should include a cover letter detailing your research interests, experience and motivation for applying, a CV, and the names of two or three referees. Applications should be uploaded through the University of Lausanne platform (link given below). All applications received by 1 April will receive full consideration, but review of applications will begin immediately.

Application link: https://bit.ly/2Ftaz9B University equality policy

The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

John Pannell <john.pannell@unil.ch>

## Lisbon EvolutionaryEcol

A 2-year post-doctoral position is available at cE3c, Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/) in Lisbon, at the laboratory of Sara Magalhães, within an ERC consolidator grant. The grant may be extended for an extra year. We are seeking a highly motivated candidate with a general interest in evolutionary ecology. He/she is expected to enjoy working in a group, know (or quickly learn) how to independently plan and analyse his/her experiments, respect the lab rules and place his/her research in a general context. To find out more about our research group visit our website at https://-mitesquad.weebly.com/ Applicants should send their CV (including the name and email of two potential recommenders) to snmagalhaes@fc.ul.pt by May 10th. Check https://ciencias.ulisboa.pt/pt/concursos for the application and selection procedure. Starting date: flexible (mid-end 2019).

Place: Faculdade de Ciências da Universidade de Lisboa.

Project title: Competition under niche construction (COMPCON) Funding: ERC Consolidator Grant, 2017-2022.

Project abstract NB: the candidate is expected to work on the parts of the project that deal with competitive ability).

Interspecific competition is arguably the best interaction to address the how individual trait variation and eco-evolutionary feedbacks shape species distributions and trait evolution, due to its indirect effects on the shared resource. However, a clear understanding of such feedbacks is only possible if each contributing factor can be manipulated independently. With COMPCON, we will address the reciprocal interactions between individual variation, niche width, niche construction and the presence of competitors using a system amenable to manipulation of all these variables. The system is composed of two spider mite species, Tetranychus urticae and T. ludeni, that up- and down-regulate plant defences (i.e., negative and positive niche construction, respectively). Mites will be colonizing tomato plants with different cadmium concentrations, allowing quantitative variation of available niches. Tomato mutant plants with low defences will be used as an environment in which niche construction is not expressed. Individual variation in niche width and niche construction will be measured in isogenic lines. Different combinations of lines will then be used to test how such variation in individual traits affects coexistence and evolution with competitors. Data generated by COMPCON will strengthen the growing link between Ecology and Evolution, as it will test recent hypotheses concerning how individual variation, niche width, niche construction and competition interact to shape species distributions and trait evolution.

Sara Magalhães, Assistant Professor, https://-mitesquad.weebly.com/ Centre for Ecology, Evolution and Environmental Changes http://-ce3c.ciencias.ulisboa.pt/ Faculdade de Ciencias da Universidade de Lisboa http://www.fc.ul.pt/ Campo Grande Lisboa researcher ID: http:/-/www.researcherid.com/rid/B-9673-2012 Sara Magalhaes <snmagalhaes@fc.ul.pt>

## LosAlamosNatlLab Bioinformatics

Description Job Title: Bioinformatics Postdoc Location: Los Alamos, NM, US Organization Name: B-10/Biosecurity and Public Health Internal job ad: https://lanl.jobs/los-alamos-nm/bioinformatics-postdoc/636672455fda4713a4dd5de6819a8916/job/
The LANL Genomics Team is looking for a highly motivated, productive, and multi-talented postdoctoral candidate to pursue research within a team of scientists

working on novel bioinformatics solutions to next generation sequencing (NGS) data analysis, with special emphasis in the fields of transcriptomics, metatranscriptomics, and epigenetics analyses. Expertise in epigenetics is preferred. The applicant will be working both on human and algal projects.

Biosciences Genomics Team capabilities include both a core sequencing facility specializing in Illumina and PacBio technologies, and a bioinformatic data analysis group adapting state-of-the-art methods and devising novel strategies and algorithms to better interpret genomic, metagenomic, transcriptomic, and epigenetic NGS data. Our group comprises experimental and computational bioscientists working on projects that span a range of topics, including algal biology/bioenergy, microbial ecology, bacterial/viral/genome evolution, host-microbe interactions (e.g. host-pathogen, fungal-bacterial symbioses, etc.), cancer biology, biosurveillance, and pathogen diagnostics. Two positions are potentially available; one will initially explore analysis of metagenomic and/or transcriptomic data analysis applied to one or more of these projects and the other will focus on epigenetics/epigenomics. Additional projects or topics of interest will also be available depending on candidate interests.

The specific subject of the applicant's PhD degree is not restricted to any specific domain, but experience in handling transcriptomic NGS data, and familiarity with one or more programming languages (e.g. C++, Python, Perl, Java), are strongly preferred. The candidate should be equally comfortable working independently as well as part of a team, be familiar with good laboratory practices and biological experiment design, have experience working with Illumina and/or PacBio sequencing data in either DNAseq, RNAseq, ChIPSeq (or related method), have experience working in a UNIX/Linux cluster environment, and must have excellent written and oral communication skills. Applicants should also have a good publication record and/or bioinformatics related publications in preparation.

Education: PhD in related field completed within the past five years or a soon to be completed PhD.

Notes to Applicants: In addition to applying on-line, candidates should submit by email their CV, a very brief letter of interest, as well as names and contact information for 3 references to Blake Hovde (hovdebt@lanl.gov). Selected candidates will be contacted for telephone interviews in late March 2019.

Additional Details: Position does not require a security clearance. Selected candidates will be subject to drug testing and other pre-employment background checks. New-Employment Drug Test: The Laboratory requires successful applicants to complete a new-employment drug test and maintains a substance abuse policy that includes random drug testing.

Candidates may be considered for a Director's Postdoc Fellowship and outstanding candidates may be considered for the prestigious Richard P. Feynman, Darleane Christian Hoffman, J. Robert Oppenheimer, or Frederick Reines Distinguished Postdoc Fellowships.

For general information go to Postdoc Program.

Equal Opportunity: Los Alamos National Laboratory is an equal opportunity employer and supports a diverse and inclusive workforce. All employment practices are based on qualification and merit, without regards to race, color, national origin, ancestry, religion, age, sex, gender identity, sexual orientation or preference, marital status or spousal affiliation, physical or mental disability, medical conditions, pregnancy, status as a protected veteran, genetic information, or citizenship within the limits imposed by federal laws and regulations. The Laboratory is also committed to making our workplace accessible to individuals with disabilities and will provide reasonable accommodations, upon request, for individuals to participate in the application and hiring process. To request such an accommodation, please send an email to applyhelp@lanl.gov or call 1-505-665-4444 option 1.

Where You Will Work: Located in northern New Mexico, Los Alamos National Laboratory (LANL) is a multidisciplinary research institution engaged in strategic science on behalf of national security. LANL enhances national security by ensuring the safety and reliability of the U.S. nuclear stockpile, developing technologies to reduce threats from weapons of mass destruction, and

— / —

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

## Lyon HorizontalGeneTransfer

WHAT: a postdoc position to explore the hypothesis that Host-Parasitoid interactions may represent a major route of Horizontal Gene Transfer. More details below

WHERE: at the ≪ Biometry and Evolutionary Biology Lab ≫, University of Lyon, France

WHEN: starting in September 2019, for 3 years

#####

We are seeking a postdoctoral researcher to be hired at the University of Lyon (Biometry and Evolutionary Biology Lab) for three years, starting in September 2019.

The project will deal with horizontal gene transfer in insects and more specifically with the hypothesis that host-parasitoid interactions may constitute a major route for this phenomenon. It builds on a long- term and extensive ecological description of associations between parasitoids and their lepidopteran hosts in a natural area of Costa Rica. Through a collaboration with the University of Pennsylvania and the University of Guelph, we will sequence the full genomes of approximately 200 species from this system to assess if horizontal transfers occur preferentially between insects that are tightly connected through host-parasitoid interactions, or, in the case of Lepidoptera, through the host plants they feed on.

The project will require heavy involvement in bioinformatics and evolutionary biology concepts and methods. The ideal candidate will have a strong interest in horizontal gene transfer, and in evolutionary biology at both molecular and phenotypic levels. He or she should be at ease with bioinformatics, modeling, phylogenetic and co-phylogenetic analysis, and be inspired by the methodological challenges in these fields.

Lyon is a beautiful and lively city, not far from the Alps. The LBBE lab (https://lbbe.univ-lyon1.fr/?lang=en) offers a very active scientific environment, dealing with many current issues in evolutionary biology, from molecules to ecosystems, with diverse approaches, from the bench and the field to big data and pure theory.

Applications should be submitted to Sylvain Charlat <sylvain.charlat@univ-lyon1.fr> by June 1, 2019. Please include your CV and the names of three individuals who are prepared to provide letters of reference. For further details, contact Sylvain or other team members: Julien Varaldi, Vincent Daubin, Vincent Miele, Damien de Vienne (CNRS - University of Lyon), Clement Gilbert (CNRS - Gif sur Yvette), Daniel Janzen (University of Pennsylvania), Paul Hebert (University of Guelph).

Sylvain Charlat sylvain.charlat@univ-lyon1.fr sylvain.charlat@gmail.com CNRS (UMR 5558) - Université Lyon 1 Laboratoire de Biométrie & Biologie Evolutive Bat. Mendel, 16, rue Raphael Dubois 69622 Villeurbanne - FRANCE Tel 1: +33 4 72 44 81 01 Tel 2: +33 6 87 18 52 21 Fax: +33 4 72 43 13 88 http://lbbe.univ-lyon1.fr/-Charlat-Sylvain-.html?lang=en CHARLAT SYLVAIN <Sylvain.Charlat@univ-lyon1.fr>

---

## MaxPlanck Ploen ModelingAntibioticResistance

Postdoc position in Mathematical Evolutionary Biology, Research Group Stochastic Evolutionary Dynamics, Max Planck Institute for Evolutionary Biology

I am looking for a Postdoc to join my research group at the Max Planck Institute for Evolutionary Biology.

Postdoc position (2 years): Evolutionary dynamics of antibiotic resistance on plasmids

The evolution of antibiotic resistance poses a severe threat to modern healthcare. Clinically relevant resistance is often encoded on plasmids. Plasmids are extra-chromosomal DNA elements that can be transmitted vertically or be transferred horizontally between cells. The location of resistance genes on plasmids can lead to special evolutionary dynamics. The aim of the project is to develop mathematical models for the evolution and spread of resistance on plasmids. On the mathematical side, the analysis will mainly be based on branching process theory, complemented by deterministic ODE systems and stochastic computer simulations.

The ideal candidate has experience in mathematical modeling in biology and is keen on working on the evolution of drug resistance. Knowledge of a programming language (C, C++, Java, R, Python. . . ) is highly desirable.

Working environment

The postdoc will join a young group at the Max Planck Institute for Evolutionary Biology. In our group, we focus on exploring the role of stochasticity in evolution. In the context of resistance evolution, we closely collaborate with experimental microbiologists at the University of Kiel. The group is part of the Department of Evolutionary Theory. The postdoc will hence be part of a larger community of researchers working at the intersection of mathematics and biology with many opportunities to take part in journal clubs, reading groups etc.

The Max Planck Institute is a lively institute with three departments (Evolutionary Theory, Microbial Population Biology, Evolutionary Genetics) and several additional research groups. It hosts several workshops per year and continuously welcomes international short-term and long-term visitors, creating a stimulating and positive research environment. We maintain close interactions with Kiel University and belong to the Kiel Evolution Center. The area is a center of evolutionary biology in Germany.

Plön

Plön is a small town, embedded into a beautiful landscape with innumerous lakes and close to the Baltic Sea. The area provides ample opportunity for free time activities such as swimming, canoeing, or biking in a stunning environment. At the same time, the cities of Kiel and Lübeck (â¥200,000 inhabitants) are only half an hour train ride away. Hamburg (Germany's second largest city) can be reached within 1.5h by train.

Application Interested students/Postdocs should send their application (motivation letter, CV, copies of certificates, contact details of two references) by email to uecker@evolbio.mpg.de. Please use the code Postdoc2019 in the subject line.

Application deadline is April 7, 2019. However, the position will remain open until filled by a qualified candidate.

Contact: Dr. Hildegard Uecker Research group Stochastic Evolutionary Dynamics Department of Evolutionary Theory Max Planck Institute for Evolutionary Biology Website: web.evolbio.mpg.de/stochdyn Email: uecker@evolbio.mpg.de Phone: + 49 4522 763-536

Hildegard Uecker <uecker@evolbio.mpg.de>

---

## MichiganStateU EvolutionPlantResilience

*Postdoctoral Position: Evolution of Plant Resilience to Abiotic and Biotic Stresses *

The Lowry lab in the Department of Plant Biology at Michigan State University (MSU) is seeking a Postdoctoral Research Associate who will conduct population genomic and/or physiological research on Pathogen Resistance and/or Cold Tolerance in switchgrass. Switchgrass is an important target species for domestic production of cellulosic biofuels. The principal aim of most switchgrass breeding programs is to develop high-yielding cultivars. However, as feedstock plantings expand, so will pathogen pressure. Unless controlled, fungal pathogens with explosive disease potential will likely drive yield declines and economic losses. Pathogen resistance can be developed through breeding programs that exploit natural genetic variation in disease resistance. Much of the functional genetic variation in switchgrass is distributed clinally with latitude as well as between lowland and upland ecotypes. In general, southern lowland cultivars of switchgrass have many advantages over northern upland cultivars because they are higher yielding, require fewer nitrogen inputs, and are more resistant to pathogens. In addition, southern lowland cultivars are generally more tolerant to heat, drought, and flooding than northern upland cultivars. However, southern lowland cultivars are more susceptible to winter kill than northern upland cultivars.

The proposed research will utilize new and powerful genetic mapping populations (QTL and GWAS) to identify genomic regions responsible for divergence in disease resistance and freezing tolerance between northern upland and southern lowland switchgrass ecotypes. These mapping populations have been planted at an unprecedented geographical scale, spanning twelve common garden field sites distributed from central Mexico to Michigan. We are studying the genetic basis of resistance to pathogens and overwintering ability across this latitudinal gradient. In addition, we are conducting laboratory experiments on fungal pathogen resistance as well as chilling and freezing tolerance. Overall, these studies will provide an improved understanding of the process local adaptation and identify loci that can be utilized in switchgrass breeding programs.

The successful candidate would work on the projects they are most interested in pursuing related to cold tolerance, pathogen resistance, and/or genomic analyses in switchgrass.

*Required Qualifications: *PhD in a field related to Genetics, Genomics, Bioinformatics, Evolutionary Biology, and/or Plant Biology at the time of hire.

*Desired Qualifications: *Expertise in genomic analyses and/or population genetics. General interest and understanding of evolution, genetics, and plant biology. Experience working in the field or laboratory with plants.

*To Apply: *Contact David Lowry (dlowry@msu.edu) with any questions. You must apply for the position at the following link to be considered for the position: http://careers.msu.edu/cw/en-us/job/500965/-research-associatefixed-term – David B. Lowry Assistant Professor Plant Biology Department Michigan State University Plant Biology Laboratories Room 268 517-432-4882 http://davidbryantlowry.wordpress.com/ David Lowry <davidbryantlowry@gmail.com>

## MichiganStateU GlacialLakeEvolutionaryEcol

Postdoctoral opportunity: Evolution of Sensory Systems & Evolutionary Genetics of Diversification

Posting snapshot: Looking for a highly motivated, creative scientist to join the Boughman research group to study the evolution of sensory systems & evolutionary genetics of diversification.

Position summary: Primary duties are to conduct research emphasizing evolutionary diversification and rapid adaptation in novel aquatic environments using stickleback fish. The project investigates adaptation, evolution of behavior and related morphological phenotypes, and evolutionary genetics/genomics relating to diversification. The postdoc will be responsible for carrying out research projects in the laboratory and field, training and supervising other personnel, analyzing data, and publishing results in a timely fashion.

Like much of the Arctic, Iceland is experiencing unprecedented climate and ecological change, much of which is caused by human activity. Against this backdrop of ecological change many species may not adapt quickly enough to survive. Understanding what facilitates and constrains rapid adaptation is crucial in our era of global anthropogenic change. We study adaptation of sight, smell, and touch in extreme and novel sensory environments (glacial lakes). We focus on sensory adaptation because animals gather information on the external environment using sight, smell, taste, sound, and touch to find prey, avoid predators, and mediate social interactions; and because sensory systems are key for survival and reproduction. This project is breaking new ground investigating adaptation of fish to glacial lakes, some of which have formed in less than 100 years as glaciers melt due to climate change. Key objectives are to investigate the pace and predictability of adaptation to changing environments in the Arctic. Our project is motivated to help understand and deal with large-scale environmental issues our society faces.

Minimum qualifications: Required experience includes: generating and analyzing phenotypic and fitness data on morphology, behavior, and other adaptive phenotypes; knowledge of quantitative and/or evolutionary genetics; experience with microscopy, photo, and video analyses; experience doing field work in challenging locales; excellent analytical skills including experience analyzing big datasets and working with databases; demonstrated ability to publish good quality papers; good communication & writing skills.

Desired qualifications: The Boughman lab studies the evolutionary process of diversification, including speciation. We study the interplay between sexual and natural selection in diversification; the creative and destructive role of hybridization; the evolution of behavior, communication, cognition, and sensory systems; and the consequences this trait evolution has for speciation. We use the charismatic threespine stickleback system because of its extraordinary power for addressing evolutionary questions. Plus, the fish are fun to work with and inherently intriguing. Ongoing research is with populations in Iceland, with some work carried out in British Columbia.

The position provides additional opportunities for independent research in related areas for motivated postdoctoral scientists.

Ph.D. required in a related field of biology. Salary and benefits are competitive.

Required application: Apply through the MSU ApplicantPage Position # 562336. To apply, please send cover letter indicating your interest and qualifications for the position, CV, names and contact information for 3 referees, and 2-3 of your papers. Candidates should also contact Dr. Janette Boughman to answer questions about the position at boughman@msu.edu. Review of applications will begin immediately. I am committed to fostering the success of women and minorities, and encourage all interested people to apply. The initial hire is for 1 year with possibility of renewal for up to 3 years depending on satisfactory progress and funding.

Janette Boughman Professor Integrative Biology Ecology, Evolutionary Biology & Behavior Program BEACON Center for the Study of Evolution in Action Michigan State University East Lansing MI 48824 boughman@msu.edu

"Boughman, Janette" <boughman@msu.edu>

## NHM LosAngeles DinosaurMacroevolution

Dinosaur Macroevolution V Postdoctoral Research Scientist, Dinosaur Institute

The *Natural History Museum of Los Angeles County* (NHMLA) *Dinosaur Institute* seeks a* Postdoctoral Research Scientist* to conduct collection-based research in dinosaur evolution broadly defined, to include systematics, paleobiogeography, paleobiology, and comparative/functional morphology.

NHMLAs Dinosaur Institute houses the Museums collection of Mesozoic tetrapods dating from 250V66 million years ago. This collection includes fossils of dinosaurs spanning the Mesozoic Era, as well as fossils of other tetrapods that lived alongside the dinosaurs, such as pterosaurs, marine reptiles, crocodiles, turtles, amphibians, and early mammals. The fossils in this collection have been acquired over nearly a century, and the collection continues to expand through an active domestic and international field program covering all Periods of the Mesozoic. The Dinosaur Institute staff provide mentorship for diverse groups including volunteers, docents, undergraduate/graduate students, and postdoctoral researchers. Additionally, educational outreach and public programming are key parts of the Institutes mission. More information about the Dinosaur Institute and staff can be found here: https://nhm.org/site/research-collections/dinosaur-institute The successful candidate will have a record of outstanding research, excellent communication skills, and a demonstrated ability to engage the public and stakeholders. A Ph.D. and a strong track record of peer-reviewed publications that focus on dinosaur paleobiology and evolutionary morphology are required. The successful candidate will develop novel projects and contribute to ongoing research in the Dinosaur Institute in collaboration with Institute Director Dr. Luis Chiappe, and Associate Curator, Dr. Nathan Smith. Current active areas of research focus on: *Dinosaur origins and early evolution; Early Mesozoic Antarctic tetrapods; dinosaur reproduction and development; and the origin and early evolution of birds*. Skills in morphometrics, phylogenetic comparative methods, 3D data processing/visualization, and programming are desirable. The successful candidate will be expected to participate actively in a broad range of museum activities, including educational programs, student mentoring, public communications and media interactions, and fundraising activities. A vision and capability to contribute to research programs that can be integrated within the NHMLAs ongoing efforts to shape the collections and research in ways that activate both its scientific and public appeal, is paramount.

NHMLA is especially interested in candidates whose background and experience have prepared them to contribute to our commitment to engage and include culturally diverse audiences in museums and in science. This is a full-time position with an initial term of one-year, with funding secured and expectation of extension for a second-year. Salary for this position is set at $52,000 per year, with Museum benefits, which include health/dental/vision coverage, as well as a 403(b) Retirement Plan with matching contributions. Additional details on NHMLA employee benefits are available here: https://nhm.org/site/about-our-museums/-working-at-nhm/employee-benefits Application deadline is May 1st, 2019. The starting date is September 1st, 2019, with some flexibility. Applicants should send: *1)* a cover letter, *2)* 1-2 page vision statement of proposed research, *3)* curriculum vitae, and *4)* the full contact information of at least three professional references *as a single PDF document* to thayden@nhm.org. Include the phrase Institute Postdoc Search in the email subject line.

*The Natural History Museum of Los Angeles County is an Equal Opportunity Employer. Please, No Phone Calls, No Fax. Research & Collections, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007, USA.*

Nathan D. Smith, Ph.D. Associate Curator The Dinosaur Institute Natural History Museum of Los Angeles County 900 Exposition Blvd Los Angeles, CA 90007

Nathan Smith <nsmith@nhm.org>

## QMUL London EvolutionEthiopianCropResiliance

Two year postdoc at QMUL London: environmental genomic analysis to enhance food security in Ethiopia

The southern Ethiopian highland agri-systems are highly robust in times of famine V they include over 78 cultivated species encompassing roots, tubers, cereals, vegetables, fruits and pulses, with a very high proportion of indigenous crops. Domestication appears to have included adaptation to environments considerably outside the environmental range of the wild ancestors.

The project is a survey of genomic diversity in key crops, to understand this adaptation, in order to develop strategies to sustain the agri-systems' resilience in the face of climate change.

This postdoc will analyse the data generated by field researchers and geneticists / bioinformaticians at Kew. It is possible, but not essential to accompany part of the field campaign in Ethiopia. Key skills are an understanding of genomic analysis and an appetite to develop new analytical methods in collaboration with Co-I Richard Nichols (https://www.qmul.ac.uk/sbcs/-staff/richardnichols.html).

Start date: as soon as possible after the formal announcement (any day now). Contact r.a.nichols@qmul.ac.uk for further details, and to be notified of the formal call for applications (which will be at very short notice).

RA Nichols <r.a.nichols@qmul.ac.uk>

---

## Switzerland ComputationalPhylogenetics

PhD /postdoc in Computational Phylogenetics

ZHAW Wädenswil, Switzerland

With the advent of new generation sequencing (NGS) bioinformatic methods must keep pace to provide robust scalable solutions to analyse large sets of molecular sequences. The evolutionary history of molecules is described by a tree structure called phylogeny, which is inferred from genomic sequences. Phylogenies are used for testing biological hypotheses with applications ranging from medicine to ecology. Phylogeny inference usually relies on an inferred alignment of homologous sequences, which ' in turn ' relies on a guide-tree reflecting their ancestral relationships. The goal is to address this apparent circularity so to improve the reliability of phylogenetic analyses. Ideally alignment and tree should be inferred jointly. For example, please see our recent article: Maiolo M, Zhang X, Gil M, Anisimova M. “Progressive multiple sequence alignment with indel evolution” BMC Bioinformatics. 2018 Sep 21;19(1):331. doi: 10.1186/s12859-018-2357-1.

In the context of the project funded by Swiss National Science Foundation, we are looking for a suitable candidate for a PhD or a postdoc position, depending on previous background and qualifications.

The successful candidate will work as part of Applied Computational Genomics Team lead by Maria Anisimova at the Institute of Applied Simulations, Zurich University of Applied Sciences (ZHAW Wädenswil) and will have a second affiliation to the University of Zurich.

The group is also part of Swiss Institute of Bioinformatics, which provides additional training and networking opportunities.

Group official ZHAW website: https://www.zhaw.ch/-de/lsfm/institute-zentren/ias/forschung/computational-genomics/ Profile requirements: Strong background in computational science, algorithms, statistics, stochastic modeling or similar; Working knowledge of C++ ; Some knowledge of phylogenetics and molecular evolution is an advantage

To apply please send an email with the title JATI2 to maria.anisimova@zhaw.ch

Your application should be in one pdf file including your CV, degree certificates and a letter of motivation.

“Anisimova Maria (anis)” <anis@zhaw.ch>

---

## Switzerland Modeling Microbial Interactions

Postdoc in modelling microbial interactions

I am looking to recruit a PostDoc researcher to study microbial interactions, in particular, bacteria dispersal through fungal hyphae networks, and bacteria-fungi interactions under different nutritional conditions, in University of Neuchâtel, Switzerland.

Bacterial dispersal is highly limited in soils because the discontinuity of water paths. Recently, it has been found that bacteria can disperse in the liquid layer on the surface of fungal hyphae. Fungal hyphae networks are like a 3D highway system that connects vast areas in the soil, providing potentially a very efficient way for bacteria to disperse. However, unlike the highways we are familiar with, fungal highways are generated by living organisms, and it is likely that the fungi providing a dispersal path interact with bacteria in complex ways. We aim to find out how bacteria spread through fungal hyphae networks, and whether the interactions between fungi and bacteria promote or impede the dispersal. In addition, we will study how nutrients influence the interactions between fungi and bacteria. Our pilot experiments have already shown that the nature of interactions between fungi and bacteria can change in function of nutrient availability. Understanding the effects of nutrients can help finding ways to manipulate fungi-bacteria interactions and their effect on soil functioning.

The successful applicant should have a PhD in mathematical modelling of biological dynamics by September 2019. Experience with modelling microbial interactions and/or microbiology lab work is an advantage. The candidate needs to be fluent in English.

To apply, please send an email to < li@evolbio.mpg.de >. Please include in your email a statement including 1) a brief overview of your previous academic and research experiences, and explain how your background fits with the project, 2) a CV or resume, and 3) a list of 2 to 3 academic references with their names and email addresses.

The position is funded by the Swiss National Science Foundation for 2 years. The starting time should be September 2019 or earlier. Applications will be reviewed continuously until the position is filled.

Xiang-Yi Li (Dr. rer. nat.) Institute of Biology University of Neuchâtel Rue Emile-Argand 11 CH-2000 Neuchâtel Switzerland

http://web.evolbio.mpg.de/ ˜ li/ Xiang-Yi Li <li@evolbio.mpg.de>

## Switzerland PhD PDF ComputPhylogenetics

PhD /postdoc in Computational Phylogenetics

ZHAW Wädenswil, Switzerland

With the advent of new generation sequencing (NGS) bioinformatic methods must keep pace to provide robust scalable solutions to analyse large sets of molecular sequences. The evolutionary history of molecules is described by a tree structure called phylogeny, which is inferred from genomic sequences. Phylogenies are used for testing biological hypotheses with applications ranging from medicine to ecology. Phylogeny inference usually relies on an inferred alignment of homologous sequences, which ' in turn ' relies on a guide-tree reflecting their ancestral relationships. The goal is to address this apparent circularity so to improve the reliability of phylogenetic analyses. Ideally alignment and tree should be inferred jointly. For example, please see our recent article: Maiolo M, Zhang X, Gil M, Anisimova M. "Progressive multiple sequence alignment with indel evolution" BMC Bioinformatics. 2018 Sep 21;19(1):331. doi: 10.1186/s12859-018-2357-1.

In the context of the project funded by Swiss National Science Foundation, we are looking for a suitable candidate for a PhD or a postdoc position, depending on previous background and qualifications.

The successful candidate will work as part of Applied Computational Genomics Team lead by Maria Anisimova at the Institute of Applied Simulations, Zurich University of Applied Sciences (ZHAW Wädenswil) and will have a second affiliation to the University of Zurich.

The group is also part of Swiss Institute of Bioinformatics, which provides additional training and networking opportunities.

Group official ZHAW website: https://www.zhaw.ch/-de/lsfm/institute-zentren/ias/forschung/computational-genomics/ Profile requirements: Strong background in computational science, algorithms, statistics, stochastic modeling or similar; Working knowledge of C++ ; Some knowledge of phylogenetics and molecular evolution is a big advantage

To apply please send an email with the title JATI2 to maria.anisimova@zhaw.ch

Your application should be in one pdf file including your CV and letter of motivation.

"Anisimova Maria (anis)" <anis@zhaw.ch>

## TexasTechU Phylogenomics

The Johnson Lab at Texas Tech University is hiring a Post-Doctoral Research Associate with expertise in Phylogenomics and Bioinformatics. The post-doc will work as part of a three-university NSF-funded collaboration to investigate the phylogeography and ploidal diversity of the moss Physcomitrium pyriforme using targeted sequence capture. More information about the project can be found at: funariaceae.uconn.edu and further information about the Johnson Lab can be found at: www.mossmatters.com Required Qualifications

* Ph.D. in Biology, Bioinformatics, Computer Science, or Related Field at time of start date * 2-3 years programming experience (C++, Java, Python, R or similar) * Fluency in English (oral and written)

Major/Essential Functions

* Analysis of next-generation sequence data using high-throughput methods. * Adapting existing bioinformatics tools for species delimitation and population genomics of non-model, polyploid organisms. * Designing novel phylogenomics packages to efficiently process target capture data. * Working with the research team to write peer-reviewed manuscripts and conference presentations. * Organizing a bioinformatics workshop to train researchers in target capture methods. * Mentoring of graduate and undergraduate students.

Preferred candidates will have experience in one or more of the following:

* Design and deployment of open source bioinformatics packages. * Data analysis (Jupyter/Pandas/R) and version control (Git). * Design and implementation of SQL and other relational databases. * Web design and interface with online databases. * Phylogenomics analysis software (MAFFT, RAxML, ASTRAL). * Evolution and biology of plants, including bryophytes.

Interested individuals should submit an application, including a statement of interest, CV, and a contact information of 3 professional interests at: https://bit.ly/-2UvN7yT or search for job 16737BR on the Texas Tech staff job page.

Review of applications will begin on March 31, 2019 and will continue until the position is filled. A tentative start date for the position is June 1, 2019, but is flexible. Women, minorities, and persons with disabilities are encouraged to apply.

For questions about the position or how to apply, contact Dr. Matt Johnson, matt[DOT]johnson[AT]ttu[DOT]edu

matt[DOT]johnson[AT]ttu[DOT]edu

## Tours France Metabarcoding

Job Offer Postdoctoral Research Assistant in Metabarcoding V CNRS, Tours, France V

job reference UMR7261-ANNTEL-002

Application only via the CNRS portal: http://bit.ly/-2GzdOPM Missions

At the CNRS, IRBI (Insect Biology Research Institute), the postdoctoral research assistant will be in charge of setting up analytical pipelines for the metabarcoding of insects and associated microbiota. IRBI is a multidisciplinary joint research institute of the CNRS and the University of Tours regrouping entomologists with expertise including evolutionary biology ecology, genomics, behaviour ecology, physiology, virology. We are currently developing large scale metabarcoding approaches in a variety of projects and in this context seeking to recrute a postdoctoral research assistant.

Work context

The postdoctoral research assistant (PDRA) in metabarcoding will work in the IMIP (Functioning and Biodiversity of Microorganism Insect Plant Interactions) team at the IRBI. The PDRA will be recruited as part of the FEDER IMPA project (Insects-Microorganisms-Heritage-Food) which aims at understanding the interactions between insects and symbiotic bacteria. The PDRA will mainly work on data of insects of agronomic (crop pests) and industrial insects (bio-conversion). The PDRA will interact with researchers using similar approaches in the ANR project IMAGHO, Region Centre Val de Loire projects MIMOSA, POLLEN, CAMPOVIGNE and the international project CLIMTREE. The PDRA will have access to a storage server and a computing cluster recently set up at the University of Tours. This recruitment is part of IRBI's scientific policy to develop a regional platform for the analyses of the entomofauna using metabarcoding approaches.

activities

- metabarcoding data analyses of insect and associated microbiota (Main)

- Biodiversity index and food web analyses (Main)
- Writing scripts usable by biologists (Main)
- Data Assembly Illumina, PacBIO or MinIon (Main)
- NGS Data Management (Main)
- Expertise in preparing DNA sequencing librairies (secondary)
- Providing expertise for the use of Oxford Nanopore technology (secondary)

skills

Biodiversity analyses using metabarcoding approaches

Expertise in at least one programming language (Python, Bash) and Linux environment, use of R and statistical tools for biodiversity analyses

Use of the BOLD database

Literature search and interactions with biologists

Further information

12-month fixed-term contract (extendable 1 year)

Send a cover letter explaining your curriculum and your areas of expertise including a description of the candidate's past experience and projects in line with the proposed position, a CV, e-mail address of 2-3 referees, the candidates retained will be interviewed between March 18 and 22, 2019.

Deadline for receipt of applications 10 March 2019 via the CNRS portal: http://bit.ly/2GzdOPM Further enquiries may be addressed to Dr Elisabeth Herniou at elisabeth.herniou@univ-tours.fr

Job Title: Postdoctoral Research Assistant in metabarcoding

Reference: UMR7261-ANNTEL-002

Place of work: TOURS

Release Date: Monday, February 18, 2019

Type of contract: Technical / Administrative contract

BAP: Life Sciences, Earth and Environment

Job Type: Postdoctoral Research Assistant in data analyses

Duration of the contract: 12 months

Planned hiring date: May 1, 2019

Working time: Full time

Remuneration: Monthly gross salary between £á 2,399 and £á 3,072 depending on experience

Required level of education: PhD

Experience: 1 to 4 years

Elisabeth Herniou <elisabeth.herniou@univ-tours.fr>

---

## TU Madrid MicrobialEvolution

POSTDOCTORAL RESEARCHER - EVOLUTIONARY SYNTHETIC BIOLOGY OF MICROBES

We are seeking to appoint a highly-motivated Postdoctoral Researcher to investigate how the conflict between robustness and plasticity drives microbial evolution. The successful candidate will construct a variety of synthetic systems involving different levels of organisation (from operons to multi-strain consortia), which s/he will then subject to high-throughput fitness assays and evolve-and-resequence experiments.

Expertise in molecular microbiology methods is required. Preference will be given to candidates with a strong background in synthetic or molecular biology, but candidates with backgrounds in plant-microbe interactions or experimental evolution are also welcome. Expertise in modular gene assembly (e.g. Gibson, golden gate) or high-throughput techniques (e.g.,TnSeq, multi-site mutagenesis) will be considered a plus. Good English communication skills, both written and oral, are expected.

We anticipate the position having a substantial degree of independence. The successful candidate will contribute to experimental design, data analysis and manuscript preparation. There will be ample opportunity for career development, including the possibility to co-supervise PhD, MSc and undergraduate students, apply for funding, teaching and present her/his work on international conferences.

The post is available as soon as possible for 2 years in the first instance. The successful candidate will join an emerging team led by Dr Couce at the Centre for Plant Biotechnology and Genomics (CBGP), a mixed research centre supported by the Technical University of Madrid (UPM) and the National Institute for Agricultural and Food Research and Technology (INIA). The project is funded through the Severo Ochoa Excellence program, the highest institutional recognition of scientific excellence in Spain, awarded only to the top research institutions across all disciplines in the country.

The everyday working language in the laboratory is English, and most administrative tasks, training and seminars arranged by the institute are conducted in English. Being the third-largest metropolitan area in the

EU, Madrid is a vibrant, multicultural hub with a high quality of life and a thriving cultural scene. The position offers a highly competitive salary with all the benefits of the Spanish National Social Security System, comprising generous sick/maternity/paternity leaves and health, unemployment and retirement insurances.

Interested candidates please send a single PDF file with a cover letter and a CV including publication list to Dr Alejandro Couce (acouce@imperial.ac.uk). Candidates short-listed for interview will be additionally requested two recommendation letters. Please include the word "EvolutionarySynthBio" in the subject line.

Dr. Alejandro Couce

Research Fellow

Department of Life Sciences, Imperial College London, UK.

&

Young Investigator Researcher

Centre for Plant Biotechnology and Genomics

Technical University of Madrid, Spain

"Couce Iglesias, Alejandro" <a.couce-iglesias@imperial.ac.uk>

---

## UArkansas NeuroEvoDevo

Postdoctoral researcher in cnidarian neural development and evolution, University of Arkansas, Fayetteville

A postdoctoral researcher position to study cnidarian neural development and evolution is available immediately in the Nakanishi lab at the Department of Biological Sciences, University of Arkansas. The laboratorys research uses the sea anemone Nematostella vectensis and the moon jellyfish Aurelia sp.1 as experimental models to investigate conserved and divergent mechanisms of neural development at the molecular and cellular levels. Specifically, the successful candidate will lead ongoing projects that involve 1) characterization of the development of neuropeptide-expressing neurons by combining immunohistochemistry, in situ hybridization and confocal microscopy, and 2) functional analyses of deeply conserved neural developmental genes, such as the class IV POU-homeobox gene, by taking a reverse genetics approach via CRISPR-Cas9.

The applicant must have a Ph.D. in biology or related field, a record of research productivity, and extensive experience in molecular biology tools, such as nucleic acid extraction, PCR, cloning, sequencing, immunohistochemistry, in situ hybridization, microinjection, microdissection, transgenesis, CRISPR-Cas9-mediated genome editing, and confocal light and electron microscopy. The postdoctoral scholar will be expected to design and perform experiments independently, analyze results, and write manuscripts. An ideal candidate will have strong interests in evolutionary developmental biology. Experience with cnidarians or other marine invertebrates is desired but not required. This is a full time, 40 hour per week position, and includes benefits. Initial appointment will be for two years, with the possibility to extend to future years contingent upon the availability of funding.

Please send inquiries about the position to Nagayasu Nakanishi at nnakanis@uark.edu.

For a complete position announcement and information regarding how to apply, visit http://jobs.uark.edu/-postings/32089 The University of Arkansas is an equal opportunity, affirmative action institution. The university welcomes applications without regard to age, race/color, gender (including pregnancy), national origin, disability, religion, marital or parental status, protected veteran status, military service, genetic information, sexual orientation or gender identity. Persons must have proof of legal authority to work in the United States on the first day of employment. All applicant information is subject to public disclosure under the Arkansas Freedom of Information Act.

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

---

## UBielefeld ShellfishPopGenomics

2-year postdoc position: population genomics of Antarctic shellfish With Dr Joe Hoffman (Bielefeld University, Germany)

An outstanding opportunity is available for a postdoctoral researcher to work on the population genomics of Antarctic shellfish. The position is available in Joe Hoffman's research group (www.thehoffmanlab.com) in the Department of Animal Behaviour at Bielefeld University. It runs from July 2019 for approx. two years and is funded by the German Research Foundation (DFG).

your tasks There is a vacancy for a postdoctoral position within the research group of Prof. Dr. Joe Hoffman in the Department of Animal Behaviour. The main aim of the project is to use genomic data in a comparative framework that facilitate cold adaptation and speciation in Antarctic invertebrates. The research will be carried out in cooperation with Prof. Dr. Lloyd Peck from the British Antarctic Survey (BAS) in Cambridge. We will search for genomic signatures of cold adaptation and their role in speciation processes in various invertebrate taxa. Numerous sample material for these questions exists already. The project will combine a genomic with a phylogeographicapproach.

research tasks (95 %) RAD-sequencing and analyses of SNP-data sets of spineless organisms in Antarctica phylogenetic analyses in conjunction with the genomic data sets statistical data analyses writing-up of the results for publication in international, peer-reviewed journals help with the running of the research group and the department (5 %)

your profile We expect completed scientific degree (e. g. Master) in biology, genetics or another relevant field PhD in a relevant field (e. g. biology, genetics, evolution) comprehensive experience with lab work, especially genomics experience with statistical analyses, preferably using R experience with genetic techniques interest in behavioral, genetic and evolutionary questions ability to work independently and as part of a team excellent written and oral communications skills in English

Preferable qualifications publications in peer-reviewed journals experience with diverse genetic and genomic techniques experience with next generation sequencing techniques experience with working with multiple, large-scale data sets

Remuneration Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L). As stipulated in §2 (1) sentence 1 of the WissZeitVG(fixed-term employment), the contract will end after three years. The employment is designed to encourage further academic qualification. The position is advertised as a full-time position. In principle, these full-time position may be changed into a part-time position, as long as this does not conflict with official needs. Bielefeld University is particularly committed to equal opportunities and the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

application procedure For full consideration, your application should be received via either post or email (a single PDF) document sent to joseph.hoffman@uni-bielefeld.deby April 3rd, 2019. Please mark your application with the identification code: wiss19036. Please do not use application portfolios and send only photocopies of original documents because all application materials will be destroyed at the end of the selection procedure. Further information on Bielefeld University can be found on our homepage at www.uni-bielefeld.de . PostalAddress Universität Bielefeld Fakultät fur Biologie Herrn apl. Prof. Dr. Joe Hoffman P.O. Box: 10 01 31 33501 Bielefeld Contact Name: apl. Prof. Dr. Joe Hoffman Phone: (+49) 521 106-2711 Email: joseph.hoffman@uni-bielefeld.de

Prof. Joseph Hoffman Department of Animal Behaviour University of Bielefeld Postfach 100131 33501 Bielefeld Germany +49 (0)521 1062711 http://www.thehoffmanlab.com Joe Hoffman <j_i_hoffman@hotmail.com>

---

## UCalgary MedicalPlantEvolution

Postdoctoral Position in Medicinal Plant Genomics

Plant specialized metabolites include some of our most important medicines, but our understanding of how these natural products are produced in plants remains incomplete, which limits our ability to exploit key biosynthetic pathways. This postdoctoral position is part of a large-scale project funded by Alberta Innovates that focuses on the establishment of genomic resources in medicinally important plants, and the deployment of plant functional genomics as a gene discovery platform supporting the reconstitution of specialized metabolic pathways in microorganisms. The specific aims of this position will be to build de novo genome assemblies and/or improve existing resources and conduct comparative genomic analysis to study the evolution of specialized metabolic pathways in Cannabis sativa (THC, CBD and other cannabinoids), Catharanthus roseus (vinblastine), Tabernanthe iboga (ibogaine), and Ephredra sinica (ephedrine). High-quality genomes for these plants will be complemented through the establishment of de novo assemblies of related species, which we will use for comparative genomic analysis. A particular area of interest is an assessment of chromosomal clustering of specialized metabolism biosynthetic genes, and an analysis of how gene clustering might have evolved.

This project will generate substantial new data with many potential avenues for analysis. A combination of high-depth PacBio and Hi-C libraries will be used to build large contigs, which will be scaffolded to near chromosome scale. The ideal postdoctoral candidate will have direct experience using these types of data and the bioinformatic processing tools necessary for building and refining genome assemblies. Experience with phylogenetics, genome annotation, orthology identification, RNAseq analysis, and advanced skills in developing personalized analysis tools in R would also be highly desirable. The project provides investigative flexibility and extra research funding is also available for well-designed side-projects, so we welcome candidates that are highly motivated and imaginative.

This work will be performed in Sam Yeamans laboratory, and in collaboration with Dr. Peter Facchini and Dr. Kenneth Ng, in the Department of Biological Sciences at the University of Calgary. The Yeaman lab will provide a dynamic work environment with lots of potential to collaborate with other postdocs and grad students working on similar (but distinct) projects.

Applicants should send an up-to-date CV, a statement of research interests, and the names and contact information of three references to samuel.yeaman@ucalgary.ca.

Samuel Yeaman <samuel.yeaman@ucalgary.ca>

---

## UCalifornia Irvine EvolutionaryGenomics

Postdoctoral Fellow in the Evolutionary Genomics/Epigenomics Lab

The Lee lab at the University of California, Irvine invites applications for one or more Postdoctoral Fellows. Our group works on the interplay between transposable elements and genome/epigenome evolution. Current projects in the lab include the epigenetic impacts of transposable elements, empirical and theoretical population genomics of transposable elements, and evolutionary epigenomics. Candidates will ideally have interests broadly relevant to these topics, but will also have opportunities to pursue their own research interests in evolutionary genetics/epigenetics.

Our lab is part of the Department of Ecology and Evolutionary Biology (https://ecoevo.bio.uci.edu/) and the Center for Evolutionary Genetics (https://evogen.bio.uci.edu/) at UCI as well as the Southern California Evolutionary Genetics Meeting. More information about our research interests can be found at http://grylee.science/ The successful candidates will have a Ph.D. in the following or related fields: evolutionary genetics, genetics, genomics, epigenetics, cell biology, bioinformatics or computational biology. Experience with high-throughput sequencing and strong quantitative skills are especially desired.

The expected start date is September 2019, but flexible.

To apply, email the following to Grace Lee (grylee@lbl.gov) with the subject line 'Postdoc application: [Your full name].' - curriculum vitae - a one-page research statement describing candidates' past experience and future research interests - contact information for three references

Please contact Grace Lee (grylee@lbl.gov) for any questions. Informal inquiries are welcome.

The University of California, Irvine is an Equal Opportunity/Affirmative Action Employer advancing inclusive excellence. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, protected veteran status, or other protected categories covered by the UC nondiscrimination policy.

Grace Yuh Chwen Lee <grylee@lbl.gov>

---

## UExeter SocialBees

POSTDOCTORAL POSITION: SOCIAL EVOLUTION IN SWEAT BEES

A 2 year full time ERC-funded postdoctoral position is available starting 1 June 2019 in the research group of Professor Jeremy Field, based in the Centre for Ecology & Conservation, University of Exeter, Cornwall Campus, UK (http://biosciences.exeter.ac.uk/staff/index.php?web_id=Jeremy_Field). The successful applicant will work on a project investigating the evolution of queen-worker caste differences and social behaviour in sweat bees (Halictidae: Lasioglossum, Halictus). Additional funding, beyond the initial 2 years, may be available depending on the needs of the project.

The post will involve work that could include carrying out field transplants, behavioural observations and experiments, together with transcriptomic work relating behaviour to gene expression (see Field et al. 2010

Current Biology 20:2028-31 for an example of our behavioural work). The successful applicant will have relevant experience in evolutionary or behavioural ecology and/or transcriptomics with non-model organisms.

The closing date for completed applications is 31 March 2019. Interviews are provisionally expected to take place during 22-30 April 2019.

For full details, including how to apply, enter the job reference number (P66687) as a keyword in the University of Exeter job search engine at: https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/etrec105gf.open?wvid817591jNg Jeremy Field Professor of Evolutionary Biology Centre for Ecology and Conservation University of Exeter Penryn Campus Cornwall TR10 9EZ

J.P.Field@exeter.ac.uk

## UGeorgia EvolutionaryGenomicsAbioticStress

A postdoctoral position studying the evolutionary genomics of abiotic stress resistance in sunflower is available in the Burke lab in the Dept of Plant Biology at the University of Georgia.

This position is part of a collaborative project that seeks to understand the genomic and physiological basis of adaptation to drought, salt, and low nutrient stress in a fascinating study system. Note that postdocs in the lab are also given the opportunity (and encouraged!) to develop independent lines of research.

The ideal candidate will have a strong background in evolutionary genetics with experience handling and analyzing large genomic and/or transcriptomic datasets. The position is available immediately, but the start date can be somewhat flexible for the right candidate.

To apply, please send your CV, a brief statement of research interests, and contact information for three references to: jmburke@uga.edu – informal inquiries are also encouraged.

Applications will be reviewed as they are received, continuing until the position is filled.

Information about the UGA Dept of Plant Biology can be found at: http://www.plantbio.uga.edu/ Information about the Burke lab can be found at: http://www.theburkelab.org/ John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 http://www.theburkelab.org/ University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

jmburke@uga.edu

## UGuelph FishEvolGenetics

A two-year postdoctoral position is available to investigate the foraging ecology and genetics of two cleaner fish species that forage on parasitic lice attached to Atlantic salmon. The position would begin between June-September 2019 and is funded for two years.

The project is led by Professor Elizabeth Boulding (Integrative Biology, U. Guelph) with co-investigator Professor Emeritus Larry Schaeffer (Animal BioSciences, U. Guelph). Our industrial collaborators are led by Dr. K.P. Ang of Kelly Cove Salmon Ltd. (KCS) a division of Cooke Aquaculture Inc. (CAI). They include Dr. J.A.K. Elliott, Dr. M. Herlin, F. Powell from KCS, and Dr. T. M. Jonassen from Akvaplan-Niva, Norway.

The objective of this NSERC Strategic Project is to provide a sustainable and pedigreed source of cleaner fish to reduce lice densities found on Atlantic salmon living in marine sea cages in Eastern Canada. This project will develop highly-repeatable methods of measuring the functional responses of two proven cleaner fishes: the lumpfish (Cyclopterus lumpus) and the cunner (Tautogolabrus adspersus). An outcome of this project will be a breeding program for lice-eating performance by lumpfish and by cunners at two existing hatcheries operated by CAI. It will also deepen our understanding of the reciprocal evolution of early mutualisms between facultative cleaner fishes and their clients.

The Postdoctoral fellow (with experience in fish applied evolution/applied ethology/behavioural ecology) will help the undergraduate and graduate students develop repeatable methods of measuring posing and other cooperative behaviors by client fish that facilitate parasite-removal by cleaner fishes. Their own project will involve assisting with salmon lice challenges of pedigreed Atlantic salmon and measuring client-posing rates near cleaner fish refuges inside the tanks. It will also involve analysis of video-assisted field observations of client behavior near cleaner-fish refuges within marine sea cages. The postdoc will be trained to estimate breeding values for lice-cleaning performance by the cleaner fish and for posing performance by their Atlantic salmon clients. Creating a breeding nucleus containing only cleaner fish and client fish with high breeding values for performance traits would be predicted to increase the reciprocal co-evolution of this mutualism in marine sea cages.

Please apply for the postdoctoral position by sending an email to Dr. Boulding (boulding@uoguelph.ca) with attachments containing: 1) your curriculum vitae/resume, 2) an electronic transcript of all your university grades, 3) a list of referees with their email addresses and telephone numbers, 4) pdf reprints of your scientific publications (if any), and 5) a statement that you are a) qualified and willing to obtain a class G Ontario Drivers License to drive a motor vehicle within Ontario, New Brunswick, Nova Scotia, and Newfoundland and b) that you are willing to travel to these sites for fieldwork for periods up to one month. She will then request references from the referees of qualified applicants.

Elizabeth Grace Boulding (Ph.D.) Professor Academic Adviser: Marine and Freshwater Biology /Biological Science Associate Editor: Journal of Molluscan Studies

University of Guelph, Ontario Canada

Office: room 1464 New Science Complex Department of Integrative Biology 50 Stone Road East University of Guelph Guelph, Ontario N1G 2W1 Canada office phone: (519) 824-4120 x54961 lab phone: (519) 824-4120 x58156 fax: (519) 767-1656 Email: boulding@uoguelph.ca webpage: http://www.uoguelph.ca/-ib/people/faculty/boulding.shtml Elizabeth Boulding <boulding@uoguelph.ca>

## UInnsbruck AquaticEvolutionaryEcol

University Assistant - Postdoc (40 hours per week), University of Innsbruck, Research Department for Limnology, Mondsee, Austria, starting on 2nd June 2019, duration 3 years.

Main tasks:

- Research as PI in the field of Aquatic Evolutionary Ecology, with focus on freshwater microzooplankton (rotifers)
- Teaching in Evolutionary Ecology
- Supervision of technical assistants and graduate students
- Acquisition of extramural funds and research management

Qualifications:

- PhD in aquatic ecology, international research experience beyond the PhD level in Evolutionary Ecology, experimental Population Ecology and microevolution of microzooplankton (rotifers)
- Teaching experience (Zoology, Ecology, Evolutionary Biology) including supervision of graduate students
- Publications in high-ranking journals, acquisition of third-party funds
- Foreign country experience
- Social and integrative abilities in team-leading and team-playing and flexibility are essential.

We are looking forward to receiving your online application by 13th April 2019. Please apply online via the Career portal of the University of Innsbruck https://lfuonline.uibk.ac.at/public/-karriereportal.details?asg_id_in465 Travel costs cannot be reimbursed.

Job profile: The description associated with this job duties and requirements can be found at https://www.uibk.ac.at/universitaet/profile-wiss-personal/post-doc.html Salary: The minimum gross salary for this position amounts to €3.804,00 per month (14 times). Furthermore, the university has numerous attractive offers. http://www.uibk.ac.at/-universitaet/zusatzleistungen/ . “Burggraf, Sonja” <Sonja.Burggraf@uibk.ac.at>

## UJohannesburg AdaptiveGenomics

The Centre for Evolutionary Genomics and Wildlife Conservation at the University of Johannesburg (South Africa) is offering a postdoctoral research position in the field of adaptive evolutionary genomics. The position is available immediately, with a duration of 1 year from the starting date. The bursary is ZAR 220 000 (~US$ 15320 or ~13621 EUR).

Applicants need to demonstrate a good working knowledge in next-generation sequencing applications, including (but not limited to) genome assembly and annotation. Experience with Unix-based software and computing clusters is vital for this position.

The research is funded by the National Research Foundation: South African National Antarctic Programme, and focuses primarily on adaptations to extreme environments in sub-Antarctic island fauna. However, the successful applicant may choose to become involved in other projects in the Centre to boost their publication outputs, which range from elasmobranch population genomics to eDNA metabarcoding of marine and river fauna. The University of Johannesburg allows postdocs to co-supervise postgraduate students.

Interested candidates should send a 1-page cover letter describing their relevant expertise and interests, a CV, and contact information for three references to both Prof Bettine van Vuuren (bettinevv@uj.ac.za) and Prof Peter Teske (pteske101@gmail.com). Review of applications will begin immediately and continue until the position is filled.

*Prof. Peter Teske* *Department of Zoology* *University of Johannesburg, Kingsway CampusAuckland Park 2006South AfricaTel +27 (0)11 559 3373* *https://sites.google.com/view/peterteske/ < https://sites.google.com/view/peterteske/ >*

For courier shipments: D3 LAB 339 (D LAB building on the far right (seen from D RING), two floors up, turn right through the glass door, last entrance on the left) Department of Zoology University of Johannesburg, Kingsway Campus (APK) Corner Kingsway and University Rd. Auckland Park 2092 Email: pteske101@gmail.com Tel.: 011 559 3373

Peter Teske <pteske101@gmail.com>

---

## UKansas DrosophilaComplexTraits

A postdoc position is available in my lab at KU to work on any of a number of evolutionary genomics projects that use flies to understand and dissect complex trait variation, especially variation in toxicological phenotypes. Projects emphasize the Drosophila Synthetic Population Resource (DSPR) that my lab is developing. The formal announcement, and links to the institutional employment website are provided below. Feel free to email me with any questions about the position. I'll also be at the fly meeting in Dallas at the end of March if anyone would like to chat in person. Stuart (sjmac@ku.edu)

The Macdonald lab at the University of Kansas seeks a postdoctoral researcher with interests in the genetics of complex trait variation. We use a range of genetic (QTL mapping, GWAS), genomic (RNAseq, ATACseq), and molecular (CRISPR/Cas9 editing) technologies to dissect the genetic basis of complex phenotypic variation using the Drosophila model. We work on numerous traits, lead the development of the Drosophila Synthetic Population Resource (DSPR, FlyRILs.org, https://bit.ly/2NwZLuF), and recently received funding to investigate the response to toxic metals (https://bit.ly/2H6Lcge). The breadth and depth of the data we are collecting, and the range of resources we have available, will enable the successful candidate to position themselves as an independent investigator. The job has an anticipated start date of June 1, 2019 (although this is negotiable).

Required qualifications include a PhD in evolution/genetics/bioinformatics (or a related field), and a first-author publication that shows your ability to initiate and execute a research project. Prior experience with Drosophila, with "big data" analysis, and with genome editing would all be useful, but are not required.

For a complete announcement and to apply online, go to employment.ku.edu/staff/13819BR

Please direct any questions about the position to Stuart Macdonald (sjmac@ku.edu).

A complete online application includes the following materials: A CV, a cover letter outlining relevant experience, research interests and accomplishments, and contact information (phone/email/address) for three referees. Initial review of applications begins 1 April 2019 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university's programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY 9for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

### Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045 ### office: 785-864-5362 email: sjmac@ku.edu ### Google Scholar: https://scholar.google.com/citations?user=-

pTXRo_gAAAAJ&hl=en ORCiD: http://orcid.org/-0000-0002-9421-002X ###

"Macdonald, Stuart" <sjmac@ku.edu>

---

## UMontana EvolutionInvasiveSpecies

Job opening:

POSTDOC MODELING ECO-EVOLUTIONARY DRIVERS of INVASIVE SPECIES (March 2019)

Project: Modeling Spread of Aquatic Invasive Species Combining Genetics & Environmental Data

Principal Investigators: Gordon Luikart, John Kimball, Brian Hand, Flathead Lake Biological Station, Division of Biological Sciences, The Univ. of Montana. gordon.luikart@umontana.edu, brian.hand@umontana.edu (406.872.4500).

Start Date & Duration: April/May 2019; 1 year with a possible 1.5-year extension.

Project Description/Summary: Aquatic Invasive Species (AIS) including rainbow trout, brook trout, bass, and zebra mussels are spreading across North America causing massive economic and ecological problems. Fortunately, large regional databases documenting spread of AIS combined with novel eDNA detections can facilitate early detection and prevention of spread. As part of a NASA-funded project, the successful applicant will help develop and apply predictive models (e.g. occupancy models, GLMs) that combine genetic, environmental, and time-series observational data on AIS spread to help forecast future hotspots of invasion. The models will help predict pathways of spread of AIS and to thereby direct managers to monitor and manage spread. The applicant will help plan and develop online software tools for managers and policy makers to visualize spread of AIS within and among water ways across North America. There will be opportunities for field work and meetings in Glacier National Park and waterways in the northern Rocky Mountains.

The successful applicant will work with scientists and managers from state and federal agencies (USGS, NPS, NISC, Montana DNRC and FWP) to coordinate combining of AIS observational and eDNA data into databases. The applicant will work with NASA and NISC (National Invasive Species Council) to facilitate reporting of data to address the United Nations on Sustainable Development Goal (SDG) number Goal 15 that seeks to "halt and reverse land degradation, and halt biodiversity loss". The applicant will also help run AIS workshops that will help build their communication network in their career.

Skills required: The applicant should have experience modeling the presence (occurrence) or movement of individuals or genes (gene flow) using occupancy or individual based simulation models. Programming ability in Python, R or similar language is required. Ideally the applicant would have experience conducting statistical (GLM) modeling to predict environmental drivers (correlates) of AIS spread. The applicant should have demonstrated ability to write and publish papers, use and manage large databases, and communicate with others from diverse groups (e.g. agencies, managers, researchers). Experience applying satellite remote sensing and other geospatial data for landscape habitat analysis & modeling directed toward aquatic ecosystems would be extremely helpful. Understanding eDNA metagenomics analyses would help.

Applications: Email us a brief letter describing your motivation and background, your CV, and contact information for three references. Review of applications will start April 1st remain open until a suitable candidate is hired.

Salary: Depends on experience and CV'.

Key references: see our web pages & contact us.

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

---

## UNewBrunswick EvolutionFloralScent

Post doc position in the Parachnowitsch Lab at University of New Brunswick

A postdoctoral position studying the evolutionary ecology of floral scent in the Penstemons is available in the Parachnowitsch lab in the Biology Department at the University of New Brunswick, Fredericton, NB, Canada.

This position is part of a larger project understanding the macro and micro-evolution of floral scent. The post doc can choose to focus on evolution of scent across the genus, geographic variation and its causes in P. digitalis or a QTL study on scent. I also encourage independent research questions.

The ideal candidate will have a strong background in evolutionary ecology and experience analysing data. Previous experience with studying floral traits, scent analysis and/or pollination is an asset but not required if the candidate is willing to learn and has strong research skills.

Position is available immediately (flexible start but earlier preferred).

To apply, please send your CV, a brief statement of research interests, and contact information for three references via e-mail to: aparachn@unb.ca ' informal inquiries encouraged.

I will review applications on an ongoing basis until the position is filled.

Dr. Amy L. Parachnowitsch

Assistant Professor Biology Department University of New Brunswick Fredericton 10 Bailey Drive Fredericton, New Brunswick E3B 5A3 Canada

Visiting Researcher Plant Ecology and Evolution Evolutionary Biology Centre EBC Norbyvägen 18 D 752 36 Uppsala, Sweden

websites: http://unb.ca/fredericton/science/depts/biology/people/parachnowitsch.html http://www.ieg.uu.se/plant/parachnowitsch-group/twitter: @EvoEcoAmy

blog (contributing member): http://smallpondscience.com/ Amy Parachnowitsch <aparachn@unb.ca>

## UNorthTexas PopulationGenomics

Use your knowledge and skills to improve the discipline of forensic genetics. The Budowle lab (https://www.unthsc.edu/graduate-school-of-biomedical-sciences/molecular-and-medical-genetics/laboratory-faculty-and-staff/) at the University of North Texas Health Science Center is a seeking a postdoctoral research associate in the fields of bioinformatics and population genomics.

Candidates must be proficient in at least one coding language, be able to work both independently and in a group setting, and be motivated to apply their talents to the field of forensic genetics. The ideal candidate would have a solid grounding in computation, population genetics and statistics. Well-qualified candidates would have proficiencies in 2 of the 3 areas. The current projects in the lab pertain to mixture interpretation and the analysis of massively parallel sequencing data, especially as it applies to short tandem repeats,metagenomics, proteomics and mitochondrial markers. The position is available for at least 1 year with the possibility of renewal after that.

Interested candidates should send their CVs and a brief statement of their research interests and goals to August at August.Woerner@unthsc.edu for more information.

"Woerner, August" <August.Woerner@unthsc.edu>

## UOtago ConservationGenomics

We are seeking a Postdoctoral Fellow to work on a Marsden-funded research project titled Resolving the genomic architecture of hatching failure to improve conservation of endangered birds' and will involve conducting genomic research on two critically endangered birds, the Alala (Hawaii) and Kakapo (New Zealand). The project will combine genomic and bioinformatic analyses with the conservation management of these threatened species, with the successful applicant spending time in both New Zealand (University of Otago) and Hawaii (University of Hawaii at Hilo, and Keauhou Bird Conservation Center, both of which are on the Island of Hawaii).

Your Skills and Experience: - A PhD and research experience in conservation genetics, evolutionary genetics or genomics of diploid organisms is essential. - Experience in population genomic and bioinformatic analyses is essential. - Experience with whole genome analyses is desirable. - Experience with different types of phenotype-genotype analyses is an advantage (e.g. genome-wide association studies (GWAS), analysis of runs of homozygosity (ROH)). - Experience with analysis of pedigrees is an advantage. - Good knowledge of conservation biology and conservation genetics, including inbreeding and inbreeding depression, is an advantage. - Knowledge of avian biology, ecology, and animal behaviour is an advantage.

Further details and how to apply can be found here: https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job00793 This role is a full-time, fixed term position for three years and is available from 1 July 2019.

Specific enquiries may be directed to the Principal Investigators of the Marsden funded project: Associate Professor Bruce Robertson, Department of Zoology, University of Otago (bruce.robertson@otago.ac.nz; Tel: +64 21 279 4110) or Dr Jolene Sutton, University of Hawaii at Hilo (jtsutton@hawaii.edu; Tel: +1 808 932 7183)

Jolene Sutton <jtsutton@hawaii.edu>

---

## UOxford EvolutionSenescence

Subject: Postdoc @ Oxford on caloric restriction in stochastic environments

I am looking for a postdoc to work on the evolution of senescence in stochastic environments in the context of caloric restriction. The post involves lab work with flatworms and demographic modelling in R. I'd appreciate if you could please direct competent candidates towards the link below. Deadline: 5th of April, noon UK time. More information about my group can be found here: https://www.zoo.ox.ac.uk/salgo-lab and https://sites.google.com/site/robresearchsite/ Job call: https://www.zoo.ox.ac.uk/job-vacancies Further details:

Postdoctoral Research Associate Department of Zoology, 11a Mansfield Road, Oxford Grade 7: Salary in the range pounds 32,236 - pounds 35,211 p.a. The SalGo Team and Aboobaker Lab are offering a Postdoctoral Researcher position in the Department of Zoology for a fixed-term of 1 year (with the possibility of extension). This position is part of the John Fell Fund project "How will immortal species respond to climate change" to investigate the impact of resource availability on the life history evolution of planarians.

We are seeking an evolutionary biologist, demographer and/or ecologist to empirically elucidate the responses of three planarian species with different modes of reproduction and varying regenerative potential to changes in timing, intensity and frequency of resource availability. This post is part of a dynamic and interdisciplinary research group: the SalGo Team, led by A/Prof Rob Salguero-Gomez. Some of the questions we study are related to the evolution of senescence, constraints of life history traits, and population responses to climate change.

The work will involve (i) setting up an experiment to test how the frequency, timing, and intensity to resource availability shapes various life history traits on three different species of flatworms (Schmidtea mediterranea, Dugesia tahitiensis and Polycellis tenuis), (ii) collection of data under laboratory conditions of survival, development and reproduction of these species, (iii) construction and analysis of integral projection models parameterised with the laboratory data, and (iv) publication and dissemination of results in high impact factor journals, conferences and the general public.

This post is ideally suited for applicants with a PhD/DPhil (or be about to obtain) with a strong background in life history evolution, demography, population ecology, and with experience in laboratory settings.

The closing date for applications is 12.00 noon on 5 April 2019.

Contact Person : Personnel Officer Vacancy ID : 139656 Contact Phone : 01865 271278 Closing Date : 05-Apr-2019

Do not hesitate to contact me if you have questions about this position. Kind regards, Rob S-G

"Aliud iter ad prosperitatem nos est: id est omnibus rebus vincere"

Dr. Rob Salguero-Gómez

Associate Professor, Department of Zoology, University of Oxford Tutorial Fellow, Pembroke College NERC Independent Research Fellow Honorary Fellow, Centre of Excellence in Environmental Decisions, University of Queensland, Australia Guest Visitor, Max Planck Institute for Demographic Research, Germany https://www.zoo.ox.ac.uk/people/-dr-rob-salguero-gomez www.compadre-db.org Rob Salguero-Gomez <r.salguero@sheffield.ac.uk>

---

## UPittsburgh EvolutionaryBiology

DEADLINE EXTENDED!! The Department of Biological Sciences at the University of Pittsburgh invites applications for a 2-year Postdoctoral Fellowship in Ecology and Evolution, broadly defined (e.g., disease ecology, microbiome, behavioral ecology, species interactions, phylogenomics, population genetics, community and eco-evo dynamics). The goal of the EE Postdoctoral Fellowship is to broaden expertise and to stimulate synergistic interactions between faculty interested in the area of Ecology and Evolution. The successful candidate will be expected to conduct original independent research that bridges the interests of two or more faculty members in the Ecology and Evolution sections of Biological Sciences and to lead a graduate seminar in their area of expertise each year.

Qualified candidates are required to submit a single, coherent 2-year research proposal to be completed under the guidance of two or more members of the ecology and evolution faculty in the Department of Biological Sciences of the Dietrich School of Arts and Sciences (https://www.biology.pitt.edu/research/ecology). The position does not include research funds so the extent of contributions from the faculty sponsors should be addressed in the proposal. We strongly encourage candidates to contact appropriate faculty sponsors before applying. Preference will be given to candidates with novel ideas, demonstrated research ability, and strong communication skills. Along with the research proposal, applications must include a CV, a short description of research accomplishments and a description of how your research, teaching or service demonstrates a commitment to diversity and inclusion. The applicant must arrange for two recommendation letters from non-UPitt faculty, and letters from the UPitt faculty sponsors to be emailed to the address below. The expected starting salary will be $48,000 per year PLUS benefits. NEW Application deadline is April 14, with position start date June-August 2019 (specific date negotiable).

Application materials should be emailed to: Dr. Tia-Lynn Ashman at: tia1@pitt.edu. The subject line should read "EE Post-doctoral application".

Dr. Tia-Lynn Ashman Distinguished Professor Department of Biological Sciences University of Pittsburgh Pittsburgh, Pa 15260

Phone: 412-624-0984

tia1@pitt.edu

---

## UQueensland CoralReefEvolutionaryGenomics

Postdoctoral Research Fellow, University of Queensland, Australia

A postdoctoral position is available immediately at the Institute for Molecular Bioscience (https://imb.uq.edu.au/) of the University of Queensland (https://www.uq.edu.au/) in Brisbane, Australia.

The role

The person appointed to this position will be responsible for assembly, analysis and interpretation of genome-scale sequence data from coral reef symbionts and related dinoflagellate species within a recently funded project. The successful applicant will collaborate as appropriate in the identification of potential genomic signatures of symbiosis and adaptive selection. There are opportunities to be part of research teams, to address individually-developed and collaboratively-generated research questions, to travel for collaborative research visits or attending conferences, and to supervise honours, masters and doctoral students.

The project

This position is created within a Discovery Projects Grant funded by the Australian Research Council to understand how genomes of differently acquired dinoflagellate algae (Symbiodiniaceae) have evolved to support symbiosis with corals. Coral reefs are sustained by symbiosis between Symbiodiniaceae and the coral host, and breakdown of this symbiosis under environmental stress results in coral bleaching and eventual death. Through genome sequencing of symbiodiniacean isolates from Australias Great Barrier Reef and their free-living relatives using cutting-edge genomic technologies, the Project aims to identify genes that have been gained, lost or shared, or are under adaptive selection, along the trajectory from free-living forms to symbionts. This project is in collaboration with Professor Debashish Bhattacharya at Rutgers University, USA.

Salary and Benefits

This is a full-time, fixed term appointment for 2 years at Academic level A, with the possibility of renewal. The remuneration package will be in the range $67,542 - $90,982) p.a., plus employer superannuation contributions of up to 17% (total package will be in the range $79,024 - $106,448 p.a.).

Employees can take advantage of UQs Sport Facilities, salary sacrificing options, on-campus childcare, discounted private health insurance, cheap parking, and many other benefits.

This position is located at our picturesque St Lucia campus, renowned as one of Australias most attractive university campuses, and located just 7km from Brisbanes city centre. Bounded by the Brisbane River on three sides, and with outstanding public transport connections, our 114-hectare site provides a perfect work environment V you can enjoy the best of both worlds: a vibrant campus with the tradition of an established university.

Here at UQ we value diversity and inclusion, and we actively encourage applications from those who bring diversity to the University. Our Diversity and Inclusion webpage contains further information and points of contact if you require additional support. Accessibility requirements and/or adjustments can be directed to recruitment@uq.edu.au.

Application of this position closes Friday 3 May 2019 at 23:55 (Eastern Australian Standard Time).

For more information about this position and to apply, please visit: http://jobs.uq.edu.au/caw/en/job/507311/postdoctoral-research-fellow Please contact Dr Cheong Xin (CX) Chan directly at c.chan1@uq.edu.au for further details.

– *Dr Cheong Xin (CX) Chan* Senior Research Officer | Affiliate Lecturer

Institute for Molecular Bioscience | School of Chemistry and Molecular Biosciences The University of Queensland Brisbane QLD 4072 Australia

*T* +61 7 3346 2617 *M* +61 416 310 786 *E* c.chan1@uq.edu.au *W* imb.uq.edu.au *TW* @dorkyM *W* cxchan.com

CRICOS code: 00025B

Cheong Xin Chan <c.chan1@uq.edu.au>

## URochester EvolutionaryGenetics

Postdoctoral fellow in evolutionary genomics Department of Biology, University of Rochester

The Fay lab in the Biology Department at the University of Rochester is seeking candidates for a postdoctoral fellow position. The lab works broadly on the genetic basis of evolutionary change, utilizing both high-throughput experimental approaches combined with statistical and computational models. Our main experimental system is yeast, focusing on the Saccharomyces species with occasional forays into Candida and other species that commonly show up in our field collections. However, we also have active collaborations working on domestication in barley, preterm birth in humans, and testing theories of diversity using experimental evolution. These interactions both stimulate project cross-fertilization and create opportunities to develop novel approaches to long-standing problems of interest to the lab.

Candidates will have the opportunity to expand on current projects or explore new areas through the development of a creative and independent project. Current projects include the evolution of gene expression dynamics, the genetic basis of interspecific differences in thermotolerance, domestication and diversification of S. cerevisiae, including wine, beer and other industrial strains, and we are initiating plans to generate barcoded mutant collections in both S. cerevisiae and S. uvarum via CRISPR. We have extensive resources in population genomics through our collection of over 4,000 wild yeast strains, probabilistic models of cis-regulatory sequences, as well as our recent acquisition of high-throughput robotics paired with both natural and constructed collections of strain, plasmid and synthetic reporter libraries.

Candidates should have a clear vision of their research interests along with expectations for training and mentorship. While there are no strict requirements for the position, strong quantitative skills, programming experience, and a population or evolutionary genetics background are desirable.

The Fay lab is located in the Biology Department, which has a strong research group in evolutionary genetics and genomics that has recently grown, providing a stimulating and interactive environment. The Department is located in Hutchinson Hall, adjacent to the Goergen Institute for Data Science, Computer Science and Biomedical Engineering Departments. Genomics and proteomics cores are available across the street at the Medical center and the Center for Integrated Research and Computing provide state of the art facilities for both parallel and large memory computing jobs.

Applicants for the position should send a curriculum vitae, a statement of research interests and contact information for three references via email. Applications will be reviewed starting in March and will continue until the position is filled.

Justin Fay Associate Professor Biology Department University of Rochester justin.fay@rochester.edu http://labsites.rochester.edu/faylab/ Justin Fay <fayjustin@gmail.com>

## USouthFlorida-Tampa HumanPopulationGenetics

Postdoctoral Fellow - Inferring demographic history of human populations. A postdoctoral fellow position in computational population genomics is available at Liu Lab (www.liulab.science) at the University of South Florida, Tampa, USA, from October 2018. The postdoctoral fellow will engage in method development and application related to inferring population demographic history using large-scale DNA sequence data (see references below). A graduate level training in population genetics or molecular evolution is required. Previous experience in methodology development and/or Java programming experience is preferred. Contact: Xiaoming Liu (xiaomingliu@helath.usf.edu). Reference: Liu X and Fu YX. (2015) Exploring population size changes using SNP frequency spectra. Nature Genetics. 47(5):555-559.

xiaoming.liu@uth.tmc.edu

---

## UTexas Austin BumblebeeCognition

A postdoc position is available in the research group of Dr Felicity Muth at the University of Texas at Austin, to work on questions in the cognitive ecology of pollination using bumblebees. The postdoc will have the opportunity to develop their own projects within the general lab areas of interest, which include exploring learning, memory and decision-making dynamics in relation to ecologically realistic foraging scenarios. Research will be primarily experimental work based in the lab and in greenhouse facilities available at the Brackenridge Field Laboratory, Austin but there is also the possibility for field-based projects.

Requirements: The candidate must have previous experience working and publishing in topics in animal cognition. While previous experience working with bees is preferred, it is not essential.

Duration and start date: The position would be full-time, benefits-eligible, and would start between September 2019 and December 2019. The position is initially for one year, but may be renewed on an annual basis for up to two years.

Salary: $47,476

Application: Please send a statement of interest, full CV including publications, and the contact information for two references to fmuth@unr.edu. Evaluation of candidates will begin at the end of March and will continue until the position is filled.

For more info see www.beecognition.com Background Checks: A criminal history background check will be required for finalist(s) under consideration.

Equal Opportunity Employer: The University of Texas at Austin, as an equal opportunity/affirmative action employer, complies with all applicable federal and state laws regarding nondiscrimination and affirmative action.

Felicity Muth, PhD Department of Biology, University of Nevada, Reno. +15206123801 < http://felicitymuth.weebly.com/ >

< http://blogs.scientificamerican.com/not-bad-science/ > Currently recruiting: https://www.beecognition.com/join-the-lab/ Felicity J Muth <fmuth@unr.edu>

---

## UToyko EvolutionaryAnthropology

Title: Postdoctoral Scholar in Evolutionary Anthropology

Laboratory: Evolutionary Anthropology ( http://www.jinrui.ib.k.u-tokyo.ac.jp/kawamura-home.html) Department: Integrated Biosciences, Graduate School of Frontier Sciences Institution: The University of Tokyo Job type: Postdoc Apply by: 31 May 2019 (could be extended) Application email: kawamura@edu.k.u-tokyo.ac.jp; use subject line 'Postdoc application'

Applications are invited for maximally two-year-and-nine-month (July 1st, 2019 ~ March 31st, 2022) postdoctoral scholar position at University of Tokyo (Kashiwa Campus), Japan. Funding is provided by the Grant-in-Aid for Scientific Research (A) (18H04005) from Japan Society for the Promotion of Science (JSPS).

This research focuses on coevolution of chemical sense and color vision in primates. Primates had long been considered as vision-oriented mammals. But recent researches have challenged this view. Our research team has played a key role in the movement. Importance of trichromatic color vision could be dependent and conditional on dietary demands and ecological settings in living environments. Various senses are likely to have evolved inter-dependently. Chemical senses, such as olfaction and tastes, in primates are now gathering researchers' attention for their importance which has long been overlooked. However, these genes belong to huge multi-gene families and their repertoire has remained less explored. Studies of them have largely relied on whole-genome sequencing databases publicly available, thus suffering from varying degrees of perfection and limited number of studied species.

We aim to cover diverse primate taxa from strepsirrhines, tarsiers, New World monkeys, Old World monkeys, apes and humans for the study of inter-species divergence and intra-species diversity of olfactory receptor (OR), taste receptor (TASR) and visual receptor (opsin) genes by applying target capture and massive-parallel sequencing ('next-generation sequencing': NGS) technologies. Analyses will integrate bio-informatics, evolutionary genetics (molecular evolution and population genetics) and functional assay using cultured-cell heterologous expression system. We also integrate the field-study information which has been accumulated by our long-term collaborators, Dr. Amanda D. Melin, University of Calgary, and Dr. Colin A. Chapman, McGill University.

Minimum requirements of applicants, by the time of appointment, are a Ph.D. degree in biological anthropology, genomics, evolutionary genetics or a related field. Strong interest in evolution is desired. Applicants must have relevant experience in analysis of genomic datasets and demonstrate a record of publication and presentation. Ideal applicants will also have experience in some of the following operations: DNA extraction, molecular cloning, PCR, Sanger sequencing, target capture and NGS.

The start date for the position is negotiable but must begin in 2019. The postdoctoral scholar will receive \250,000-300,000 JPY per month, as well as health benefits. Interested applicants should email application materials (letter of application summarizing interests, skills and goals, CV, and contact information for 2 referees) to Shoji Kawamura ( kawamura@edu.k.u-tokyo.ac.jp).

The University of Tokyo is an Equal Opportunity Employer. There are no citizenship requirements. All qualified applicants will receive consideration for employment without regard to race, color, religion, age, sex, sexual orientation, gender identity or expression, national origin, genetic information, or disability or any other legally protected basis.

Shoji Kawamura <kawamura@edu.k.u-tokyo.ac.jp>

## UTromso Norway AncientDNA

Postdoctoral Fellow in ancient sedimentary DNA About the Position

The Arctic University Museum of Norway has a 2.5 year fixed term contract vacant at the post-doctoral level. The applicant will join the international team of researchers in the ERA-NET BiodivERsA project “Future ArcTic Ecosystems (FATE): drivers of diversity and future scenarios from ethnoecology, contemporary ecology and ancient DNA” < https://www.biodiversa.org/1400 >. The project will conduct a circumarctic investigation of long-term biodiversity change based on ancient DNA from lake sediment cores, with a specific focus on the role of herbivory and climate in shaping vegetation. We will use this data, in conjunction with data from contemporary ecology and indigenous and local knowledge, to develop scenarios of future biodiversity and ecosystem services.

The position of Postdoctoral Fellow is a fixed-term position for a period of 2.5 years starting on May 1st 2019. The main objective of the appointment as a postdoctoral research fellow is to qualify for work in senior academic position. No one may be appointed to more than one fixed term-period as a Postdoctoral Fellow at the same institution.

The position’s field of research The postdoc will generate and analyse paleogenetic data on vegetation, mammals and fungi/lichens using lake sediment cores from Norway and Svalbard. The project will involve fieldwork in both areas. He/she will also contribute to identify long-term, broad-scale drivers and develop scenarios of ecosystem change at pan-Arctic scale through literature review and data collection. The work will be carried out in close collaboration with the ancient DNA labs at the Alfred-Wegener-Institute (AWI) Research Unit Potsdam, the University of California Santa Cruz and McMaster University. This position will have a special responsibility for vascular plant aDNA protocol development. The project builds strongly on interdisciplinary exchange leading to joint analyses and publications with the other international members of the BiodivERsA project. https://www.jobbnorge.no/en/available-jobs/job/-166189/postdoctoral-fellow-in-ancient-sedimentary-dna
Inger Greve Alsos <inger.g.alsos@uit.no>

## UWisconsin Madison Evolution

The Payseur lab at the University of Wisconsin-Madison invites applications for a new postdoctoral position.

We use genetics and genomics to understand mechanisms of evolution. Members of our group gain valuable experience computationally analyzing genomic data, collecting new data in the lab, and interpreting findings within a powerful evolutionary framework. The labs work covers three areas: speciation, extreme phenotypes in island populations, and the evolution of recombination. The postdoctoral researcher will have substantial flexibility in setting a research focus within one of these areas.

The Payseur lab offers a stimulating, interactive, and supportive climate with rich opportunities for professional development. In the 14 years since the group was founded, alumni have earned positions as tenure-track faculty, industry researchers, and graduate program coordinators. Bret Payseur meets regularly with each member of the group to discuss individualized training goals and all aspects of the scientific process. The lab convenes as a group to share research updates and to critically evaluate scientific literature. We strive for an inclusive environment in which all experiences are valued and ways to expand diversity in academics are freely discussed.

The Payseur lab is located in the Laboratory of Genetics at the University of Wisconsin-Madison V a department with a storied history in genetics and evolutionary biology. The department and the university are home to a highly interactive collection of faculty with broad and deep expertise across the life sciences. The lab enjoys local collaborations with leaders in genomics, statistical genetics, computational biology, molecular genetics, and evolutionary biology. The University of Wisconsin-Madison is consistently ranked as a top public university and is renowned for its strength in biological research. Madison is rated as one of the best places to live (https://livability.com/best-places/top-100-best-places-to-live/2019), offering excellent restaurants, a thriving arts community, and an impressive assemblage of parks, bike paths, and lakes only a few hours driving distance from Chicago and Milwaukee.

The successful candidate will demonstrate a strong research record in the life sciences. Evidence of productivity in the form of first-authored publications is required. Experience analyzing genomic data is desirable. Applicants should be highly motivated and interested in working as part of a research team. A Ph.D. in biology or a related field is required. The initial appointment will be for two years. The appointment may be renewed, contingent upon progress.

To apply, please email to Bret Payseur (payseur@wisc.edu) a SINGLE PDF consisting of three pieces: (1) a brief (less than one page) research statement that clearly explains the motivation for applying, (2) an updated CV, and (3) contact information for two references. Review of applications will begin immediately. Interested individuals are encouraged to contact Bret Payseur with any questions. Informal inquiries are welcome.

Bret Payseur <bret.payseur@wisc.edu>

---

## UWisconsin Madison EvolutionaryGenomics

The research group of John Pool at the University of Wisconsin - Madison invites applications for a postdoctoral research position. We have multiple opportunities for projects to work on, with an overarching theme of addressing big questions in population/evolutionary genetics. The candidate's own research interests can play an important role in developing a research program of shared interest.

Potential research areas could include:

* Measuring Genetic Diversity to Predict Adaptive Potential Both within-population genetic variation and between-population adaptive differentiation may provide raw material for future evolution, but it's unclear which is more important. It's also unclear how we should summarize within- and between-population diversity if our goal is to predict adaptive potential. Experimental and methodological progress on these issues will inform basic science and conservation.

* Fundamental Population Genetics We are interested in leveraging data (such the >1000 genomes from our Drosophila Genome Nexus), along with simulation and statistical/computational methods to ask basic population genetic questions. Examples could include new angles on the classic but unresolved controversy over the relative roles of selective sweeps and background selection, and the relative roles of hard and soft sweeps on autosomes versus the X chromosome.

* The Genetic Architecture of Reproductive Isolation Partial prezygotic and postzygotic isolation exists between African and European populations of D. melanogaster, which diverged only ~10 kya but now occupy very different environments and show both experimental and genomic evidence for multiple incompatibilities. We are developing this untapped system as a prime model for the evolution of reproductive isolation.

* The Genetic Architecture of Adaptive Evolution When traits evolve in nature, we'd like to understand how many genes are involved, whether selection acts on standing variation or new mutations, whether it ultimately fixes the causative variants, and how predictable these changes are across populations evolving in parallel. Our focus on local adaptation among Drosophila melanogaster populations from contrasting natural en-

vironments provides a powerful and efficient system for addressing these questions.

Our research group was founded 7 years ago and currently includes 1 postdoc and 5 PhD students. I have advised 4 former postdocs, and the publication records of Amir Yassin and Justin Lack show what a productive environment our lab can be. I also welcome postdocs taking important components of our research with them when they found their own labs. Further lab info: http://www.johnpool.net UW-Madison offers a superb scientific environment with a supportive, collaborative, and egalitarian culture. Many labs focus on population genetics, evolutionary genomics, and Drosophila research: http://www.evolution.wisc.edu/view_faculty https://genetics.wisc.edu/drosophila-and-other-insects/ Madison offers an exceptional quality of life in a beautiful landscape, and has been ranked as the best US city for young adults. Downtown and campus are bordered by lakes, and Madison features diverse art, music, cultural, and culinary offerings. http://www.visitmadison.com/media/rankings/ To apply, send a CV, contact info for 3 references, and a statement of research interests (up to 1 page) addressing: * Your own long term scientific interests and specific overlap with the Pool lab's research. * Your background in the concepts of population/evolutionary genetics and relevant research skills.

I am interested in adding to the diversity of our lab in a broad sense, including gender balance, cultural perspectives, and intellectual backgrounds and skill sets.

Start dates are flexible from June 2019 onward. Salary follows the NIH scale (currently $50K for new postdocs). Individual or family health insurance is offered.

Applications are due April 1. However, earlier applications are welcome, and later applications may still be considered. Informal pre-application inquiries (e.g. to discuss potential research topics) are also welcome at any time.

John Pool Associate Professor Laboratory of Genetics University of Wisconsin - Madison

jpool@wisc.edu

---

## UWisconsinMadison MutationEvolutionaryGenetics

A postdoctoral researcher position is available in the lab of Dr. Nathaniel Sharp to train in the Genetics Department at the University of Wisconsin-Madison. The goals of the Sharp Lab are to improve our understanding of the mutation process and its consequences for evolving populations. We start from a foundation of evolutionary theory to develop and test hypotheses using experiments with yeast and fruit flies, often involving genome sequence analyses. Potential research topics would include assessing the roles of standing genetic variation, genome architecture and reproductive mode in the rate and spectrum of mutations. The successful candidate will have expertise in evolutionary genetics, population genetics, genomics, or a related field, and will be familiar with statistical analysis in R. UW Madison is home to many research groups that address a broad array of topics in biology, and the Genetics Department has a long and distinguished history. The city of Madison offers many cultural and recreational opportunities with a low cost of living. The Sharp Lab is a safe and inclusive environment, and diverse candidates are encouraged to apply. For more information visit sharp.genetics.wisc.edu and contact nathaniel.sharp@wisc.edu.

NATHANIEL SHARP <nathaniel.sharp@wisc.edu>

---

## UWisconsin Milwaukee Bioinformatics

Dr. Rebecca Klaper at the Great Lakes Genomics Center at the University of Wisconsin-Milwaukee, School of Freshwater Sciences, is seeking a postdoctoral scholar to work on several functional, comparative, and environmental genomics projects. The ideal candidate will have:

- Ph.D. in Biology, Environmental Sciences, Genetics or Bioinformatics

-Mastery of BASH, proficiency in programming with Perl, and some competency in R, Python, SQL

-Familiarity with UNIX environments and computing clusters.

-Two years experience in analyzing genomic data including de novo transcriptome and assemblies and RNA-Seq, management of large datasets, and experience with gene and protein prediction, neural network analysis.

The position will involve:

-Contributing to several projects of scientists in the Great Lakes Genomics Center with the expectation of developing new analyses and original research leading to first author publications. These include examining differential gene expression in several non-model organisms (ecological models), analysis of methylation patterns, genomic changes in populations and other analyses

-Presenting research results locally and at professional meetings.

-Collaborating with a diverse group of scientists.

-Facilitating collaborations between the Great Lakes Genomics Center and scientists at other institutions.

-Writing and assisting with the writing of research proposals and peer-reviewed journal articles.

-Training and mentoring graduate and undergraduate student researchers.

To apply please send a statement of Interest, resume, and contact information for three references. Please be sure to provide a list of any relevant coursework in your resume, or cover letter and describe your experience related to the criteria above. Papers published that document work in this area also appreciated.

Rebecca Klaper

Professor and Director of the Great Lakes Genomics Center

Editor, Environmental Toxicology and Chemistry

School of Freshwater Sciences

University of Wisconsin-Milwaukee

Rebecca D Klaper <rklaper@uwm.edu>

## UWisconsin StevensPoint WhitefishGenomics

The Larson Lab at UW-Stevens Point (https://larsonlab.wordpress.com/) is looking for a postdoctoral researcher to conduct genomics research on fish populations across the Great Lakes and beyond. The main focus of this position will be to develop genomic tools for whitefish in Lake Michigan to improve resolution of population structure and understand local adaptation. However, the successful applicant will have significant freedom to develop other projects, likely involving genome resequencing. Competitive applicants should have a strong background in bioinformatics and proficiency in one or more scripting languages such as Perl or Python. We will strongly consider applicants who have experience in population genetics regardless of past study organisms; previous experience in fish genetics is not required. Applicants must have a PhD. However, we are open to exceptional applicants that will be completing their PhD within the next six months. The position will be open until filled and start dates are negotiable. The salary is $50,000 per year plus benefits. Funding is available for two years with a possibility for renewal depending on job performance and funding situation. Applicants should submit a cover letter describing your previous research and research goals, a full CV, and names and contact information for three references to Wes Larson (Wes.Larson@uwsp.edu).

“Larson, Wes” <wlarson@uwsp.edu>

## UZurich 2 EvolutionaryBiol

Postdoc in experimental evolutionary biology

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study the evolution of new protein functions through experimental evolution, and the role of robustness, epistasis, or cellular noise in adaptive evolution. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and lifes fundamental organizational principles. Ongoing experimental work in the lab ranges from the directed evolution of proteins to laboratory evolution of microbes (e.g., Bratulic et al. Nature Communications 2017; Sprouffske et al. PLoS Genetics 2018). The successful candidate will have flexibility in designing their own project, as long as it falls within the purview of the labs general research area (see http://www.ieu.uzh.ch/wagner/).

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will help develop. The successful candidate will have a strong background in microbiological techniques and molecular cloning. Experience with flow cytometry, as well as with computational analysis of high-throughput DNA sequence data will be a plus, as will be a research history in evolutionary biology. The position offers a highly competitive salary of up to three years on annually renewable contracts.

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 jobs.wagner@ieu.uzh.ch: CV including publication list, academic transcripts, three academic references, and a statement of research interests not exceeding three pages that includes a sketch of an experimental evolution project that the applicant would like to pursue. Please include the word $^{o}$EXPPDOC19± in the subject line. Applications will be considered until March 25, 2019, or until the position has been filled. The starting date is flexible.

jobs.wagner@ieu.uzh.ch

---

Postdoc in computational or theoretical evolutionary biology

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The laboratory is working on a broad range of research topics that include the origin of evolutionary adaptations and innovations, the evolution of metabolic networks and gene regulatory networks, the evolution of genome organization, and the evolution of protein and RNA molecules. (e.g., Aguilar-Rodrguez et al., Nature Ecology and Evolution 2017, Hosseini and Wagner, PNAS 2018, Payne et al., PNAS 2018). Lab members have diverse backgrounds and research projects, but are unified by their interests in evolution and lifes fundamental organizational principles. The successful candidate will have flexibility to develop their own research project within the purview of the labs broad research area (see http://www.ieu.uzh.ch/-wagner/).

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will help develop. The successful candidate will have a strong background in an area of computational science. Fluency in a major scripting language such as python, and experience in computational data analysis or mathematical modeling is a must. A strong background in biology and a demonstrated interest and research history in evolutionary biology will be a plus.

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 jobs.wagner@ieu.uzh.ch: CV including publication list, academic transcripts, three academic references, and a statement of research interests not exceeding three pages that includes a sketch of a project that you would like to pursue. Please include the word $^{o}$COMPPDOC19± in the subject line. Applications will be considered until March 25, 2019, or until the position has been filled. The starting date is flexible

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

— / —

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

## WorkshopsCourses

AuburnU Bioinformatics Jun3-7 . . . . 125
Berlin BioinformaticsInR Sep16-20 . . . . 125
Berlin ComparativeGenomics Oct7-11 . . . . 126
Berlin eDNA Jul8-12 . . . . 127
Berlin MachineLearning Jun3-7 . . . . 127
Berlin Phylogenomics May20-24 . . . . 128
Berlin PopulationGenomics May13-17 . . . . 128
BrighamYoungU HHMI EvolutionReligion Jul11-13 129
Calgary GeometricMorphometricsUsingR Jul8-12 . 129
FridayHarborLabs EvolutionaryQuantGenetics Jun10-14 . . . . 130
InstPascal France ModelingEvolution Jul8-12 . . . . 130
Madrid StatisticalPhylogenetics Jun10-19 . . . . 130
MichiganState Avida-ED Aug7-9 . . . . 131
MichiganStateU Avida-ED Aug7-9 . . . . 131
MountainLakeBiolStation EvolutionaryBiology Jul28-Aug4 . . . . 132
NorthCarolinaStateU EvolutionaryMedicine May20-24 132
Poland MolecularPhylogeny Jul15-18 . . . . 133
Providence AnalysisOfIntegratedTraits Jun26 . . . . 133
Squamish BC TamingTheBeast Aug12-16 . . . . 134
UCDavis EnvironmentalOmicsHackathon May8-10 134
UGeorgia ComputationalModeling May13-17 . . . . 134
UK 3PythonCourses Jun10-28 . . . . 135
UK LandscapeGenetics Mar25-29 FinalCall . . . . 136
UK MicrobiomeAnalysisUsingQIIME2 Sep9-13 . . . 137
UK ModellingAdaptiveVariation Jun17-21 . . . . 138
UK PythonForBiologists Jun10-14 . . . . 139
UYork GeneExpression Mar26-28 . . . . 140
Valencia Phylogenomics Oct7-11 . . . . 141
YaleU SustainingBiodiversityInfrastructure Jun12-14 141
YosemiteNatlParl Symbiosis May17-19 . . . . 141
Yunnan Metabarcoding Oct15-26 . . . . 142

## AuburnU Bioinformatics Jun3-7

Dear EvolDir list,

I am writing to announce:

the 6th Annual Bioinformatics Bootcamp at Auburn University June 3-7, 2019

The College of Sciences and Mathematics (COSAM) will sponsor the 6th Annual Bioinformatics Bootcamp at Auburn University June 3V7, 2019. Instructed by Les Goertzen, Scott Santos, Ken Halanych, Laurie Stevison, Rita Graze, Jamie Oaks, and Xu Wang from the Department of Biological Sciences at Auburn University.

The Bootcamp is a week-long workshop emphasizing hands-on training in numerous aspects of next generation DNA sequencing data analyses such as sequence assessment and quality control, genomic and transcriptomic assembly, annotation, differential expression, phylogenomics and more. Additionally, the workshop provides instruction in the Linux operating system command-line environment, basic scripting and many widely used open-source software packages. Registration for the workshop is $600.

Please see http://www.auburn.edu/bioinformatics for more information.

To apply:

Please provide a brief (half page) statement of interest describing how the AU Bioinformatics Bootcamp will benefit your research and a 2-page CV.

Application materials should be submitted by March 31th, 2019 as a single PDF via email to bioinformatics@auburn.edu. Notifications will be sent to applicants starting April 15th, 2019.

Kenneth M. Halanych Schneller Chair, Alumni Professor Curator of Marine Invertebrates Biological Sciences Department Life Sciences Bld. 101 Auburn University Auburn, AL 36849

http://metazoan.auburn.edu/halanych/lab/index.html Phone: (334)-844-3222 e-mail: ken@auburn.edu

Editor-In-Chief The Biological Bulletin http://www.journals.uchicago.edu/toc/bbl/current Kenneth Halanych <ken@auburn.edu>

## Berlin BioinformaticsInR Sep16-20

Dear all,

registrations are now open for the course “Bioinformatics with R and Bioconductor” this September (16-20) in Berlin (FU University).

Instructor: Dr Ludwig Geistlinger (City University of New York School of Public Health)

Overview: This course will provide biologists and bioinformaticians with practical statistical analysis skills to perform rigorous analysis of high-throughput genomic data. The course assumes basic familiarity with genomics and with R programming, but does not assume prior statistical training. It covers the statistical concepts necessary to design experiments and analyze high-throughput data generated by next-generation sequencing, including: exploratory data analysis, principal components analysis, clustering, differential expression, and gene set analysis.

Program: ( https://www.physalia-courses.org/courses-workshops/course19/curriculum-19/ )

Here is the full list of our courses and Workshops: ( https://www.physalia-courses.org/courses-workshops )

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org ( http://www.physalia-courses.org/ ) Twitter: @physacourses mobile: +49 17645230846

( https://groups.google.com/forum/#!forum/physalia-courses )

"info@physalia-courses.org" <info@physalia-courses.org>

---

## Berlin ComparativeGenomics Oct7-11

Dear all, happy to inform you that the registrations are now open for the 2nd edition of our Comparative Genomics course in Berlin (Free University of Berlin)

When: 7-11 October 2019

Instructors:

Dr Fritz J. Sedlazeck (https://fritzsedlazeck.github.io/)

Prof. Dr. Ingo Ebersberger (https://scholar.google.com/citations?user=-LOOY3kYAAAAJ&hl=en)

Course overview

This course will introduce biologists and bioinformaticians into the field of comparative genomics. Different techniques will be introduced to identify single nucleotide polymorphism (SNP) and structural variations (SVs) as well as the annotation of these variations and the assessment for their functional impact.

Course format

The course is structured in modules over five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at researchers interested in learning how to compare genomes and what can be learned from genomic similarities as well as variations. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of comparative genomics. On this basis, we will then continue to describe all major analysis steps from the raw sequencing data via the identification of variations to an assessment of their impact on the phenotype.

Attendees should have a background in biology. There will be a mix of lectures and hands-on practical exercises using command line Linux. We will therefore dedicate one session to introduce basic and advanced Linux concepts for processing data on Amazon cloud (AWS). Attendees should have also some familiarity with genomic data such as that arising from NGS sequencing experiments.

LEARNING OUTCOMES

Setting up a comparative genomics analysis environment with the CONDA package management system Identification of SNPs and SVs using de novo genome assembly and read mapping strategies Assessment of strengths and weaknesses of the different DNA sequencing technologies, Illumina, Pacific Bioscience, Oxford Nanopore, for the detection of variations Strengths and pitfalls of de novo assembly and mapping approaches for comparative genomics Hands on experience of state of the art methods to compare multiple genomes Annotation of variations and comparative genomics analysis Familiarity with biological sequence analysis in an evolutionary context

For more information about the course, please visit our website: ( https://www.physalia-courses.org/courses-workshops/course33/ )

Here is the full list of our courses and Workshops: ( https://www.physalia-courses.org/courses-workshops/ )

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/-#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

---

## Berlin eDNA Jul8-12

Course: Intro to Environmental DNA research and analysis

Where: Free University Berlin (Germany)

When: 8th -12th July 2019

Instructors:

1) Dr. Mathew Seymour (Bangor University, UK)

2) Luke E. Holman (University of Southampton, UK)

Overview:

This course focuses on the use of eDNA to detect eukaryotic species form environmental samples. Here, we offer an introduction into eDNA based science with key emphasis on how to design, implement and analyze 1) species specific (targeted) eDNA using qPCR and 2) community based analyses using metabarcoding and high throughput sequencing.

After completing the course, students should be in a position to (1) Design their own eDNA study based on their research needs (2) understand the principles of qPCR, including in-silico primer development and experimental setup (3) analyse high throughput sequencing eDNA metabarcoding data (4) Perform preliminary analyses of both qPCR and metabarcoding data and (5) Create publication quality figures 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.

This course is aimed at researchers and technical workers with a background in ecology, biodiversity or community biology who want to use molecular tools for biodiversity research. The course is intentionally broad with an aim of providing a a general overview of the current state-of-the-art in eDNA research as well as equipping practical researchers with some basic tools to begin their own research projects.

No programming or scripting experience is necessary and we will assume no prior knowledge of command line programming, those with previous expertise using the Linux console or R are most welcome and we aim to provide something new for everyone. The practical sessions will be run using Amazon Web Services (AWS) linux servers, participants must bring their own computer system. Instructions for pre-installing software will be provided.

For more information and for the full program, please visit our website: ( https://www.physalia-courses.org/-courses-workshops/course40/ )

Should you have any questions, please feel free to contact us: ( mailto:info@physalia-courses.org )

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/-#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

---

## Berlin MachineLearning Jun3-7

Introduction to Machine Learning

When: 3rd-7th June 2019

Where: Free University of Berlin

Registration deadline: 4th May 2019

Instructor: Prof. Paolo Frasconi (University of Florence, Italy; http://ai.dinfo.unifi.it/paolo/)

This course is aimed to students and researchers aiming to understand the basic principles of machine learning. It will focus on supervised learning, starting with linear models (regression, logistic regression, support vector machines) and will extend to the basic technologies of deep learning and kernel methods for vector data, signals, and structured data. Basic principles of learning theory that are useful to analyze results of practical applications will be also covered. Finally, there will be practical sessions using scikit-learn, TensorFlow, and Keras. After completing the course, students should able to understand the most popular learning algorithms, to apply them to solve simple practical problems, and to analyze and interpret the results. 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.

The syllabus has been planned for people with zero or very basic knowledge of machine learning.

For more information about the course, please visit our website: https://www.physalia-courses.org/courses-workshops/course43/ Here is the full list of our courses and Workshops: ( https://www.physalia-courses.org/-courses-workshops/ )

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org ( http://www.physalia-courses.org/ ) Twitter: @physacourses mobile: +49 17645230846 ( https://groups.google.com/forum/-#!forum/physalia-courses )

info@physalia-courses.org

## Berlin Phylogenomics May20-24

Phylogenomics Course

Where: FU University Berlin (Germany)

When:20-24 May 2019

Instructor: Dr. Michael Matschiner (University of Basel (Switzerland))

Course website: ( https://www.physalia-courses.org/-courses-workshops/course21/ )

Overview: In this workshop we will present theory and exercises to infer time-calibrated phylogenies from multi-locus, RADseq, and whole-genome data sets while accounting for these confounding factors.

Who Should Attend: This workshop is aimed at researchers, PhD or postdoc level planning to infer phylogenetic relationships and divergence times from multi-locus, RADseq, or whole-genome data.

Requirements: Attendents should have basic knowledge of UNIX and will need to use the command line on their laptops. Familiarity with a scripting language such as Ruby, Python, or Perl will be helpful but is not required.

Full list of our courses and Workshops: ( https://-www.physalia-courses.org/courses-workshops/ )

Should you have any questions, please feel free to contact us at: info@physalia-courses.org

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org ( http://www.physalia-courses.org/ ) Twitter: @physacourses mobile: +49 17645230846 ( https://groups.google.com/forum/-#!forum/physalia-courses )

"info@physalia-courses.org" <info@physalia-courses.org>

## Berlin PopulationGenomics May13-17

Dear all,

still a few places available for 4th edition of our course "Introductory Population Genomics: From Data to Inference" this May (13th-17th) in Berlin, with Dr. Martin Taylor and Dr. Lewis Spurgin from the University of East Anglia, UK.

The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

For more information, please visit our website: https://www.physalia-courses.org/courses-workshops/-course392/ Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/ )

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/-#!forum/physalia-course info@physalia-courses.org

## BrighamYoungU HHMI EvolutionReligion Jul11-13

Join us for an HHMI-funded workshop at Brigham Young University designed to build bridges between Evolutionary Biology and Religion.

When: July 11 - 13, 2019

Where: BYU Campus, Provo, UT

Who: We invite any faculty members from an institution where students face conflict between religious influences and learning evolutionary science. We require that participants come in teams of three:

-A faculty member from a Biology-related discipline who teaches undergraduate students in Biology -A faculty member from a theology-related discipline who can speak to the predominant faith traditions of students -A local minister representative of the majority of the student body

Details: All travel and lodging expenses will be covered. Additional stipends may be available for participation in follow-up activities related to the research. Attendees will be co-authoring a set of learning materials that can be shared broadly and that are specific to a faith tradition that offer students a way to reconcile faith and evolution without promoting or degrading religion. Attendees will also have the opportunity to participate in the building of video vignettes with the same purpose.

To register, please visit https://goo.gl/forms/-7VUDKz0DjTfADsWS2 Our Goal:

Many students struggle with the scientific information presented to them as it may appear confrontational to their religious beliefs. Well-meaning scientists have approached the intersection between faith and science in ways that lengthen the divide between these two ways of interpreting the world. Ultimately, our goal is to replace these approaches with a 'Reconciliatory Model'. To reconcile is to “cause to coexist in harmony”; to “make or show to be compatible”; or to “restore friendly relations between” (Oxford Dictionary, 2017). By involving theologians, scientists, and clergy in a combined effort toward a solution, we can create a mutually respectful and highly effective method to help students reconcile these two ways of knowing toward a more scientifically literate society.

Thank you! Please direct any questions to Dr. Jamie Jensen, Brigham Young University: Jamie.Jensen@byu.edu, 801-422-6896.

seth.bybee@gmail.com

---

## Calgary GeometricMorphometricsUsingR Jul8-12

Dear Colleagues,

Registration is open for the course Introduction to Geometric Morphometrics using (mostly) R.

Instructors: Dr. Paula Gonzlez (CONICET-HEC-UNAJ, Argentina) and Dr. David Katz (University of Calgary, Canada).

Dates and place: July 8th-12th, 2019, Alberta (Canada).

This course is intended as an introduction to the major aspects of 2D and 3D landmark-based shape analysis. While we will spend some time on shape theory and mechanical aspects relevant statistical analyses, the goal of doing so will be to develop your intuition for how to&#8212;and how not to&#8212;design and interpret your geometric morphometrics research.

Students will learn the foundations of geometric morphometrics through lectures and daily exercises. The exercises are designed around a mouse skull shape sample from a controlled experiment with longitudinal design, though for most exercises, students are welcome to work with their own data instead.

Students lacking a rudimentary understanding of R will be asked to complete a short series of introductory exercises prior to attending the course. Most analyses will be done in R, although we will also use Meshlab for landmarking 3D models, and tpsDig for 2D landmarking.

The program includes analysis of relatedness (pedigree, phylogeny) and morphological integration and modularity.

More information and registration: https://www.transmittingscience.org/courses/geometric-morphometrics/introduction-geometric-morphometrics-using-mostly-r or writing to courses@transmittingscience.org

Places are limited to 20 participants and will be occupied by strict registration order.

This course is organized by Transmitting Science and Calgary University.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org

Soledad De Esteban Trvigno <soledad.esteban@transmittingscience.org>

## FridayHarborLabs EvolutionaryQuantGenetics Jun10-14

Applications for this year's Evolutionary Quantitative Genetics Workshop, to be held June 10 - 14, 2019 at the Friday Harbor Laboratories of the University of Washington, are still open, until the end of the day on the 15th of March. There are still some places in the workshop. For a description of the workshop, its lecturers and costs, and links to the blog pages for last year's workshop, see this web page:

https://fhl.uw.edu/courses/course-descriptions/course/-evolutionary-quantitative-genetics-workshop-2019/ The application form is

https://tinyurl.com/EQG2019Application/ and is also linked to at the workshop web page. Please pass this on to anyone who might be interested in applying.

Joe Felsenstein and Steve Arnold

Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USA

Joe Felsenstein <joe@gs.washington.edu>

## InstPascal France ModelingEvolution Jul8-12

Dear colleagues,

A quick reminder to register for the upcoming summer school "Data and Models in Ecology and Evolution" taking place at the Institut Pascal (Saclay, FRANCE) from 8 to 12 July 2019 and dedicated to Post-Docs and PhD students in Mathematics and Biology.

The deadline for registration is the 15/04/2019.

For more information and to apply, see here :

https://www.universite-paris-saclay.fr/fr/data-and-models-in-ecology-and-evolution Funding for travel and accommodation can be provided by the Institut Pascal.

Sincerely, The organizing and scientific committee D. Abu Awad, G. Achaz, A. Becheler, C. Coron, S. Dupas, F. Jay, A. Olivier, M. Sedki, S. Stoeckel, A. Véber

"Abu Awad, Diala" <diala.abu-awad@tum.de>

## Madrid StatisticalPhylogenetics Jun10-19

MADPHYLO 2019: Madrid Workshop in Statistical Phylogenetics

Where: Real Jardin Botanico (CSIC), Madrid, Spain

When: 10th-19th June 2019

www.madphylo.com Course overview:

Darwin founded the field of evolutionary biology on the concept that all organisms are related to one another through an unknown evolutionary tree. Phylogenetic or evolutionary inference has become an essential tool in many disciplines across the life sciences, from molecular epidemiology to paleontology. In this workshop, the participants will learn the theoretical and technical basis of stochastic modeling in evolutionary biology and phylogenetics. The workshop will also provide full training in the open software RevBayes, an R-like interactive environment based on graphical model concepts for the modeling of complex evolutionary problems. At the end of the workshop, the student will have an understanding of the assumptions behind state-of-the-art methods used in modern phylogenetic analysis, as well as being able to build up new models from existing functions in RevBayes.

Instructors:

The lecturers are prominent analytical systematists and evolutionary biologists, who are behind the development of many of the methodological and computing tools routinely used in modern phylogenetic inference and evolutionary biology: Prof. John Huelsenbeck (University of California, Berkeley), Prof. Brian Moore (University of California, Davis), Dr. Michael R. May (University of California, Davis), Prof. Sebastian Hoehna (University Ludwig-Maximilians, Munich), . The Workshop is organized and directed by Dr. Isabel Sanmartin (Real Jardin Botanico, CSIC, Madrid), who will also lecture.

Workshop details:

The course will be taught from June 10, 2019 to June 19, 2019. Lectures and practicals will be tightly linked, meaning that you will learn the theory and also how to apply the theory on the same day. Students are encouraged to bring their own laptops. The tuition for the course is deliberately low, at only 450 Euros. This tuition includes coffee breaks and an informal American-style make-your-own-sandwich lunch every day of the workshop. However, tuition does not include lodging. You will be required to find a place to stay if you are from outside of Madrid.

More details and how to register can be found on the website: https://www.madphylo.com Email isanmartin@rjb.csic.es or johnh@berkeley.edu for any questions.

Dr. Isabel Sanmartin, PhD Department of Plant Biodiversity and Conservation Vicedirector of Communication and Educational Outreach Real Jardin Botanico, CSIC Plaza de Murillo 2 28014 Madrid, SPAIN 0034-(91)-4203017 isanmartin@rjb.csic.es Google Scholar webpage https://scholar.google.com/citations?user=HNhEAN8AAAAJ&hl=en Personal webpage

http://www.rjb.csic.es/jardinbotanico/jardin/contenido.php?PagA3&tipo=cientifico&codÂ&len=es SYNTHESYS plus If you work in an EU country or a country associated with the EU Framework Programmes and want to do research in a major European Taxonomic Facility, visit http://www.synthesys.info. New Call Open Now

Isabel Sanmartin <isanmartin@rjb.csic.es>

---

## MichiganState Avida-ED Aug7-9

DEADLINE EXTENDED. We are now accepting applications on a rolling basis.

We are currently soliciting applications for participants in a training workshop to teach faculty how to use Avida-ED, a free, web-based program designed to teach both principles of evolution and the nature of science, based on the research platform Avida. This summer, we are holding two such workshops, one at the University of Texas in Austin from June 12-14; the other at Michigan State University (in East Lansing) from August 7-9. Workshop participants will learn how to use this program, and incorporate it into courses that they teach. We will give priority to applications submitted as teams of two, though we are also accepting applications from single individuals. Full details on the workshops, and information on how to apply, are available at https://avida-ed.msu.edu/active-lens-train-the-trainers-workshop-2019-edition/ . Due to grant constraints, we are limited to participants within the US. If you have any questions about the workshop or application procedure, please don't hesitate to contact Mike Wiser at mwiser@msu.edu

mwiser@msu.edu

---

## MichiganStateU Avida-ED Aug7-9

We are currently soliciting applications for participants in a training workshop to teach faculty how to use Avida-ED, a free, web-based program designed to teach both principles of evolution and the nature of science, based on the research platform Avida. This summer, we are holding two such workshops, one at the University of Texas in Austin from June 12-14; the other at Michigan State University (in East Lansing) from August 7-9. Workshop participants will learn how to use this program, and incorporate it into courses that they teach. We will give priority to applications submitted as teams of two, though we are also accepting applications from single individuals. Full details on the workshops, and information on how to apply, are available at https://avida-ed.msu.edu/active-lens-train-the-trainers-workshop-2019-edition/ . The initial application deadline is March 3rd; we will likely switch to rolling acceptance after this date for the slots that remain open. Due to grant constraints, we are limited to participants within the US. If you have any questions about the workshop or application procedure, please don't hesitate to contact Mike Wiser at mwiser@msu.edu

mwiser@msu.edu

## MountainLakeBiolStation EvolutionaryBiology Jul28-Aug4

Join Drs. Amanda Gibson (University of Virginia), Lynda Delph (Indiana University), and Curt Lively (Indiana University) for a six-day workshop on evolutionary biology for early career graduate students (Master's or PhD students in their first or second year). We've modeled this workshop off of the Evolutionary Biology Workshop in Guarda, Switzerland that was initiated by Stephen C. Stearns in 1988.

When: July 28 V August 4 2019

Where: Mountain Lake Biological Station, Pembroke VA

Cost: $447.75

During this week, you'll have the time and support to think deeply about the evolutionary questions that most excite you and to engage in focused conversations with a small group of peers. As you shape your ideas into a research proposal, you'll practice communicating with others and articulating yourself in writing. Profs. Lively, Delph, and Gibson will lead sessions on developing questions and writing effectively. Participation is limited to 12.

The objectives of this workshop are to: identify important questions in evolutionary biology; formulate testable hypotheses and design targeted experiments; express your ideas clearly through writing and speaking; have focused conversations with your peers about shared scientific interests

For more information and to register, visit https://mlbs.virginia.edu/evolution-workshop-2019 "Gibson, Amanda K (akg5nq)" <akg5nq@virginia.edu>

## NorthCarolinaStateU EvolutionaryMedicine May20-24

Announcing the TriCEM Evolutionary Medicine Summer Institute

We are excited to announce that we are now accepting applications for the 2019 Evolutionary Medicine Summer Institute (EMSI https://urldefense.proofpoint.com/v2/url?u=https-3A__tricem.us14.list-2Dmanage.com_track_click-3Fu-3Dd5d89ab81579d70d38dccfe2b-26id-3D762ccb0a7d-26e-3D222dbf443b&d=DwMFaQ&c=imBPVzF25OnBgGmVOlcsiEgHoG1i6YHLR0Sj_gZ4adc&r=z-zb0FnOpOVAS-BuPlBRUY1ezjGg6vxsnsOiIiSX94qU&m=FV9v6sUDjZX0Y0vIWDnpPZCiBCprHBoOypCnx3-KQO30&s=DjOqTb6PE0Jxhv5KNR76DoBSw9IbwM8S_c1lLXBFIf4&e=) May 20-24. The goal of EMSI is to introduce core evolutionary concepts to a wide range of topics in human health and disease, including public health, and to train physicians and medical scientists in computational methods used in evolutionary and ecological research.

EMSI will bring together internationally recognized experts in evolutionary biology with students and health practitioners who want to apply these perspectives to cancer, infectious disease, evolution of microbial resistance, neurology, autoimmune disease, the microbiome, and more. Lectures on key concepts will be complimented with hands-on computational exercises. Our goal is to give participants the background on evolutionary principles and the tools to apply evolutionary biology to questions of medical importance. For more information and the application form, please visit our EMSI website https://urldefense.proofpoint.com/v2/url?u=https-3A__tricem.us14.list-2Dmanage.com_track_click-3Fu-3Dd5d89ab81579d70d38dccfe2b-26id-3Dfb5949d47b-26e-3D222dbf443b&d=DwMFaQ&c=imBPVzF25OnBgGmVOlcsiEgHoG1i6YHLR0Sj_gZ4adc&r=z-zb0FnOpOVAS-BuPlBRUY1ezjGg6vxsnsOiIiSX94qU&m=FV9v6sUDjZX0Y0vIWDnpPZCiBCprHBoOypCnx3-KQO30&s=xjIFoUgzNXi-WrhWGyJrAlU01BeobOeqJggs2_xrL5c&e=.

This year, EMSI will be held at North Carolina State University.

To apply, and for more information, please fill out this form https://urldefense.proofpoint.com/v2/url?u=https-3A__tricem.us14.list-2Dmanage.com_track_click-3Fu-3Dd5d89ab81579d70d38dccfe2b-26id-3D2dec736c62-26e-3D222dbf443b&d=DwMFaQ&c=imBPVzF25OnBgGmVOlcsiEgHoG1i6YHLR0Sj_gZ4adc&r=z-zb0FnOpOVAS-BuPlBRUY1ezjGg6vxsnsOiIiSX94qU&m=FV9v6sUDjZX0Y0vIWDnpPZCiBCprHBoOypCnx3-KQO30&s=NM37Ohbaech5jLUNe7IVQISaDRcoSeHrb0kZ1OgaVvo&e=.

Please direct questions to Grace Farley (grace.farley@duke.edu), James Herrera (james.herrera@duke.edu ), or Charles Nunn (clnunn@duke.edu).

Our contact information is:

Duke University Box 90383 Durham, NC 27708 919.681.6363 www.tricem.org "Dr James Herrera, Ph.D." <james.herrera@duke.edu>

---

## Poland MolecularPhylogeny Jul15-18

Course title: DNA-sequence data and phylogenies in biodiversity

When: 15-18 july 2019

Where: University of Lodz (Poland)

Instructor: Dr. Diego Fontaneto (https://scholar.google.de/citations?user=-WO97K4QAAAAJ&hl=en)

Overview: This course will introduce scientists interested in biodiversity to the use of DNA-sequence data to address questions that cannot be addressed by using only morphological and ecological data in their studies. After a short introduction on how to obtain DNA sequences and reliable molecular phylogenies, the focus of the questions that could be addressed will be on taxonomy, community ecology, and comparative methods.

LEARNING OUTCOMES

- Understand how to read, interpret and obtain molecular phylogenies, with a focus on the concepts and rationale behind phylogenetic methods
- Learn tools from DNA taxonomy
- Learn how to include phylogenies in the analyses of community ecology and in comparative analyses
- Hand-on experience on all the steps
- Learn how to R including molecular phylogenies in ecological analyses

For more information, please visit the course website: https://www.physalia-courses.org/courses-workshops/course28/ Here is the full list of our courses and Workshops: ( https://www.physalia-courses.org/-courses-workshops/ )

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/-#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

---

## Providence AnalysisOfIntegratedTraits Jun26

Short Course: Phylogenetic comparative analysis of integrated anatomical traits https://scate.phenoscape.org/-2019-workshop-cfp.html Where: Providence, RI When: June 26, 2019 (Wednesday), 9 am-12 pm

Course overview:

Ontologies encode information about a domain of knowledge, such as how anatomical structures are related, which is crucial information for modeling character evolution. Phenoscape, in its current Semantic Comparative Analyses for Trait Evolution (SCATE; http://-scate.phenoscape.org) project, is developing tools that use the computable knowledge in ontologies to improve phenotypic character modeling and inform analyses of trait evolution. To train evolutionary biologists and developers of comparative analysis tools to adopt these new capabilities, the SCATE team will be holding a short course on using ontologies in comparative analyses of integrated anatomical traits, in conjunction with iEvoBio and the Evolution Meetings, on June 26, 2019 in Providence, Rhode Island.

Attendees will learn how to use R packages such as RPhenoscape (http://rphenoscape.phenoscape.org) to access a knowledgebase of ontology-linked phenotypes (kb.phenoscape.org), build character matrices that take anatomical dependencies into account, and use these to construct stochastic character maps on a phylogeny. The course will also include a practical introduction to community ontologies for biodiversity domain knowledge (anatomy, taxonomy, phenotypic attribute).

Graduate students, postdocs, faculty, and software developers with interests in comparative analyses, morphology, and phylogenetics are encouraged to apply.

Free registration: Applications accepted until May 15th or capacity is reached. Register by filling out the form at https://goo.gl/forms/802KN6cd6cQOI01Q2 Wasila.Dahdul@usd.edu

## Squamish BC TamingTheBeast Aug12-16

Hi Brian,

The BC Centre for Excellence in HIV/AIDS and the JC Wilt Infectious Diseases Research Centre are hosting the first North American Taming the BEAST workshop this summer in Squamish, British Columbia. Taming the BEAST is a workshop focused on BEAST2, an open-source software package for Bayesian phylogenetic analyses of molecular sequences. The workshop consists of invited talks, lectures and hands-on tutorials by leading experts in the field. The aim of the workshop is to equip participants with the skills and core knowledge to confidently perform phylogenetic and phylodynamic analyses of their own. It is open to graduate students and scientists interested in the analysis of genomic data and molecular evolution. The link to the workshop page is https://taming-the-beast.org/workshops/ Francois (Frank) Cholette JC Wilt Infectious Diseases Research Centre Public Health Agency of Canada Winnipeg, MB francois.cholette@canada.ca

"Cholette, Francois (PHAC/ASPC)" <francois.cholette@canada.ca>

## UCDavis EnvironmentalOmicsHackathon May8-10

Dear Colleagues,

Please find below an announcement for an exciting series of workshops focused on 'Speeding up Science' in Environmental -Omics research fields. Travel funding for all participants is being generously sponsored by the Moore Foundation, and the inaugural workshop will be taking place May 8-10, 2019 at UC Davis.

Full workshop description and provisional schedule: http://bit.ly/2JMm957 Application to participate (deadline April 12): https://goo.gl/forms/-11i9KTaMwOLdBqBw2 We're looking for people with metabarcoding, metagenomics, and metatranscriptomics data/code/scripts to join us for a Jupyter/Binder hackathon - the goal is to improve data analysis tools for Environmental -Omics studies, by producing reproducible workflows for common data processing and visualization steps.

If you are a researcher or software developer using high-throughput sequencing approaches in any ecosystem (marine, terrestrial, human microbiome, etc.), please apply!

International applicants outside the USA are also welcome to apply (the exact number of international participants we can support will depend on the applicant pool and how far we can stretch the travel budget).

Any questions can be directed to workshop organizers Holly Bik ( holly.bik@ucr.edu) and C. Titus Brown (ctbrown@ucdavis.edu).

– Holly Bik Assistant Professor Department of Nematology University of California, Riverside 3401 Watkins Drive Riverside, CA 92521 Email: holly.bik@ucr.edu Phone: (+1) 951-827-4230

Web: https://www.biklab.org/ Twitter: https://-twitter.com/hollybik Holly Bik <holly.bik@gmail.com>

## UGeorgia ComputationalModeling May13-17

Dear EvolDir,

The Center for the Ecology of Infectious Diseases (CEID) at UGA is pleased to announce that registration is open for the 2019 CEID-IDEAS Computational Modeling Workshops, taking place Monday May 13th to Friday May 17th at the Odum School of Ecology in Athens, GA. Comprised of two back-to-back workshops, this series introduces students and healthcare professionals to the field of quantitative modeling as it relates to the dynamics of infectious diseases. Through a combination of lecture and laboratory practicums, participants will synthesize the advanced techniques of statistics, computer science, and mathematics to help them frame biological questions in mathematical parlance, embark on analyses of these models, and work with a diverse array of data using advanced computational methods. Upon completion, participants should be able to:

* Write code in R to perform research analysis * Create reproducible workflows * Extend understanding through independent study using web-based resources * Express hypotheses as mathematical models * Manipulate and

analyze diverse data types

Course Information

Workshop I. Introduction to Scientific Programming Monday & Tuesday, May 13th & 14th, 8:00AM-5:00PM & Wednesday, May 15 8:00AM-Noon Instructors: John Drake & Andrew Park

Workshop II. Modeling Infectious Diseases Wednesday, May 15 from 1:00PM-5:00PM & Thursday & Friday, May 16th & 17th, 8:00AM-5:00PM Instructors: John Drake & Pej Rohani

Participants are welcome to register for one or both sessions using the registration portal here: https://estore.uga.edu/C27063_ustores/web/classic/store_main.jsp?STOREID19 Full information is available in the program brochure here: http://ideas.ecology.uga.edu/wp-content/uploads/2019/01/IDEAS-Computational-Modeling-Workshop-Program-2019-1.pdf Please contact IDEAS@uga.edu with any questions or concerns!

Trippe Ross Administrative Specialist Center for the Ecology of Infectious Diseases 203 D.W. Brooks Drive University of Georgia Athens, GA 30602 706-542-1930 ceid.uga.edu

tross312@uga.edu

---

## UK 3PythonCourses Jun10-28

Dear Brian, can you please post the following to the courses and workshops page of evoldir, thanks in advance, Oliver

3 different Python courses for Biologists scheduled for June in Scotland

Introduction to Python for Biologists (IPYB06) 10 June 2019 - 14 June 2019 https://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb06/ Advanced Python for Biologists (APYB03) 17 June 2019 - 21 June 2019 https://www.prinformatics.com/course/advanced-python-biologists-apyb03/ Genomic data Visualisation and Manipulation using Python (DVMP02) 24 June 2019 - 28 June 2019 https://www.prinformatics.com/course/data-visualisation-and-manipulation-using-python-dvmp02/ Email oliverhooker@prinformatics.com

Check out our sister sites, www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. March 25th V 29th 2019 LANDSCAPE GENETIC DATA ANALYSIS USING R (LNDG03) Glasgow, Scotland, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg03/ 2. April 1st V 5th 2019 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy02/ 3. April 1st V 5th 2019 INDIVIDUAL BASED MODELS FOR ECOLOGSITS (IBME01) Glasgow, Scotland, Dr Aristides (Aris) Moustakas

https://www.prstatistics.com/course/individual-based-models-using-r-and-netlogo-ibms01/ 4. April 8th V 12th 2019 MACHINE LEARNING (MLUR01) Glasgow, Scotland, Dr Aristides (Aris) Moustakas https://www.prstatistics.com/course/machine-learning-using-r-mlur01/ 5. April 15th V 19th 2019 INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB06) Athens, GREECE,, Dr. Martin Jones http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb07/ 6. April 22nd V 26th 2019 GIS USING R (GISR) Glasgow, Scotland, Dr Luca Nelli https://www.prstatistics.com/course/gis-using-r-gisr01/ 7. April 29th V May 3rd 2019 MULTIVARIATE ANALYSIS OF ECOLOGICAL COMMUNITIES IN R WITH THE VEGAN PACKAGE (VGNR02) Orford Musique, Quebec, Canada, Dr. Guillaume Blanchet https://www.prstatistics.com/course/multivariate-analysis-of-ecological-communities-in-r-with-the-vegan-package-vgnr02/ 8. May 6th V 10th 2019 AN EXPLORATION OF R FOR PSYCHOLOGISTS: FROM DATA HANDLING TO MULTILEVEL MODELLING (XPLR01) Myuna Bay, AUSTRALIA, Dr. Sean Murphy https://www.psstatistics.com/course/an-exploration-of-r-for-psychologists-from-data-handling-to-multilevel-modelling-xplr01/ 9. May 20th V 24th 2019 MODEL BASE MULTIVARIATE ANALYSIS OF ABUNDANCE DATA USING R (MBMV03) Myuna Bay, AUSTRALIA, Prof. David Warton https://www.prstatistics.com/course/model-based-multivariate-analysis-of-abundance-data-using-r-mbmv03/ 10. May 20th V 24th 2019 MACHINE LEARNING (MLUR02) Myuna Bay, AUSTRALIA, Dr Aristides (Aris) Moustakas https://www.prstatistics.com/course/machine-learning-using-r-mlur02/ 11. June 10th V 14th 2019 STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR (SIMM04) Glasgow, Scotland, Dr. Andrew Parnell, Dr. Andrew Jackson www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm04/ 12. June 17th V 21st 2019 SPATIAL MODELLING AND ANALYSIS OF ADAPTIVE GENOMIC VARIATION (SPGN01) Glasgow, Dr. Matt Fitzpatrick

— / —

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

---

## UK LandscapeGenetics Mar25-29 FinalCall

Landscape genetic data analysis using R (LNDG03)

https://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg03/ This course will be delivered by Prof. Rodney Dyer form the 25th - 29th March in Glasgow City Center.

Course Overview:

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 Program

Monday 25th V Classes from 09:30 to 17:30

Module 1: Spatial & Ecological Data. Installation & configuring R & RStudio Acquiring spatial data, projections, and visualization Vector and raster data

Tuesday 26th V Classes from 09:30 to 17:30

Module 2: Genetic markers and basic analyses Genetic markers and sampling Genetic distance, diversity, and structure Ordination techniques based upon genetic markers

Wednesday 27th V Classes from 09:30 to 17:30

Module 3: Integrating spatial and genetic data Barrier detection & population division Resistance Modeling Mantel and distance regressions Remote sensing V LiDAR and Hyperspectral data

Thursday 28th V Classes from 09:00 to 17:00

Module 4: Integrating spatial and genetic data Spatial autocorrelation Network Approaches PCMN & Redundancy

Friday 29th V Classes from 09:30 to 16:00

Module 5: Adaptive Genetic Variance Outliers & gradients Quantitative genetics, why we should care. Chromosome walking

Email oliverhooker@prstatistics.com

Check out our sister sites,

www.PRstatistics.com (Ecology and Life Sciences)

www.PRinformatics.com (Bioinformatics and data science)

www.PSstatistics.com (Behaviour and cognition)

1. March 11th V 15th 2019

ECOLOGICAL NICHE MODELLING USING R (ENMR03)

Glasgow, Scotland, Dr. Neftali Sillero

http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr03/ 2. March 18th V 22nd 2019

INTRODUCTION TO STATISTICS AND R FOR EVERYONE (IRFE01)

Athens, GREECE, Dr Aristides (Aris) Moustakas

https://www.prstatistics.com/course/introduction-to-statistics-and-r-for-anyone-irfe01/ 3. March 25th V 29th 2019

LANDSCAPE GENETIC DATA ANALYSIS USING R (LNDG03)

Glasgow, Scotland, Prof. Rodney Dyer

http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg03/ 4. April 1st V 5th 2019

INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01)

Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre

http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy02/ 5. April 1st V 5th 2019

INDIVIDUAL BASED MODELS FOR ECOLOGSITS (IBME01)

Glasgow, Scotland, Dr Aristides (Aris) Moustakas

https://www.prstatistics.com/course/individual-based-models-using-r-and-netlogo-ibms01/ 6. April 8th V 12th 2019

MACHINE LEARNING (MLUR01)

Glasgow, Scotland, Dr Aristides (Aris) Moustakas

https://www.prstatistics.com/course/machine-learning-using-r-mlur01/ 7. April 15th V 19th 2019

INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB06)

Athens, GREECE,, Dr. Martin Jones

http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb07/ 8. April 22nd V 26th 2019

GIS USING R (GISR)

Glasgow, Scotland, Dr Luca Nelli

https://www.prstatistics.com/course/gis-using-r-gisr01/ 9. May 6th V 10th 2019

AN EXPLORATION OF R FOR PSYCHOLOGISTS: FROM DATA HANDLING TO MULTILEVEL MODELLING (XPLR01)

Myuna Bay, AUSTRALIA, Dr. Sean Murphy

https://www.psstatistics.com/course/an-exploration-of-r-for-psychologists-from-data-handling-to-multilevel-modelling-xplr01/ 10. May 16th V 19th 2019 (please note this a 4-day course from Thursday

— / —

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

---

# UK MicrobiomeAnalysisUsingQIIME2 Sep9-13

Microbiome Data Analysis Using QIIME2 (MBQM01)

https://www.prinformatics.com/course/microbiome-data-analysis-using-qiime2-mbqm01/ This course will be delivered by Dr. Yoshiki Vazquez Baeza and Dr. Antonio Gonzalez Pena from the 9th - 13th September in Glasgow City Centre.

Course Overview: This course will provide a theoretical, analytical and practical introduction to QIIME 2 (canonically pronounced ¥chime two), which stands for Quantitative Insights into Microbial Ecology 2, and Qiita (canonically pronounced ¥cheetah), a multiomics and multi-study online tool. QIIME 2 and Qiita are open source software packages for comparison and analysis of microbial communities, primarily based on high-throughput amplicon sequencing data (such as SSU rRNA) generated on a variety of platforms, but also supporting analysis of other types of data (such as shotgun metagenomic, metabolomics or proteomics). The main Qiita deployment ( http://qiita.microbio.me/) allows users to manage and analyze large studies, their metadata and the multiple data types generated from the same samples. Additionally, it allows users to combine their samples with other published and public studies available in the system. QIIME 2 is a stand-alone environment for the analysis of individual microbiome data sets that can be used on your laptop, university computational resources, and cloud computing resources.

Course objectives: By the end of the course, participants will be able to: 1) Understand the most recent QIIME2 and Qiita features for microbial community analysis 2) Select the best workflow and parameters to perform the different steps for microbial community analysis 3) Understand and apply on their own datasets different phylogenetic and non-phylogenetic metrics to compare microbial diversity samples 4) Upload and analyze their own datasets using Qiita and compare their studies with other public studies

Course Programme Monday 24th V Classes from 09:30 to 17:30 Module 1: Introduction to the microbiome. Module 2 (optional): Refresher of the command line interface and UNIX-like systems. Module 3: Bioinformatics challenges in the microbiome. Module 4: Introduction and search for public studies via Qiita.

Tuesday 25th V Classes from 09:30 to 17:30 Module 1: Connecting to workshop server and CLI Refresher. Module 2: QIIME 2 concepts (artifacts, visualizations, methods, plugins, interfaces, etc). Module 3: Sample, sequence, and phylogeny processing. Module 4: Importing and exporting data in QIIME 2.

Wednesday 26th V Classes from 09:30 to 17.30 Module 1: Diversity analyses (alpha diversity). Module 2: Diversity analyses (beta diversity). Module 3: Taxonomic classification for target gene data.

Thursday 27th V Classes from 09:30 to 17:30 Module 1: Differential abundance testing. Module 2: Meta-analyses using Qiita. Module 3: Creating a study in Qiita. Module 4: Searching for sequences and environments using redbiom.

Friday 28th V Classes from 09:30 to 16:00 Module 1: Compare the commands and tools we reviewed in the workshop with recent papers. Module 2: Review other

Qiime2 plugins available and tools: PICRUSt, 'ili, time series analysis, etc. Module 3: The Python API for QIIME2. Module 4: Open science considerations before and after publication.

email oliverhooker@prinformatics.com

Check out our sister sites! www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. March 25th V 29th 2019 LANDSCAPE GENETIC DATA ANALYSIS USING R (LNDG03) Glasgow, Scotland, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg03/
2. April 1st V 5th 2019 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy02/ 3. April 1st V 5th 2019 INDIVIDUAL BASED MODELS FOR ECOLOGSITS (IBME01) Glasgow, Scotland, Dr Aristides (Aris) Moustakas https://www.prstatistics.com/course/individual-based-models-using-r-and-netlogo-ibms01/ 4. April 8th V 12th 2019 MACHINE LEARNING (MLUR01) Glasgow, Scotland, Dr Aristides (Aris) Moustakas https://www.prstatistics.com/course/machine-learning-using-r-mlur01/

— / —

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

---

## UK ModellingAdaptiveVariation Jun17-21

Spatial modelling and analysis of adaptive genomic variation (SPGN01)

https://www.prstatistics.com/course/spatial-modelling-and-analysis-of-adaptive-genomic-variation-spgn01/ This course will be delivered by Dr. Matt Fitzpatrick from the 17th - 21st June in Glasgow City Centre.

Course Overview: Local adaptation to climate and other environmental drivers increasingly is being studied at the molecular level using high-throughput sequencing methods, with applications spanning both model and non-model organisms. At the same time, statistical tools for modeling and mapping patterns of biodiversity have seen increasing application, including to the challenge of understanding the drivers of spatial variation in adaptive genomic variation and mapping these patterns under current and future climate. This 5-day course will provide the skill set necessary to analyze sequence data for signatures of natural selection and to apply spatial modeling techniques to these patterns to quantify and map population-level genetic variation using two spatial modelling algorithms V Generalized Dissimilarity Modelling (GDM) and Gradient Forest (GF).

The course will include introductory lectures, instruction on using the Linux command line for manipulation of genomic data, guided computer coding in R, and exercises for the participants, with an emphasis on visualization and reproducible workflows. Portions of each day will be allotted for students to work through their own datasets with the instructors.

This course is intended for research scientists, postdoctoral researchers, and graduate students interested in learning how to analyze genomic data for signals of adaptation using population genetic tools and the application of spatial modeling understanding and mapping landscape genomic patterns in R.

After successfully completing this course students will: 1) Understand the theory and techniques for detecting signals of natural selection using genomic data, focusing on multi-population and landscape approaches 2) Understand the statistical underpinnings of spatial modeling methods (GDM and GF) for analyzing and mapping adaptive genomic variation 3) Be able to develop, evaluate and apply GDM and GF for quantifying and mapping spatial genetic patterns 4) Estimate population-level vulnerability to climate change

Students are highly encouraged to bring their own data to the course.

Course Programme

Monday 17th V Classes from 09:30 to 17:30 Day 1 V Background and introduction 1) Introduction to approach 2) Data types (spatial, environmental, and genomic) 3) Considerations (quality control, SNP calling, filtering)

Tuesday 18th V Classes from 09:30 to 17:30 Day 2 V Natural Selection I 4) Introduction to the genomics of natural selection 5) Review of population genomic approaches to inferring selection 6) Implementing FST- and differentiation-outlier tests and interpreting results

Wednesday 19th V Classes from 09:30 to 17:30 Day 3 V Natural selection II 7) Principles of inferring selection from environmental association analyses 8) Review of landscape genomics approaches to inferring selection 9) Preparing SNP data from VCF and environmental data from rasters 10) Implementing multiple association methods (e.g., LFMM, RDA, etc.) and interpreting results

Thursday 20th V Classes from 09:30 to 17:30 Day 4 V Spatial Modeling I 11) Introduction to GDM and GF 12) Review of genetic and environmental data preparation 13) Interpreting model results 14) Model fitting / testing / validation / variable selection

Friday 21st V Classes from 09:30 to 16:30 Day 5 V Spatial Modeling II 15) Predictions & Applications of GDM / GF 16) Transforming environmental grids 17) Visualizing spatial variation in genetic composition 18) Calculating genetic differences between locations / times 19) Projecting patterns under climate change

Email oliverhooker@prstatistics.com

Check out our sister sites, www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. March 25th V 29th 2019 LANDSCAPE GENETIC DATA ANALYSIS USING R (LNDG03) Glasgow, Scotland, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg03/ 2. April 1st V 5th 2019 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy02/ 3. April 1st V 5th 2019

— / —

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

---

## UK PythonForBiologists Jun10-14

Introduction to Python for Biologists (IPYB06)

https://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb06/ This course will be delivered by Dr. Martin Jones from the 10th - 14th June in Glasgow City Center.

Course Overview:

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackle problems in their own research and (2) continue their Python education in a self-directed way. In biology Python is often applied to sequence analysis and data manipulation e.g. calculating base composition statistics, removing adapter sequences, translating DNA to protein, counting kmers, filtering tables etc. In this course we use these applications as examples during the exercises as a way of illustrating how to use the tools that Python has because it makes sense given the background of most of the people who attend. However, it should be possible to apply what you learn to any type of programming problem.

Course Program

Monday 10th V Classes from 09:30 to 17:30

Module 1: Introduction. We will start with a general introduction to Python and explain why it is useful and how learning to program can benefit your research. Some time will be taken to explain the format of the course. We will outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place. Core concepts introduced: source code; text editors; whitespace; syntax and syntax error; and Python versions.

Module 2: Output and text manipulation. This session will show students how to write very simple programs that produce output to the terminal and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that well rely on in future sessions. We will run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages and learn how to go about fixing them methodically. Core concepts introduced: terminals; standard output; variables and naming; strings and characters; special characters; output formatting; statements; functions; methods; arguments; comments.

Tuesday 11th V Classes from 09:30 to 17:30

Module 3: File IO and user interfaces. We will discuss about the importance of files in bioinformatics pipelines and workflows during this session, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects and a bit of discussion about how Python interacts with the operating system. The practical session is spent combining the techniques from session 2 with the file IO tools to create basic file-processing scripts. Core concepts introduced: objects and classes; paths and folders; relationships between variables and values; text and binary files; newlines.

Module 4: Flow control 1: loops. A discussion of the limitations of the techniques learned in session 3 quickly reveals that flow control is required to write more sophisticated file-processing programs, at this point we will progress on to the concept of loops. We look at the way in which Python loops work, and how they can be used in a variety of contexts. We explore the use of loops and lists together to tackle some more difficult problems. Core concepts introduced: lists and arrays; blocks and indentation; variable scoping; iteration and the iteration interface; ranges.

Wednesday 12th V Classes from 09:30 to 17.30

Module 5: Flow control 2: conditionals. We will use the idea of decision-making in session 5 as a way to introduce conditional tests and outline the different building-blocks of conditions before showing how conditions can be combined in an expressive way. We look at the different ways that we can use conditions to control program flow, and how we can structure conditions to keep programs readable. Core concepts introduced: Truth and falsehood; Boolean logic; identity and equality; evaluation of statements; branching.

Module 6: Organizing and structuring code. In session 6 we will discuss functions that we would like to see in Python before considering how we can add to our computational toolbox by creating our own. We examine the nuts and bolts of writing functions before looking at best-practice ways of making them usable. We also look at a couple of

— / —

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

---

## UYork GeneExpression Mar26-28

Dear all,

Registration is now open for the following course at the University of York in the UK. Please see the link below for details.

Many thanks

John Davey York Bioinformatics john.davey@york.ac.uk

Gene Expression Technologies 26-28 March 2019 https://www.york.ac.uk/biology/technology-facility/genomics/gl-courses/gl-gene-expression-course/ Gene expression technologies are central to a wide range of biological research projects, from medical research, such as looking at effects of drug candidates at the molecular level or understanding the cellular changes during cancer development, through to ecological work, such as measuring the changes in complex microbial communities under different environmental stresses.

This three-day course covers the dominant technologies that are used to measure gene expression: qPCR and RNASeq. For each technology, the principles of the technique are described followed by the details of the implementation.

The data produced by each methodology is described, and the steps required to go from raw data to reliable measures of differential gene expression are demonstrated. In addition, an outline of the preparation of samples is described, along with the quality control steps necessary to ensure that these technologies can produce reliable results.

Course Outline: - Introduction to Gene Expression - Preparation of RNA Samples - qPCR Methods and Data Analysis - RNASeq library preparation - Read alignment and pseudoalignment - Differential expression analysis - Functional analysis

John Davey <john.davey@york.ac.uk>

## Valencia Phylogenomics Oct7-11

Registration is open for the course 'Introduction to Phylogenomics' organized by Transmitting Science.

October 7th-11th, 2019 in Valencia, Spain

This workshop will introduce participants to the theory and tools for phylogenetic inference in the era of genome sequencing. Course material will focus on statistical methods for phylogeny estimation, software implementing these methods, applications of these methods to large molecular datasets, and discuss trade-offs and tools for improving the accuracy of phylogenomic analyses. In hands-on practical sessions, participants will gain experience working with bioinformatic and statistical tools for analyzing large datasets. The course is intended to facilitate ongoing or planned phylogenomics projects by students, so they are encouraged to notify instructors in advance about the topics of greatest relevance to their own work.

Instructors: Dr. Jeremy Brown ( Louisiana State University, jembrown@lsu.edu,); Dr. Robert Thomson (University of Hawaii, thomsonr@hawaii.edu) Coordinator: Dr. Soledad De Esteban-Trivigno (soledad.esteban@transmittingscience.org, Transmitting Science)

More information and registration: https://www.transmittingscience.org/courses/evolution/introduction-to-phylogenomics/ or writing to courses@transmittingscience.org

Robert C. Thomson Associate Professor Department of Biology University of Hawaii Honolulu, HI 96822

808.956.6476 http://thomsonlab.org/ thomsonr@hawaii.edu

## YaleU SustainingBiodiversityInfrastructure Jun12-14

Organized by ESA, funded by NSF: Discover Success with our 3-day course

Designed with leaders of digital data resources, collections, field stations, and laboratories in mind, Sustaining Biological Infrastructure: Strategies for Success is a 3-day course organized by ESA and funded by NSF to skyrocket the success of your project or program. Join us June 12-14th, 2019 at Yale University to learn from our expert faculty with decades of experience in fundraising, strategic planning, marketing, and communication and develop an action plan for your project.

We're also co-located with the Digital Data in Biodiversity Research < https://www.eventbrite.com/e/3rd-annual-digital-data-conference-methods-protocols-and-analytical-tools-for-specimen-based-tickets-54760252389 > Conference! If you come for the whole week and attend both course and conference, your conference fee is only $50. https://www.eventbrite.com/e/3rd-annual-digital-data-conference-methods-protocols-and-analytical-tools-for-specimen-based-tickets-54760252389 Access our colleague discount: Our alumni have found that bringing a colleague to learn and brainstorm with is invaluable- so we're offering $200 off the second registration!

Learn more at www.esa.org/sbi . Not sure if your project or program is a good fit? Please reach out to us, and we will tell you more about the course- emily@esa.org.

The May 17th deadline is approaching- but apply < https://esa.org/sbi/how-to-apply/ > soon to access reduced-rate lodging and secure your spot! www.esa.org/sbi/how-to-apply Emily Mastrianni <emily@esa.org>

## YosemiteNatlParl Symbiosis May17-19

Dear Colleagues,

Registration is now OPEN for the 9th Annual Yosemite Symbiosis Workshop!

EARLY BIRD REGISTRATION DUE IN 5 DAYS

The Ninth annual Yosemite Symbiosis Workshop will take place on May 17-19, 2019 at the Sierra Nevada Research Institute, Yosemite National Park.

Keynote speaker 2019: Dr. Martha (Molly) S. Hunter from The University of Arizona!

Information about our meeting:

Why: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis and microbiome research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our ninth annual meeting and we have been consistently attracting scientists from all over the country and overseas.

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

When: The talks and formal meeting will be held 18-19, 2019, though we make accommodation arrangements available for attendees to arrive on Friday the 17th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Past attendees and talks can be found here: http://www.sachslab.com/symbiosis-2015.php Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room. Costs: See details in the registration page (up soon). We will only be able to accept credit card payments this year

Register here: < https://t.co/i1hTGwqI15 > https://snri.ucmerced.edu/form/symbiosis-workshop-2019-registration Pay here:

https://commerce.cashnet.com/cashneti/selfserve/EditItem.aspx?PC˜n03_W2-SYWK&ItemCount=1 Payment is required to confirm your registration.

Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

–

*Joel L. Sachs* *Professor & Vice Chair* Department of Evolution Ecology & Organismal Biology Department of Botany & Plant Sciences (Cooperating Member) Department of Microbiology & Plant Pathology (Cooperating Member) University of California, Riverside

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

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

---

## Yunnan Metabarcoding Oct15-26

Yunnan Metabarcoding School 2019 (China)

We are pleased to announce the Yunnan Metabarcoding School, 2019 edition.

DNA metabarcoding is a rapidly evolving method of eukaryotic biodiversity assessment that combines two technologies: DNA taxonomy and high-throughput DNA sequencing. Applications range widely, from environmental impact assessment, to diet reconstruction, to paleoecology, to targeted species detection, among others. Metabarcoding draws from methods developed in field ecology, systematics and phylogenetics, molecular biology, bioinformatics, and statistics.

The 2019 Yunnan edition is allied to the metabarcoding school started by the metabarcoding.org team and shares some of the same instructors. This edition will be hosted by the Kunming Institute of Zoology and is financed by a special fund from the Chinese Academy of Sciences (CAS) focused on aspects of China's Belt and Road Initiative (BRI). As such, the school will be preceded by a separate, one-day international conference to launch a Horizon Scanning exercise for the BRI.

The Yunnan Metabarcoding School will be held from 15 - 26 October 2019, in two sections.

14 Oct 2019: Belt and Road Initiative (BRI) Conference, Horizon Scanning 15-21 Oct 2019: Metabarcoding School I (MSI): Metabarcoding & Metagenomics 22-26 Oct 2019: Metabarcoding School II (MSII): R & Laboratory Practicals

The school will fund airfares, in-China ground travel, lodging, and meals for 30 students (including Ph.D. students, postdocs, and professional researchers, defined broadly). Students will be responsible for providing a suitable laptop computer (details below) and paying for their own out-of-China ground travel, tourist visa, and personal purchases.

MSI: Our goal is to host 15 students from within China and 15 students from other countries.

MSII: We expect approximately half the MSI students to stay on for MSII.

Application, selection criteria, and preparation

Candidates can apply for the school by sending an English-language email to the following address before

31 May 2019: metabarcoding_CAS at mail.kiz.org

The email must contain the following in a single PDF attachment (no portrait photos):

1. a brief CV 2. a letter of motivation indicating how the applicant's research will benefit from DNA-based methods of biodiversity assessment (please first review the curriculum below, as we will cover both PCR-based and metagenomic methods). The core of the letter is a 150-200 word description of your research project. Please indicate if you wish to attend MSI or MSI and II.

In the (likely) case that we receive more than 30 applications (or more than 15 applications from outside China), preference will be given to students

1. whose described project in the cover letter is well developed and likely to benefit immediately from the skills learned, 2. who come from a Belt and Road Initiative (BRI) country 3. who are able to demonstrate basic fluency in molecular-ecology and bioinformatic techniques (e.g. can use Unix and R on the command line, can teach how PCR works) 4. who have sufficient English-language skills

Students must bring a laptop computer with the following capacity: 8 GB RAM, 150 GB SSD free storage, and natively boots into macOS or Ubuntu Linux.

We will assign preparatory homework to the accepted students.

Instructors

Â Kristine Bohmann (Natural History Museum of Denmark) Â Frédéric Boyer (LECA, CNRS, France) Â Anthony Chariton (Macquarie University, Australia) Â Shyam Gopalakrishnan (Natural History Museum of Denmark) Â Min Tang (China Agricultural University) Â Shanlin Liu (Natural History Museum of Denmark) Â Douglas Yu (Kunming Institute of Zoology; University of East Anglia, UK) Â Additional instructors from the Kunming Institute of Zoology

Curricula

The school will be divided into lectures and practicals, taught in English, with Chinese-fluent instructors present.

Metabarcoding School I: The lectures will cover different aspects of DNA metabarcoding and metagenomics as applied to eukaryotes. The obitools and DAMe practicals will let students run metabarcoding pipelines from raw sequences to species x sample tables, plus visualisations in R. The i/eDNA practical will introduce students to water sampling using filters. We will also run computer-based practicals in PCR primer design, taxonomic assignment, and metagenomic methods as applied to eukaryotic species (see Ji et al. 2019, Peel et al. 2019). Note that this course does not cover bacterial/archaeal/viral biodiversity.

All students will have to give a flash talk (7 mins) about their project and how it will benefit from DNA-based methods of biodiversity assessment. In the evenings, we will run a "Saw One, Did One, Now Teach One" exercise, in which students will divide into groups of three and

— / —

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

## 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.