

---

# E v o l D i r

May 1, 2019

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

---

## Foreword

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at [Golding@McMaster.CA](mailto: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 .....	16
Jobs .....	51
Other .....	73
PostDocs .....	80
WorkshopsCourses .....	117
Instructions .....	134
Afterword .....	135

---

## Conferences

Albufeira Portugal VultureConservation Oct1-4 ..... 2	Padova Italy AncientDNA Apr15Abst ..... 8
Berlin WildlifeConservation Sep30-Oct2 AbstractDead- line ..... 3	Padova Italy Evolution Sep1-4 ISEBawards ..... 8
Berlin Wildlifeconservation Sep30-Oct2 AbstDeadlin- eApr30 ..... 3	Padova Italy ISEB Sep1-4 ..... 9
Bristol SystematicsAssociation Jun17-19 ..... 4	PalmSprings EvolutionMobileDNA Jun23-28 ..... 9
Bristol Systematics Jun17-19 ..... 4	Portland Oregon Sex Asex Jun2-4 ..... 10
Freiburg GalaxyCommunity Jul1-8 ..... 4	Portland Oregon SexAsex Jun2-4 ..... 10
FrenchAlps GenomicsProbabilisticModeling Oct6-9 . 5	Providence RI Evolution Jun21-25 ..... 11
Ghent Polyploidy Jun11-14 ..... 5	Seville SpanishSocEvolBiol Feb5-7 ..... 12
Goettingen ReticulateEvolution Nov22-24 ..... 6	SMBE SatelliteRegionalMeetings2020 CallProposals 12
Lausanne Drosophila Sep5-8 ..... 6	Split Croatia EvoKE EvolutionOutreach Sep26-29 . 13
London MolluscComparativeGenomics Sep16-17 .... 7	Tucson PlantEvol Jul27-31 ..... 13
Marseilles EvolBiol Sep24-27 ..... 7	UCambridge EvolutionaryGenetics Apr16-18 ..... 14
NewHampshire GordonEvoGenomics Jul14-19 ..... 7	UK MolluscanGenomics Sep16-17 programme registra- tion ..... 15

---

### Albufeira Portugal VultureConservation Oct1-4

We, the Vulture Conservation Foundation, will be bringing together scientists, conservationists and the public in the Algarve, Portugal for an international congress looking at the latest research and conservation of vultures in Europe and beyond, in our first European Vulture Conference. <https://www.4vultures.org/european-vulture-conference/> or <https://www.eventbrite.com/e/european-vulture-conference-2019-tickets-59441903333>

Confirmed key-note speakers:

Andre Botha (Endangered Wildlife Trust), speaking about vulture conservation in Africa François Sarrazin (University Sorbonne & Paris Natural History Museum), who will give a talk on restoration and conservation of scavengers populations Iñigo Fajardo (Junta de Andalucía), speaking about wildlife-crime and vulture conserva-

tion Olivier Duriez (University of Montpellier), presenting on social foraging ecology of vultures Ran Nathan (University of Jerusalem), speaking on movement ecology of vultures

Several symposia are also being planned, including on:

Current status of supplementary feeding strategies and where to next? Monitoring and mitigating disturbance: should we hide or reveal important vulture areas? Human aspects of vulture conservation: ecosystem services; social perceptions; promoting positive change Vultures and human infrastructures (wind energy, power lines, railways, airports)

Abstract submission currently forseen until the end of May with most likely extension of the deadline - so check it out and register to join us for four days on Vultures!

Vulture Conservation Foundation

Franziska Lorcher

Scientific and conservation coordinator

VCF- Vulture Conservation Foundation Wuhlrstrasse 12,

CH-8003 Zurich

Tel.: +41 44 450 68 14 f.loercher@4vultures.org  
[www.4vultures.org](http://www.4vultures.org) \*Visit the VCF also on our  
 facebook and twitter site: [www.facebook.com/vultureconservationfoundation](https://www.facebook.com/vultureconservationfoundation) and [www.twitter.com/4vultures](https://www.twitter.com/4vultures)

Franziska Lorcher <f.loercher@4vultures.org>

---

### Berlin Wildlife Conservation Sep30-Oct2 AbstractDeadline

Dear colleagues,

ABSTRACT SUBMISSION for WRC2019 ends on Tuesday, APRIL 30, 2019!

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 - Conservation genetics (poster presentations) - Importance of social behaviour and application of social networks across wildlife biology and conservation (poster presentations) - 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?

Find all important information on abstract submission here: <http://www.izw-berlin.de/abstract-submission-373.html> . SUBMIT YOUR ABSTRACT NOW at <https://www.bayceer.uni-bayreuth.de/wrc2019/en/> . When submitting your abstract, you will be asked to register.

If you wish to attend Wildlife Research and Conservation 2019 (September 30 - October 2, 2019), register before April 30 to benefit from the early bird discount!

REGISTRATION FEES: Early bird registration fees (until April 30, 2019): Early bird fee: 210 Euro Early bird student fee: 130 Euro

Regular registration fees (after April 30, 2019): Regular fee: 280 Euro Regular student fee: 170 Euro

REGISTER NOW to secure your early bird discount: <https://www.bayceer.uni-bayreuth.de/wrc2019/en/> . CONFERENCE VENUE: Botanical Museum and Botanic Garden Berlin Konigin-Luise-Str. 6-8 14195

Berlin Germany How to get to the venue: <https://www.bgbm.org/en/how-get-here>

Please circulate information about Wildlife Research and Conservation 2019 by email, twitter, facebook and other social media! For those who have twitter we ask you to use #WRC2019Berlin to refer to the conference. Many thanks!

We look forward to welcoming you and your colleagues 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](mailto:symposium@izw-berlin.de) Conference website: <http://www.izw-berlin.de/welcome-234.html> Abstract submission and online registration: <http://www.bayceer.uni-bayreuth.de/wrc2019/en/> "Prugel, Josepha" <prugel@izw-berlin.de>

---

### Berlin Wildlife Conservation Sep30-Oct2 AbstDeadlineApr30

Dear colleagues,

There are only 4 days left to submit your abstract for Wildlife Research and Conservation 2019!

ABSTRACT SUBMISSION DEADLINE: Tuesday, April 30, 2019

Submit your abstract now: <https://www.bayceer.uni-bayreuth.de/wrc2019/en/> 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 - Conservation genetics (poster presentations) - Importance of social behaviour and application of social networks across wildlife biology and conservation (poster presentations) - 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?

Find all important information on abstract submission

here: <http://www.izw-berlin.de/abstract-submission-373.html> When submitting your abstract, you will be asked to register. If you wish to attend Wildlife Research and Conservation 2019 (September 30 - October 2, 2019), register before April 30 to benefit from the early bird discount!

Register now to secure your early bird discount: <https://www.bayceer.uni-bayreuth.de/wrc2019/en/> Please circulate information about Wildlife Research and Conservation 2019 by email, twitter, facebook and other social media! For those who have twitter we ask you to use #WRC2019Berlin to refer to the conference. Many thanks!

We look forward to welcoming you and your colleagues in Berlin!

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

CONTACT: Conference Organisation Leibniz Institute for Zoo and Wildlife Research (IZW) 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](mailto:symposium@izw-berlin.de) Conference website: [www.izw-berlin.de/welcome-234.html](http://www.izw-berlin.de/welcome-234.html) Online registration and abstract submission: [www.bayceer.uni-bayreuth.de/wrc2019/en/](http://www.bayceer.uni-bayreuth.de/wrc2019/en/) "Prugel, Josepha" <[pruegel@izw-berlin.de](mailto:pruegel@izw-berlin.de)>

---

## Bristol Systematics Association Jun17-19

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. The keynote speakers include Fredrik Ronquist, Tandy Warnow, and Tom Brooks. Abstracts can be submitted until 24th May.

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  
Jordi Paps <[jordipaps@gmail.com](mailto:jordipaps@gmail.com)>

---

## Bristol Systematics Jun17-19

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. The keynote speakers include Fredrik Ronquist, Tandy Warnow, and Tom Brooks.

Early bird registration ends in 5th April 2019 and abstracts can be submitted until 26th April. There are especial 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  
Jordi Paps <[jordipaps@gmail.com](mailto:jordipaps@gmail.com)>

---

## Freiburg Galaxy Community Jul1-8

2019 Galaxy Community Conference (GCC2019) 1-8 July, Freiburg, Germany <https://galaxyproject.org/gcc2019> Deadlines 22 April: Oral Presentation and Lightning Talk abstracts due 17 May: Early registration ends

The 2019 Galaxy Community Conference (GCC2019) will be held 1-8 July in Freiburg, Germany. GCC brings together hundreds of faculty, clinicians, researchers, and students, all working in and supporting data intensive science that is accessible, sharable and reproducible.

GCC2019 features oral presentations, lightning talks, posters, demos, birds-of-a-feather gatherings (BoFs), training, a CollaborationFest, and plenty of opportunities for networking.

Presentations will cover the full spectrum of Galaxy applications, enhancements and deployments. If you are working in data intensive science then GCC2019 is an ideal conference for sharing your work, learning from

others, and finding new collaborators.

Present your work! Abstract submission for talks, lightning talks, demos and posters is now open. If you work in data-intensive science then please consider presenting your work at GCC2019. This is a chance to present to 200+ researchers, all addressing challenges in data intensive science. Review of oral presentations starts on 22 April. Submit an abstract (or two) now!

Registration Early registration starts at 49/day for students and postdocs, and 79 / day for other academics and non-profit researchers. Childcare is available and travel fellowships are available as well. Early registration ends 17 May, when rates go up by 60%. So, register early.

About Galaxy Galaxy (<https://galaxyproject.org/>) is a platform for data integration and analysis in the life sciences. It enables researchers to build, run, share, and repeat their own complex computational analyses using only a web browser and without having to first learn system administration and command line interfaces.

The Galaxy Project is driven by a vibrant community who publish workflows and analyses, wrap new tools, maintain and enhance the source code, provide support, and write documentation and training materials. Galaxy is open-source and freely available, and is deployed in hundreds of organizations, running on everything from laptops through supercomputers to public and private clouds. Over 150 of these platforms are publicly available and can be used with little or no setup. Thousands of tools have been ported to Galaxy (“wrapped”) and are deployable from the Galaxy Tool Shed. Galaxy was developed to support life science research, but the software is domain agnostic and is now used in domains as diverse as natural language processing, constructive solid geometry, and social science.

We hope to see you in Freiburg! GCC2019 Organizers

– <https://galaxyproject.org/gcc2019/> <https://galaxyproject.org/> <https://usegalaxy.org/> Dave Clements <clements@galaxyproject.org>

---

**FrenchAlps**  
**GenomicsProbabilisticModeling**  
**Oct6-9**

Dear Colleagues,

We are pleased to announce the 5th Probabilistic Mod-

eling in Genomics meeting (ProbGen19), to be held in Aussois, in the French Alps, Oct 6-9, 2019 (<https://-probgen2019.sciencesconf.org/>).

The goal of this meeting is to cover a wide variety of topics in genomics, ranging from population genomics to systems biology and cancer genomics, with a particular focus on the use of novel mathematical and computational models and inference methods to address timely and important biological questions. What makes the meeting special, in our view, is that it has substantial mathematical and theoretical depth yet remains well grounded in the practical and scientific concerns of modern genomics. We invite abstract submissions on a range of topics including functional genomics, molecular evolution, phylogenetics, epidemiology, methods for genome-wide association studies, quantitative genetics, etc.

We will have three keynote speakers: Barbara Engelhardt (Princeton University) Gil McVean (Big Data Institute, University of Oxford) Caroline Colijn (Simon Fraser University, Vancouver)

Alongside invited speakers, oral presentations will be selected from submitted abstracts. We particularly encourage abstract submissions from junior investigators, including postdoctoral fellows and graduate students. A few grants will be available for students and postdocs.

Best wishes and hope to see some of you at the meeting,

Organizing committee: Laurent Duret, Michael Blum, Nicolas Lartillot & Franck Picard

ProbGen steering committee: Thomas Bataillon, Richard Durbin, Barbara Engelhardt, Anders Krogh, Gerton Lunter, Molly Przeworski, Adam Siepel, Yun S. Song

Laurent Duret <Laurent.Duret@univ-lyon1.fr>

---

**Ghent Polyploidy Jun11-14**

International Conference on Polyploidy

Abstract submission deadline 11 April 2019

The International Conference on Polyploidy will present cutting edge research into the importance of polyploidy and whole genome duplication for genetics, evolution and ecology. For the 2019 meeting, which will take place at the beautiful city of Ghent, we are trying to put together an exciting program focusing on many different

aspects of polyploidy, such as the short- and long-term ecological and evolutionary consequence of polyploidy for plant and animal systems, but also polyploidy in somatic cells and clonal populations will be discussed.

The International Conference on Polyploidy will present a unique opportunity to meet and discuss with colleagues, get updated on the newest developments and insights into recent and ancient polyploidy and whole genome duplication, and will provide unique possibilities to network and discuss collaborations. We are delighted to announce that Dr. Ilia Leitch (Kew Gardens) has agreed to deliver the plenary lecture on Tuesday afternoon, June 11th, opening the meeting.

Prof. Dr. Yves Van de Peer Department of Plant Biotechnology and Bioinformatics, Ghent University VIB - UGent Center for Plant Systems Biology Technologiepark 71, B-9052 Ghent, Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 email: yves.vandeppeer@psb.ugent.be

Yves Van de Peer <yves.vandeppeer@psb.vib-ugent.be>

---

## Goettingen Reticulate Evolution Nov22-24

Dear colleagues,

the 61st Phylogenetic Symposium with the topic “\*Reticulate Evolution\*” will take place at the University of Göttingen from November 22-24, 2019.

Ever since Darwin’s theory of evolution suggested a common ancestry of all life on earth phylogenetic trees have been used to visualize its relationships. However, evolutionary histories cannot always be adequately represented as bifurcating phylogenetic trees. Prime example is the symbiogenic origin of eukaryotes from the merger of an archaean and a bacterium. Besides symbiogenesis, other processes such as horizontal gene transfer, hybridization, divergence with gene flow result in reticulation of phylogenetic trees, the origination of lineages through complete or partial merging of two or more ancestor lineages. Reticulate evolution is well documented across the tree of life, including many examples from plants and animals. We are looking forward to bring together experts from different backgrounds to summarize recent progress in the field of reticulate evolution.

Confirmed speakers (in alphabetical order):

\*Eric Baptiste\*(Université Pierre et Marie Curie,

France)

\*Marta Barluenga\*(Museo Nacional de Ciencias Naturales Madrid, Spain)

\*Mathilde Cordellier\*(University of Hamburg, Germany)

\*Judith Fehrer\*(Academy of Sciences of the Czech Republic, Prague, Czech Republic)

\*Christoph Oberprieler\*(University of Regensburg, Germany)

\*Bengt Oxelman\*(University of Gothenburg, Sweden)

\*Pamela S. Soltis\*(University of Florida, USA)

\*Alexander Suh\*(Uppsala University, Sweden)

Registration for this symposium is free of charge, but we will charge for the participation at the conference dinner. Please register via email to uschach@gwdg.de. Poster presentations are welcome and the deadline for abstract submission to the same email address is October 31, 2019. Further information and updates will be available at:

<https://www.uni-goettingen.de/de/-phylogenetic+symposium+2019/605388.html> Sincerely,

Christoph Bleidorn

Elvira Hörandl

Prof. Dr. Christoph Bleidorn Georg-August-Universität Göttingen Johann-Friedrich-Blumenbach Institute for Zoology & Anthropology Animal Evolution and Biodiversity Untere Karspuele 2 37073 Göttingen Germany

Follow me on twitter! [https://twitter.com/C\\_Blei](https://twitter.com/C_Blei) “Bleidorn, Christoph” <cbleido@gwdg.de>

---

## Lausanne Drosophila Sep5-8

The EDRC 2019 takes place in Lausanne (Switzerland) on 5-8 September. The conference covers any research topic involving Drosophila, including a session on evolutionary biology and population genetics and a special workshop on interactions between sexes. More information at [edrc2019.com](http://edrc2019.com). Early-bird registration and abstract submission deadline: April 30.

Tadeusz Kawecki <tadeusz.kawecki@unil.ch>

---

**London**  
**MolluscComparativeGenomics**  
**Sep16-17**

Pearls of wisdom: synergising leadership and expertise in molluscan genomics Monday 16 - Tuesday 17 September 2019 Kavli Royal Society Centre, Chicheley Hall, Newport Pagnell, Buckinghamshire, MK16 9JJ, UK Organised by Dr Angus Davison and Dr Maurine Neiman

I wanted to let you know that the Royal Society is holding a Theo Murphy meeting, Pearls of wisdom: synergising leadership and expertise in molluscan genomics, from 16 - 17 September 2019. The meeting is a 2-day event, held at Chicheley Hall, Buckinghamshire, and has a poster session for increased networking.

Although molluscs are ecologically, economically, and medically important, progress in understanding their biology has been limited by problems associated with genome sequencing and assembly. As technology breakthroughs overcome these challenges, this meeting will bring together experts in molluscan biology and genomics to share best practice in how to use these developments in elucidating the biology of this diverse and ill-understood phylum. More information on the speakers and programme is available on the website < <https://royalsociety.org/science-events-and-lectures/-2019/09/pearls-of-wisdom/> >.

Registration for this meeting is free, but participants are required to register in advance of the meeting.

Sophia Coe Scientific Programmes Officer

T +44 20 7451 2503

The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG royalsociety.org

Registered Charity No 207043

This email is sent on behalf of The Royal Society, 6-9 Carlton House Terrace, London SW1Y 5AG, United Kingdom.

“Coe, Sophia” <Sophia.Coe@royalsociety.org>

---

**Marseilles EvolBiol Sep24-27**

23rd Evolutionary Biology Meeting 24-27 /09.

Goal : To gather together International scientists interested in the mechanisms of evolution that generate the incredible diversity of living things found on Earth .

DL June 30.

web : aeb.fr twitter :EvolBiolMeetingMarseilles

Best regards Pierre

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

---

**NewHampshire**  
**GordonEvoGenomics Jul14-19**

Ecological and Evolutionary Genomics Gordon Research Conference

July 14 - 19, 2019

\*\*\*SCHEDULE NOW ONLINE\*\*\* \*\*\*More than 10 talks will be selected from abstract submitted by young investigators (trainees and PIs)\*\*\*

Chairs : Christian Landry and Angela Douglas Vice-chairs : Camille Berthelot and Sarah D. Kocher

See list of invited speakers and details here:

<https://www.grc.org/ecological-and-evolutionary-genomics-conference/2019/> \*\*\*Note new location, closer to Boston (70 min) and Manchester (20 min) airports\*\*\*

Southern New Hampshire University 2500 North River Road Manchester, NH, US

Meeting description Genomics tools have never been so powerful and accessible to biologists interested in how the interplay between ecological and evolutionary forces is shaping biodiversity. The 2019 Gordon Research Conference on Ecological and Evolutionary Genomics will explore how the genome-scale processes that underpin organismal phenotypes interact with ecological and evolutionary processes over multiple spatiotemporal

scales. The meeting will be preceded by a Gordon Research Seminar (GRS), which will provide opportunities for early career researchers (students and postdocs) to present their projects and will include a special mentorship session. Topics highlighted at the meeting will include: the ecological and evolutionary significance of novel genes and variation in genome architecture, including genomic conflicts; the role of hybridization and introgression as drivers of diversity; genome-scale perspectives on the role of the microbiome in host adaptations; and the increasing contribution of genomics to explanations of ecosystem function. This meeting will also bring the latest technological developments in genomics and genome manipulation, emphasizing their application to non-model species. Join us to participate in creative discussions in an inclusive social and scientific atmosphere, to empower the future research in the field.

Christian Landry <Christian.Landry@bio.ulaval.ca>

---

### Padova Italy AncientDNA Apr15Abst

Please send your abstract to [aaiconference2019@gmail.com](mailto:aaiconference2019@gmail.com) using the template provided on the website ( [www.aaiconference2019.it](http://www.aaiconference2019.it) ) and specifying whether it is intended for a talk, a poster or either of them. Please note: only one abstract per registered presenting author will be considered - Abstract submission deadline (final extension): \*15 April 2019\*

Presenters will be notified by email about acceptance of their abstract and assignment to a talk/poster by 15 May 2019

The bi-annual meeting of the Italian Anthropological Association aims at bringing together the various streams of Biological Anthropology in a three-day long international conference. In recent years a number of ground breaking discoveries have been made possible by several technological advances in the fields of ancient and modern genomics, isotopic analysis and virtual anthropology. Also, new developments in the field of applied anthropology have changed our approach to the study of living and past human populations. All these, and other topics, will be distilled in this year' conference, in search of what will be the next relevant research questions. In addition, a joint symposium with SIBE will promote a dialogue among invited speakers on “what is

a population” and on communication of science.

The conference will be structured in four main sessions, harboring contributions from all fields of Biological Anthropology: 1) Hominids and Palaeolithic humans - covering all subjects up to the Palaeolithic 2) From prehistory to history - from the Neolithic and Bronze Age cultural revolutions and demographic expansions all the way to contemporary populations 3) Contemporary human populations - mostly based on living populations, with support from ancient data 4) Applied Anthropology - including biomechanics, biomedical, forensic and all other branches of applied Anthropology.

Looking forward to seeing you all there, Luca Pagani, Researcher at the University of Padova, Italy on behalf of the organizing committee

Luca Pagani <[lp.lucapagani@gmail.com](mailto:lp.lucapagani@gmail.com)>

---

### Padova Italy Evolution Sep1-4 ISEBawards

The Italian Society for Evolutionary Biology is pleased to announce the ISEB Awards that will be assigned during its 8th Congress to be held in Padova on 1-4 September 2019 (<https://sibe2019.sibe-iseb.it>)

Doctor Darwin Prize

Established by the Italian Society of Evolutionary Biology with the aim to stimulate interest and research related to the Evolutionary Medicine. The award consists in the amount of 1,000 granted to young researchers (up to 40 years old) members of the SIBE.

SIBE Prize

The Italian Society of Evolutionary Biology especially wants to promote the participation to the Congress of young researchers (younger than 40 years old), with a prize of 500 for the best published (or in press) article on Evolutionary Biology, in the period 2018-2019.

NEW!!! Best outreach project

The Italian Society for Evolutionary Biology decided to establish, for the first time, a prize of 500 for the best project of science communication, outreach, dissemination, and popularization in the fields of evolutionary biology, implemented in the period 2017-2019.

Best poster

The best poster will be voted by the congress attendees during the Congress, 300 for the winner.



Best PhD student presentation

The best PhD presentation will be voted by the scientific committee of the Congress, 300 for the winner.

Please find all details about rules and procedures for assignment on SIBE 2019 website

<https://sibe2019.sibe-iseb.it/awards.php> We look forward to receiving your applications,

Lisa Locatello on behalf of the Organizing Committee  
Department of Biology University of Padova, Italy

Italian Society for Evolutionary Biology: [www.sibe-iseb.it](http://www.sibe-iseb.it) Lisa Locatello <lisa.locatello@unipd.it>

---

## Padova Italy ISEB Sep1-4

The Italian Society for Evolutionary Biology (ISEB) is pleased to announce its 8th Congress that will be organized by the Department of Biology of the University of Padova on 1-4 September 2019.

The congress will be hosted in two wonderful locations of the University of Padova: the historical Botanical Garden, the most ancient botanical garden in the world and UNESCO world heritage, and the 'Galileo Galilei' Main Hall of the XVI century Palazzo Bo.

SIBE 2019 warmly welcomes all professional and non-professional Evolutionary Biologists, as well as teachers and science writers. Through an informal and easygoing atmosphere, the Congress aims at promoting exchanges and synergies among scientists and/or amateur, and is especially addressed to young students and scientists.

The Organizing Committee and the Scientific Committee are pleased to invite you to submit an abstract for consideration via the online participant portal <https://sibe2019.sibe-iseb.it/call-for-abstracts.php> Deadline: 15 May 2019

Six symposia, encompassing many different fields in evolutionary biology and with eminent invited speakers, may host your contribution:

1) Units of diversity: tools, strategies and case-studies to define species limits. Invited speaker: Birgit Schlick-Steiner (University of Innsbruck, Austria) 2) Evolution in marine environments. Invited speaker: Lloyd Peck (British Antarctic Survey, Cambridge, UK) 3) Social behaviour: ecology and evolution. Invited speaker: Daniela Campobello (University of Palermo, Italy) 4) Conservation and evolution. Invited speaker: Christo-

pher Clements (University of Bristol, UK) 5) Phylo3: Phylogenetics, Phylogenomics & Phylogeography. Invited speaker: Daniele Silvestro (University of Gothenburg, Sweden and University of Lausanne, CH) 6) Population genetics and population genomics (organized in partnership with the Italian Anthropological Association on September 4th) Invited speaker: Montgomery Slatkin (University of California at Berkeley, CA, USA)

and of course you can't miss the rich and surprising programme of social events!

Please, visit SIBE 2019 website <https://sibe2019.sibe-iseb.it> for all detailed information about the Congress and to register.

Looking forward to seeing you in Padova,

Lisa Locatello on behalf of the Organizing Committee

Lisa Locatello Department of Biology University of Padova <lisa.locatello@unipd.it>

Italian Society for Evolutionary Biology: [www.sibe-iseb.it](http://www.sibe-iseb.it) Lisa Locatello <lisa.locatello@unipd.it>

---

## PalmSprings EvolutionMobileDNA Jun23-28

FASEB Mobile DNA is coming this summer!

The Mobile DNA Conference: 25 Years of Discussion and Research June 23-28, 2019 in Palm Springs, California. Please be aware that registration for the 2019 meeting is NOW OPEN and the early registration deadline is fast approaching.

For detailed information, visit <https://src.faseb.org/-mobile-dna/> Important dates: Advance registration deadline Wednesday, May 8, 2019 Last day to register Saturday, June 1, 2019

Travel awards are available from FASEB and other sponsoring organizations. <http://www.faseb.org/Science-Research-Conferences/Awards-and-Travel-Grants.aspx> (Note: The Society for Molecular Biology and Evolution (SMBE) is sponsoring four travel awards, \$500 each, to junior evolutionary biologists specifically for this conference.)

Organizers for this year's meeting are: David Ray - Texas Tech University Wenfeng An - South Dakota State University Victoria Belancio - Tulane University Stephane Boissinot - NYU Abu Dhabi Richard Cordaux - Centre National de la Recherche Scientifique

Please contact any of us if you have questions not answered at the website.

See you this summer!

–

David A. Ray

Associate Professor Department of Biological Sciences Texas Tech University Phone: (806) 834-1677 [www.davidraylab.com](http://www.davidraylab.com) [www.crocgenomes.org/-david.4.ray@gmail.com](http://www.crocgenomes.org/-david.4.ray@gmail.com)

Even the best of us have bad days. “I am very poorly today and very stupid and hate everyone and everything.”  
- Charles Darwin - Oct. 1, 1861

David Ray <david.4.ray@gmail.com>

## Portland Oregon Sex Asex Jun2-4

Early bird registration for AGA 2019 closes this coming Monday, April 15! Don't forget to register.

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 Solem Stoeckel, INRA Rennes, France Jennifer Anderson, Uppsala University, Sweden Mercedes Burns, University of Maryland Jeanette Whitton, University of British Columbia

ccough-schulze@cvm.tamu.edu

## Portland Oregon SexAsex Jun2-4

June is soon!

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

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>  
Key Distinguished Lecturer: Sally Otto, University of British Columbia, Canada

Selective interference and the evolution of sex

Invited Speakers:

Matthew Hartfield, University of Edinburgh, Scotland

Determinants of genetic diversity in facultative sexuals

Laura Katz, Smith College

Germline/soma distinction across the (eukaryotic) tree of life

Stacy Krueger-Hadfield, University of Alabama, Birmingham

Whats ploidy got to do with it? Mating system variation in haplodiplontic algae

Curt Lively, Indiana University

Through the looking glass: host/parasite coevolution and sex

Tanja Schwander, Universite de Lausanne, Switzerland

Genomic consequences of asexual reproduction in animals

Rebecca Zufall, University of Houston

Amitosis and the Evolution of Asexuality in Tetrahymena ciliates

Catherine Rushworth, UC Davis

Disentangling the fitness effects of hybridization and asexuality in natural plant populations

Jennifer Anderson, Uppsala University, Sweden

Life history lessons from Neurospora crassa and other filamentous fungi

Solemn Stoeckel, INRA Rennes, France

The dynamics of genetic diversity in partially clonal populations

Nadia Singh, University of Oregon

Variation in Recombination Rate: Causes and Consequences

Mercedes Burns, University of Maryland Baltimore County

Maintenance of sex via geographic heterogeneity and facultative parthenogenesis in a Japanese harvestman

Jeannette Whitton, University of British Columbia, Canada

How important is male function in the maintenance of sex? Data from plant systems

Oral Presenters (Short talks):

Elora Lopez, Stanford University

Patterns and frequency of variation among asexual clones in a long-lived coral species

Karen Barnard-Kubow, University of Virginia

Mechanisms and consequences of balancing selection in a model cyclic parthenogen

Trung Huynh, University of Texas Arlington

Differentially expressed genes between reproductive modes: a primer to identifying the genetic basis of facultative apomixis in *Daphnia*

Sissi Donna Lozada Gobillard, Institute of Biochemistry and Biology, Potsdam, Germany

Patterns of genetic diversity of plant species occurring in a metapopulation wetland system is explained by clonality rather than dispersal mechanisms

Linnea Sandell, University of British Columbia

Sex, drugs, and mating competition: effects of frequent outcrossing in *Saccharomyces cerevisiae*

Jamie Schwock, Portland State University

Somatic mutation and cell lineage selection during vegetative growth promotes rapid adaptation in plants

Mark Smithson, Washington State University

Epigenetic variation in asexual adaptation: explaining shell shape variation

Karel Janko, Institute of Animal Physiology and Genetics, Czech Republic

Why do animals abandon sex? On the interconnection between asexuality hybridization and speciation

Anjanette Baker <theaga@theaga.org>

## Providence RI Evolution Jun21-25

\*\*\*Early registration discount ends 10 PM Eastern Daylight time on Apr. 15, 2019\*\*\*

EVOLUTION 2019 – Annual joint meeting of the ASN/SSB/SSE June 21-25, Rhode Island Convention Center in Providence, RI <http://www.evolutionmeetings.org> Talks are accepted on a first-come, first-served basis until May 15 or until capacity is reached, WHICHEVER IS EARLIER. It is possible that capacity will be reached prior to the Apr. 15 early registration deadline. You can only access the talk submission process by first completing online registration. A noticed will be posted on the meeting website when talks are full.

ALL posters are accepted until May 15.

Also closing on Apr 15: - Application for various forms of travel support including ASN, SSE and ESEB travel supplements and volunteering at the conference - Application for Mayr and Hamilton awards \*\*\*Eligible students wanting to apply should register for a regular talk ASAP (and tick the appropriate box) as these may fill prior to Apr. 15 (you can edit your talk details later)\*\*\*

\*\*Answers to nearly all question you may have about the conference can be found on the meeting website.

OTHER INFORMATION: - Consider giving a poster; our poster invite app will allow you to invite up to 3 attendees of your choice to come view it. This can dramatically change the relative value of a poster compared to a talk

- Free professional childcare available on-site. Bookings are done during conference registration.

- There are MANY optional events before and during the conference. Some required pre-registration. Details on the website.

- Hotel accommodations: <https://www.evolutionmeetings.org/accommodation.html>

- Dorm accommodations are booked DURING conference registration. The majority of rooms are double and you must specify your roommate to reserve a room. Help finding a roommate here: <https://docs.google.com/spreadsheets/d/1ePZ72-2FrTVZpucANJVQDhmfL3Wg8Yn2e9JeObIxWVv0/>

[edit?usp=sharing](#) - Sponsor/exhibitor registration is also open.

---

## Seville SpanishSocEvolBiol Feb5-7

Dear colleagues,

The 7th biennial Meeting of The Spanish Society for Evolutionary Biology (SESBE) will be held in Seville, from 5 to 7 February 2020, organized by the School of Biology, University of Seville (US), the Doñana Biological Station (EBD-CSIC) and the Centro Andaluz de Biología del Desarrollo (CABD-CSIC and University Pablo de Olavide). Please save the dates and pay attention to the launching of the first circular and web page by next June 2019. We encourage all researchers, teachers and interested non-professionals, particularly those in early career stages, to attend an exciting conference in a relaxed academic environment.

The Organizing Committee

C. Alonso, EBD M. Arista, US J. Arroyo, US F. Balao, US M. Escudero, US I. Gómez-Mestre, EBD J.L. Gómez-Skarmeta, CABD P. Jordano, EBD X. Picó, EBD

Dr. Juan Arroyo [arroyo@us.es](mailto:arroyo@us.es) Departamento de Biología Vegetal y Ecología. Dept. of Plant Biology and Ecology Universidad de Sevilla Apartado 1095 -E41080 Sevilla, Spain phone: desk office: +34 954 557 058 lab: +34 955 420 845 fax: +34 954 557 059 Research group: <http://grupo.us.es/grnm210/> <https://scholar.google.es/citations?user=sq1zWekAAAAJ&hl=es> [orcid.org/0000-0003-4749-2519](https://orcid.org/0000-0003-4749-2519) ResearcherID: J-2562-2012 Sociedad Española de Biología Evolutiva: <http://sesbe.org> Peer Community in Evolutionary Biology <https://evolbiol.peercommunityin.org>

Juan Arroyo <[arroyo@us.es](mailto:arroyo@us.es)>

---

## SMBE SatelliteRegionalMeetings2020 CallProposals

SMBE Satellite and regional meetings 2020 - call for proposals

Each year, SMBE provides funds in aid for \*SMBE

SATELLITE MEETINGS\*. These are workshops or small, topically focused regional meetings with fewer than 100 participants that are organized and held independent of the SMBE annual meeting. In the past five years, SMBE has supported multiple satellite meetings on diverse topics (e.g., “The Origin of Life” 2014, “Causes of Genome Evolution” 2014, “Phylogenomic Networks in Microbial Genome Evolution” 2014, “Investigating biological adaptation with NGS: data and models” 2015, “Mutation, Repair and Evolution” 2015, “Phylogenetics and Biodiversity” 2015, “Mechanisms of Protein Evolution III” 2015, “Genome Evolution in Pathogen Transmission and Disease” 2016, “Genetics of admixed populations” 2016, “RNA modification and its implication on adaptation and evolution” 2016, “Mitochondrial Genomics and Evolution” 2017, “Evolution of microbes in natural and experimental populations ’ synthesis and synergies” 2017, “Molecular evolution and medicine” 2017, “Evolution of genome architecture” 2017, “Molecular evolution and the cell” 2018, “Genome Evolution in Pathogen Transmission and Disease” 2018, and “Modern Methods for the study of ancient DNA” 2018)

SMBE is now calling for proposals for workshops/satellite meetings to be held between Jan 1st 2020 and Dec 31st 2020. Funds will be awarded on a competitive basis to members of the molecular evolution research community to run workshops/satellite meetings on an important, focused, and timely topic of their choice. The deadline for submission of proposals is May 15th 2019.

\*SMBE INTERDISCIPLINARY AND REGIONAL ACTIONS\*. In addition to supporting its annual meeting and satellite meetings, SMBE will promote interdisciplinary research and extend its actions worldwide by sponsoring (1) joint meetings with meetings of other societies; symposia or plenary lectures on molecular biology and evolution at meetings whose primary focus is not molecular evolution; (2) regional meetings outside the US, Europe, and Japan; (3) small regional meetings in the US, Europe, or Japan targeted towards PhD students and postdocs with the purpose of helping them develop their presentation skills and facilitate networking. Funds will be awarded on a competitive basis to members of the molecular evolution research community to run all three types of actions. SMBE is now calling for proposals to be held between Jan 1st 2020 and Dec 31st 2020. The number of awards will depend on the quality of proposals and total cost. The deadline for submission of proposals is May 15th 2019.

\*Guidelines\*

Â SMBE will provide financial support for up to 80%

of the cost of each satellite meeting, up to maximum of \$40,000 USD per meeting (most meetings are funded at \$20,000-\$30,000 each). SMBE will provide financial support for up to 80% of the cost for the joint and regional meetings, up to maximum of \$25,000 USD per meeting (up to \$10,000 USD for small regional meetings in the North America, Europe, or Japan). SMBE will cover the cost of plenary lectures, up to a maximum of \$3,000 USD per lecture. A detailed projected budget, including the expected number of participants, travel/food/lodging costs, and registration fees must be submitted with the application. Please note that SMBE funds cannot be used for indirect costs or overhead costs.

\*Â\* At least one of the organizers must be a member of SMBE. Current SMBE Council members, or members who have rotated-off Council in the last calendar year, are not eligible to serve as meeting organizers or co-organizers.

Â For satellite meetings, funds will be awarded on a competitive basis to members of the molecular evolution research community that propose an important, focused, and timely topic. Topics not well represented in symposia of SMBE annual meetings will be favored over those that are already well represented at the annual meetings or previous SMBE satellite meetings. For Interdisciplinary and Regional actions, meetings/symposia/lectures will be selected based on the scientific importance, timeliness and anticipated impact on the fields of molecular biology, genome biology, and evolution.

§Proposals are encouraged to include details for plans about the recruitment of speakers and participants that will ensure broad representation across SMBE membership, including gender and geographical location. We would like to gather information on the number of male and female speakers, where the speakers are coming from and their status summarized as senior/mid-career/junior faculty/trainee. Proposals for meetings to be organized in geographical areas that have been traditionally under-represented in SMBE meetings (annual or satellite) are especially encouraged.

Â Proposals will be received and reviewed by three SMBE Council Members that will make a recommendation to SMBE Council, whose decision is final.

— / —

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>

---

## Split Croatia EvoKE EvolutionOutreach Sep26-29

Dear evolution enthusiasts!

Registration deadline for the next EvoKE Conference has been extended to the 5th of May 2019!

EvoKE 2019 conference will take place in Split, Croatia, from 26 to 29 of September. Registration for the event is open and will end on the 5th of May 2019. Be one of the 100 participants, ranging from researchers and educators to media and policymakers, that will work together to transform evolution education and outreach in Europe.

The 2.5 days will include plenary talks by invited speakers (listed <https://evokeproject.org/plenary-speakers-2/>) and multiple workshops (listed <https://evokeproject.org/workshops/>) which will allow you to:

- co-construct international and interdisciplinary collaborative teams;
- improve your science education and outreach skills;
- share your expertise in evolution education and outreach;
- learn about new tools and resources;
- and prototype new evolution education and outreach projects.

To register please visit [bit.ly/evoke19apply](http://bit.ly/evoke19apply) and fill in the registration form. You can learn more about the registration process and the conference here: <https://evokeproject.org/applying-for-evoke-2019/> The EvoKE Team

Szymon Drobnik <[szymek.drobnik@gmail.com](mailto:szymek.drobnik@gmail.com)>

---

## Tucson PlantEvol Jul27-31

PLANTS Undergraduate travel awards enhancing diversity at BOTANY 2019 meetings, July 27-31, 2019, Tucson, Arizona [botanyconference.org](http://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](http://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](mailto:HCacanindin@Botany.org).

CONTACTS: If you have questions, please contact one of the organizers: Anna Monfils – [anna.monfils@cmich.edu](mailto:anna.monfils@cmich.edu)

Heather Cacanindin – [hcacanindin@botany.org](mailto:hcacanindin@botany.org) Ann Sakai' [aksakai@uci.edu](mailto:aksakai@uci.edu)

[aksakai@uci.edu](mailto:aksakai@uci.edu)

---

## UCambridge Evolutionary Genetics Apr16-18

Hi All,

Registration for this years annual Ecological Genetics Group meeting, in association with the British Ecological Society and Genetics Society has been extended for one week!! It will close on the 8th of April. Get registering so you don't miss out- Last chance!

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 < <https://www.plantsci.cam.ac.uk/directory/-davey-matthew> > [www.plantsci.cam.ac.uk](http://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 < <https://www.zoo.cam.ac.uk/directory/william-amos> > [www.zoo.cam.ac.uk](http://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 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 forget 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](http://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! All talk and poster slots now filled.

Looking forward to seeing you in Cambridge.

Cheers

Gemma

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

---

## UK MolluscanGenomics Sep16-17 programme registration

Mollusks! Molluscs! Genomes and Long-reads!

The draft programme is now out for "Pearls of Wisdom", the first conference focused on molluscan genomics, at the Royal Society of London's Chicheley Hall, UK, 16th-17th September 2019. Co-organised by Dr Angus Davison, University of Nottingham ([angus.davison@nottingham.ac.uk](mailto:angus.davison@nottingham.ac.uk)) and Dr Maurine Neiman, University of Iowa ([maurine-neiman@uiowa.edu](mailto:maurine-neiman@uiowa.edu))

#pearls19

While all speaker slots have been allocated, we still have plenty of space for attendees. Posters welcome. Please request an invite via the Royal Society web page: <https://royalsociety.org/science-events-and-lectures/2019/09/pearls-of-wisdom/>. There is no registration fee!

We anticipate that some funding may be available, especially to early-career scientists - email Angus for UK/EU-based scientists and Maurine for graduate students or postdocs who are US citizens or green-card holders.

Confirmed speakers:

Menno Schilthuizen @schilthuizen, Suzanne Saenko, Jeanne Serb @jeanne\_serb, Mark Blaxter, Carrie Albertin @CarrieOcto, Jin Sun, Matt Loose @matloose, Andrew Calcino @AndrewCalcino, Marina Panova, Noriyuki Satoh, Marie-Agnes Coutellec, Peter Fields @peterdfields, Maurine Neiman @mneiman (co-organiser), Coen Adema, Otto Seppala @otto\_seppala, Michael McCartney, Yale Passamanek, Kim Perry, Ximing Guo, Angus Davison @angus\_davison (co-organiser)

Provisional programme: <https://royalsociety.org/science-events-and-lectures/2019/09/pearls-of-wisdom/>  
– Dr Angus Davison | Reader and Associate Professor in Evolutionary Genetics School of Life Sciences | University Park | University of Nottingham | NG7 2RD +44 (0) 115 8230322 | [angus.davison@nottingham.ac.uk](mailto:angus.davison@nottingham.ac.uk) | @angus\_davison | [angus.davison.org](http://angus.davison.org)

[Angus.Davison@nottingham.ac.uk](mailto:Angus.Davison@nottingham.ac.uk)

---

## GradStudentPositions

AarhusU TropicalPlantDiversification . . . . . 16	PrincetonU EEBPreview Oct3-6 . . . . . 34
Bolzano Italy Microbe aDNA . . . . . 17	Rennes PlantGenomeEvolution . . . . . 34
CharlesU FishControlGeneEvolution LastCall . . . . 18	RyersonU PlantPopulationBiology . . . . . 35
CharlesU MimicryAposematism . . . . . 19	SLU Uppsala PlantGenomics . . . . . 36
CharlesU PlantRadiations . . . . . 19	SouthDakotaStateU PlantPhylogenetics . . . . . 37
CharlesU Prague BodySizeEvolution . . . . . 20	ThunenInst Germany eDNA . . . . . 37
CharlesU ReptileSexChromosomes . . . . . 20	UAberdeen BeetleExptEvolution . . . . . 38
ClarkU Massachusetts ReptileEvolution . . . . . 21	UAlabama Huntsville EvolutionaryBiol . . . . . 39
ETH Zurich FungalPopGenetics . . . . . 21	UBasel 2 EvolutionRangeLimits . . . . . 39
HIE Sydney AdaptiveCapacityToDrought . . . . . 22	UBasel AlpineButterflyEvolution . . . . . 40
HongKongU AnimalCommunicationMicrobiome . . 23	UBasel PlantPhylogeneticsEvolution . . . . . 41
IntlMaxPlanck 5 EvolutionaryBiol . . . . . 23	UBern FishEvolutionaryEcol . . . . . 42
JagiellonianU AdaptiveEvolution . . . . . 24	UFlorida EvolutionaryEcol . . . . . 43
JagiellonianU Poland InsectSymbioses . . . . . 25	UHongKong BehaviouralEvolutionElephants . . . . 43
JustusLiebigU ComparativeVenomic . . . . . 26	UKiel MarineEvolutionaryGenomics . . . . . 44
LaTremblade France GenomicSelection . . . . . 27	UManitoba BeeSystematics . . . . . 45
LeipzigU BiodiversityEcolEvol . . . . . 27	UmeaU ModelingEukaryoteOrigins . . . . . 45
LinkopingU PhylogeneticComparativeMethods . . . 28	UMontpellier InvasiveInsectPopulationGenomics . . 46
LundU SpeciationGenomics . . . . . 28	UNorthernColorado PlantPopConservationGenetics 47
MasarykU EvolMouseHybridSterility . . . . . 28	UPorto FishPopulationGenomics . . . . . 47
MaxPlanckInst ShrewBrainSizeChanges . . . . . 29	UppsalaU AvianGeneRegulatoryEvol . . . . . 48
MemorialU Canada RarePlantConservation . . . . . 29	UQueensland UExeter SexualConflict . . . . . 48
Montpellier VaginalMicrobiotaDynamics . . . . . 30	Vienna PopulationGenetics . . . . . 49
NHM UOslo Norway EvolutionaryBiolOrnithology 30	VLIZ Belgium 2 MarineBiodiversity . . . . . 49
NHM UOslo Norway EvolutionaryGenomicsZool . . 31	WesternConnecticutStateU WildlifeDiversity . . . . 50
NortherArizonaU TreeClimateAdaptation . . . . . 32	
NTNU Trondheim AvianEvolutionaryEcol . . . . . 33	

---

### AarhusU TropicalPlantDiversification

Applications are invited for a PhD fellowship/scholarship at Graduate School of Science and Technology, Aarhus University, Denmark, within the Bioscience programme. The position is available from 1 August 2019 or later. Read more and apply here: <http://phd.scitech.au.dk/for-applicants/apply-here/may-2019/plant-diversification-in-the-tropics-why-are-there-so-many-species-in-rainforests/> Title: Plant diversification in the tropics: why are there so many species in rainforests?

Research area and project description: Tropical rain-

forests are famous for their biological 'hyperdiversity': they are estimated to harbor around half of the world's species on less than 10 percent of the world's land surface. Despite decades, if not centuries, of scientific interest, this exceptional concentration of biodiversity remains enigmatic. Evolutionary processes of speciation, extinction and migration are almost certainly implicated, but the data to measure them remain scarce. Phylogenetic methods, drawing on new genomic data, can help getting new insights into the evolutionary engine of rainforest hyperdiversity (<https://doi.org/10.1111/nph.14516>).

This PhD project is part of TropiToL, a five-year project funded by VILLUM FONDEN aiming to use the Tree of Life to understand the biological hyperdiversity of tropical rainforests. We will build and apply phylogenetic trees of plants at different scales, and use a combination of macroevolutionary and ecoinformatics methods to statistically test different candidate drivers of rain-



forest plant diversity. Plants are the structural and trophic foundation of terrestrial ecosystems, including rainforests, and can serve as a model to understand the biological richness of rainforests more broadly. This, in turn, can help us understand the processes that generate and maintain high biodiversity in general.

The candidate will work on one or more tropical rainforest plant groups, generating genomic data, building phylogenetic trees at species and/or population level, gathering additional data (traits, occurrences) to characterize species' ecology, and applying cutting-edge macroevolutionary methods to understand (1) what drives speciation, extinction and migration in tropical rainforest groups, and (2) how do these processes individually and in combination affect biodiversity.

The PhD project is likely to focus, at least in part, on the island of Madagascar, which our team is using as a model system for understanding the diversification of tropical forests. The candidate will have access to existing datasets on the palms of Madagascar, but will be expected to collect complementary data. There will be opportunities to conduct fieldwork, depending on the exact scope of the PhD project, which will be determined in consultation with the successful candidate. An extended (>3 months) research stay at a collaborating institution abroad is expected.

Place of employment and place of work: The PhD student will be enrolled in the Graduate School of Science and Technology (GSST) at Aarhus University. The place of employment is Aarhus University, and the place of work will be Section for Ecoinformatics and Biodiversity (ECOINF), Department of Bioscience, Ny Munkegade 116, 8000 Aarhus C, Denmark.

Contacts: Applicants seeking further information are invited to contact: Associate professor Wolf Eiserhardt, phone +45 8715 6136, e-mail: wolf.eiserhardt@bios.au.dk

wolf.eiserhardt@bios.au.dk

---

## Bolzano Italy Microbe aDNA

Job Announcement

PhD position in the field of mummy microbiome research  
Institute for Mummy Studies, Eurac Research, Bolzano, Italy

We are looking for a microbial ecologist with expertise

in advanced molecular, bioinformatics and microscopic techniques and an interest in applying innovative methods to the field of mummy microbiome research. Our Institute is internationally renowned for its research on the Iceman and other mummified and skeletal human remains of different periods from all over the world. Our research aim is to assess the microbiome composition in mummified human remains. There is increasing evidence that mummified human remains still contain traces of the original endogenous microbial community members. Often, however, this ancient microbiome is masked by the DNA of post-mortem upgrown organisms and environmental microbial contaminations. Therefore, mummy microbiome research can discover both traces of the ancient host microbiome and metabolic key-players in the mummy ecosystem that potentially foster a slow but constant degradation process of unique mummified remains. The aim of this project is to characterize both the ancient endogenous and still active microbial community members in mummified human remains.

The main research objectives are:

- \* In-depth taxonomic characterization of the microbial community members in various mummified human remains from all over the world
- \* Comparison of ancient and modern human microbiomes
- \* Characterization of the still active microbial community members: Implications for the conservation of the human mummies.

We offer a three years PhD position at the Eurac Research - Institute for Mummy Studies. The position is available as early as September 2019.

What we seek We are looking for a highly motivated and independently working young scientist with a conceptual and practical background in the application of a holistic microbial ecology approach on the ancient human remains. To decipher both the ancient endogenous microbiome and the still active microbial community members this holistic approach combines molecular biology (DNA/RNA based analysis) and shotgun metagenomics (binning, assembly, taxonomic/functional assignment, phylogeny) with microscopic analyses of the microbes (Fluorescence in situ Hybridisation).

Experience in most of the mentioned areas/techniques is requested. Proficiency in spoken and written English is mandatory.

What we offer We offer up to three years of appointment as a PhD student according to the salary scheme of the EURAC. The candidate will work in a young and international team with a highly stimulation research environment. The EURAC is an equal opportunity employer.

How to apply Please send an E-mail before 31.05.2019 to [mummy.studies@eurac.edu](mailto:mummy.studies@eurac.edu) containing a pdf-file with a short cover letter and a detailed CV (including a brief description of research interests and of the educational background). Please mention in your E-mail the subject: PhD mummy microbiome.

Please attach, after reading the privacy policy in compliance with the EU Regulation No. 2016/679 (GDPR) and the national legislation, the following consent to your personal record: 'I have read the privacy policy under <http://www.eurac.edu/en/aboutus/Jobs/Pages/default.aspx> and hereby authorize Eurac Research to use my personal data in accordance to EU Regulation No. 2016/679 and national legislation.' We inform you that we will not be allowed to consider any application without this compliancy declaration.

Please add the following consent if it is of interest to you: "I hereby explicitly authorize Eurac Research to store my personal data for the purpose of being contacted for potential future job openings".

Maixner Frank <[frank.maixner@eurac.edu](mailto:frank.maixner@eurac.edu)>

---

## CharlesU FishControlGeneEvolution LastCall

We are seeking a motivated Ph.D. student to join an interdisciplinary project combining basic research and its forensic application for fish species control. The main focus of the project is on 1) development of the universal molecular tools for forensic fish species identification (e.g. in the food trade, fish production), and, 2) the molecular evolution of parvalbumin genes in fishes. The selected Ph.D. candidate will be focused on the following topics under the co-supervision of three supervisors from different fields, and will perform the study at the Charles University in Prague and Food Research Institute in Prague.

PhD topic title: Molecular characterization of fish parvalbumin gene and application for fish production control

Parvalbumin is an important protein of muscle tissue. Highly conserved exons in the protein-coding part of the parvalbumin gene are separated by three introns, which are quite unique among various fish species. This feature makes nuclear intron sequences convenient as a molecular marker for PCR-based species determination, as well as the subsequent Real Time PCR-based

quantification in a complex mixed samples. Results of the parvalbumin research will be reflected in fish species determination for forensic application in fish trade, food industry etc. The goal of the research part is to characterize parvalbumin gene (including the number and sequences of the pseudogenes and/or functional paralogs) throughout the ray-finned fishes and focus on the evolution of the genes. Ultimately, this should serve as a reference for identification of the intron-based PCR markers for fish species determination.

The research group is located in Prague (Czech Rep.) and the selected Ph.D. student will process reference material (collected in the field or via fish trade), as well as will have an option to actively participate in the field sampling. The project is funded by the Czech Ministry of Agriculture. Selected candidate is expected to participate in the development of the forensic tool, actively participate at scientific conferences and produce research publications.

Start: October 2019, Duration: 4 years

The salary is composed of the standard university scholarship (126'000 CZK) and project employment (84'000 CZK), and can be additionally increased by 24'000 CZK according to the progress of the study duties, which in total sufficiently covers living expenses in the Czech Republic (student standard).

Required: motivation and enthusiasm for biology, nature and science; fluency in English; a M.Sc. degree in biology or related fields (or to be finished until September 2019).

Desirable (but not necessary): previous experience with laboratory work, especially molecular genetic methods; (basic) experience with research projects evidenced by a (co)authorship of research papers or conference contributions.

Deadline: 10th April 2019. Selected candidates will be then invited for the Skype interview, which will happen between April 15th - 17th. The final selected candidate has to be assigned to the position by the end of April in order to fulfil the administrative conditions of the Charles University.

All questions and applications (CV + half-page motivation letter + 2 contacts for possible reference) should be sent directly to the main supervisor, Petr Hanak ([petr.hanak@vupp.cz](mailto:petr.hanak@vupp.cz))

Zuzana Musilova, PhD. ([zuzmus@gmail.com](mailto:zuzmus@gmail.com))

Department of Zoology Charles University Vinicna 7, CZ-128 44 Prague Czech Republic - Europe

---

## CharlesU MimicryAposematism

A PhD position on aposematism and mimicry at Department of Zoology, Charles University, Prague

We are looking for a highly motivated candidate for a PhD position to join our project focused on evolution and maintenance of imperfect mimicry. The selected PhD candidate will become part of the research team within the grant project: Mimetic Complexes and the Evolution of Inaccurate Mimics funded by Czech Science Foundation (Czech Republic).

Mimicry, a phenotypic resemblance between different species due to the selection by predators, represents one of intriguing topics in evolutionary biology. Species that form mimetic complexes may either possess some anti-predatory defensive mechanisms or be palatable (forming Batesian- Muellierian continuum), and their mutual resemblance may be accurate or, in many respects, inaccurate. In this project, we study two mimetic complexes of European arthropods: the myrmecomorphic (ant-resembling) complex formed mainly by ants, true bugs, and spiders, and the red-and-black complex including mainly true bugs, beetles, and velvet spiders. We aim to determine the diversity of these mimetic complexes, quantify similarities between the mimetic species, and reconstruct the evolution of their mimetic characters. We shall compare the efficacy of defensive mechanisms of the mimetic species against different predators (birds, spiders, mantids, predatory bugs), test how predators learn, generalize and categorise the mimics, and evaluate several hypotheses explaining the evolution of inaccurate mimicry.

The PhD project will be focused mainly on various aspects of predator cognition (learning, generalisation, categorisation, decision making), their role in evolution and maintenance of imperfect mimicry, and their effects on mimetic relationships between prey species. The work shall combine behavioural experiments with image processing and analyses.

Our research group is a part of Department of Zoology, Faculty of Science, Charles University, and we are based in Prague (Czech Republic). More information about the Department of Zoology and its Ethology and Ecology Research Group can be found at: <http://web.natur.cuni.cz/zoologie/eko/en/>. Start date: October 2019. Duration: 4 years.

Required: high motivation and genuine enthusiasm for science in general and for evolutionary and behavioural ecology in particular; proficiency in English; MSc degree in biology or related fields (to be completed until September 2019).

Desirable (but not necessary): experience with designing behavioural experiments and with methods of recording and analysing animal behaviour; advanced statistical skills; experience with image processing and analysis; experience with research projects.

Charles University has a 4-year PhD programme in Zoology; a standard scholarship amounts to 10500 CZK (420 EUR) per month with further increase by up to 4000 CZK (160 EUR) per month according to publication activity, and additional funding from the grant project of 6000 CZK (240 EUR), which in total sufficiently covers living expenses.

Deadline for application is 24 April 2019 (the selected candidate has subsequently to apply for a PhD position at Charles University, Faculty of Science via university webpages by 30 April 2019 (interviews usually scheduled for the beginning of June).

Applications: a motivation letter, CV (including education, research experience and publication list), and contact details for a person who can provide a reference) should be sent to Alice Exnerova ([exnerova@gmail.com](mailto:exnerova@gmail.com), [exnerova@natur.cuni.cz](mailto:exnerova@natur.cuni.cz)).

Contact: Alice Exnerova, PhD Phone: +420 221 95 1835  
E-mail: [exnerova@natur.cuni.cz](mailto:exnerova@natur.cuni.cz), [exnerova@gmail.com](mailto:exnerova@gmail.com)  
<http://web.natur.cuni.cz/zoologie/eko/en/lide/alice-exnerova-en/>).

“doc. Mgr. Alice Exnerová, Ph.D.”  
<[alice.exnerova@natur.cuni.cz](mailto:alice.exnerova@natur.cuni.cz)>

---

## CharlesU PlantRadiations

A Ph.D. position is available in the research group of Dr. Roswitha Schmickl at the Department of Botany of Charles University in Prague.

\*Title of the Ph.D. project:\* Cytogenomics of a Cape plant radiation V the role of whole genome duplication and transposable elements

\*Starting date:\* October 2019

\*Project summary:\*

Both the ubiquity of recent polyploids and association

of ancient whole genome duplication (WGD) events with evolutionary radiations are frequently taken as indirect evidence of the adaptive value of polyploidy. However, in stark contrast to this stands the discovery that recent polyploids diversify at lower rates, which re-appraised older notions about polyploids as evolutionary dead-ends. This Ph.D. project focuses on the radiating southern African \*Oxalis\* clade (SoAO). Within-species ploidy diversity in SoAO is more than three times higher than global estimates of angiosperm intraspecific ploidy variation. Within this project it will be tested which processes lead to the extensive polyploidization in this plant group and if there is a ploidy-dependent diversification rate shift. In addition, the role of transposable elements in radiating SoAO and their interrelation with WGDs will be addressed. Methods will focus on phylogenomic analyses, common garden experiments, and flow cytometry.

The successful candidate is expected to have a broad and strong interest in plant evolution, phylogenetics and bioinformatics. Previous experience in any of these fields is a plus.

If you are interested, please send your CV and motivation letter to Roswitha Schmickl (roswitha.schmickl@natur.cuni.cz) until April 30th 2019.

“Roswitha Schmickl, Ph.D.”  
<roswitha.schmickl@natur.cuni.cz>

---

## CharlesU Prague BodySizeEvolution

A Ph.D. position is available at the Charles University, Faculty of Science, Prague, Czech Republic Project title: Ontogeny of sexual size dimorphism in lizards

Application deadline: Review of applications will begin immediately; for full consideration please apply before April 11, 2019 Starting date: October 2019

Background and aims: Body size is a crucial trait connected to nearly every aspect of animal life. It is very often sexually dimorphic. Despite its central importance, proximate mechanisms of intra- and interspecific variability in body size are still not well understood. The aim of the Ph.D. project is to compare the ontogeny of structural size, steroid levels, bone growth plates and mainly gene expression of genes associated with growth hormone/insulin-like growth axis and of receptors for androgen and estrogen between female-larger

and male-larger gecko species.

The successful applicant must hold a Master of Science (M.Sc.) in Biology/Ecology or related fields, has experience with methods for quantifying gene expression, enthusiasm, reliability and good knowledge of written and spoken English.

We offer: Funded Ph.D. position at the Faculty of Science, Charles University, Prague, Czech Republic for four years - scholarship 10500 CZK (410 EUR) per month plus part time job funded from the grant project (5000 CZK (195 EUR), until Dec 2021), increase in scholarship as a bonus for submitted manuscript or passed state doctoral exam (starting from additional 2000 CZK (78 EUR) per month)

If interested, please apply with one pdf file which contains: a letter describing your motivation for this project and your experience, CV, publication list and contact details of two referees. Please send your application by email to zuzana.starostova@natur.cuni.cz

For further information and submitting your application, please contact Zuzana Starostova (Department of Zoology, Faculty of Science, Charles University) email: zuzana.starostova@natur.cuni.cz; Web page: <https://-zuzanastarostova.webnode.cz/> “Mgr. Zuzana Starostová, Ph.D.” <zuzana.starostova@natur.cuni.cz>

---

## CharlesU ReptileSexChromosomes

Project description: The aim of the project is to examine the evolution of sex chromosomes and their homology based on gene content in selected lineages of reptile, a specie-rich group, involving lineages with either XX/XY, ZZ/ZW or temperature-dependent sex determination. Despite the recent advances in the field, our knowledge about their sex determination systems and sex chromosome homology is limited only to few lineages of reptiles (eg. iguanas, advanced snakes), while the majority of reptilian lineages remain unstudied. The successful candidate will study the evolution of sex chromosomes in a multi-directional approach, involving cytogenetics (FISH, chromosome painting), molecular genetics (qPCR) and/or bioinformatics (genomics/transcriptomics).

Qualifications: The applicant should possess Master degree (or equivalent title) and a proven expertise in a related field of biology: evolutionary biology, cytogenetics, phylogenetics, genomics and/or bioinformatics.

Previous experience in herpetology is not necessary.

Application: The applicant should send a short motivation letter (max 2 pages) explaining his/her background, a CV and contact information for two references to Dr. Michail Rovatsos (rovatsom@natur.cuni.cz). Good knowledge of the English language is required.

Financial support: The PhD position will be financially supported with stipend for maximum time of 4 years, starting from October 2019. Additional support will be provided from projects financed from Grant Agency of Czech Republic.

Suitable candidates will be interviewed until Friday 26/4. For any additional information, do not hesitate to write an email. Info about the team's activities in our website: <https://mirovatsos.wordpress.com/> Michail Rovatsos

Assistant Professor Department of Ecology Faculty of Science Charles University Vinicna 7, 12844 Prague Czech Republic

“Michail Rovatsos, Ph.D.”  
<michail.rovatsos@natur.cuni.cz>

Bergmann (pbergmann@clarku.edu) prior to applying with any questions they may have, a cover letter that includes their research interests, CV, and names and e-mail addresses for two references. The Biology Department at Clark University is small but vibrant, providing students the opportunity to gain experience in research, teaching, mentoring, and outreach. Support by way of Teaching Assistantship is guaranteed for five years, and includes tuition waiver. Although this year's application deadline has passed, we are accepting applications.

For more information, visit: Bergmann Lab: <http://www2.clarku.edu/faculty/pbergmann/> Biology Department: <http://www2.clarku.edu/departments/biology/> Graduate Admissions: <http://www.clarku.edu/admissions/graduate-admissions> Philip J. Bergmann Associate Professor Biology Department Clark University 950 Main Street Worcester, MA 01610

Philip Bergmann <PBergmann@clarku.edu>

---

## ETH Zurich FungalPopGenetics

---

### ClarkU Massachusetts ReptileEvolution

Dr. Philip Bergmann's Evolutionary Functional Morphology Lab at Clark University is recruiting a Ph.D. student to begin in Fall 2019 or Spring 2020. The Bergmann lab studies form-function relationships in an evolutionary and ecological context, primarily using reptile and amphibian locomotion as a study system. The main research foci are (1) how form-function relationships work and are affected by factors such as ontogeny and substrate, and (2) the evolution of snake-like body shapes from phenotypic, functional, and ecological perspectives. Tools used by the lab to address these questions include high-speed video, force plates, EMG, dissection, behavioral observations, field work, and modeling/simulation approaches. Some exciting areas that might be of interest to new PhD students include the ontogeny of performance, connecting performance with habitat use, performance in predator-prey interactions, and integrating form-function relationships with genetic architecture of performance traits.

Graduate students should be self-motivated and have prior research experience. They will be encouraged to develop their own projects within the context of the lab research. Interested students should contact Dr.

Title: Global population genetics of *Cercospora beticola*, cause of cercospora leaf spot on sugar beets

Summary: *Cercospora beticola* causes the most important fungal disease on sugar beets worldwide. A global collection of ~1000 strains of *C. beticola* will be assayed for 20 SSR markers. Population genetic analyses of these neutral loci will be used to elucidate global population structure and infer effective population size, reproductive mode, and extent of gene flow. 150 of the strains will be used to conduct an FST/QST analysis to determine the importance of local adaptation in selected populations. Using complete genome sequences from these 150 strains, a GWAS will be conducted to identify candidate genes underlying each trait.

Description: *Cercospora* leaf spot (CLS) caused by the fungus *Cercospora beticola* (Cb) is an important disease on sugar beets. CLS is typically controlled with fungicides, but resistance has become a problem in many locations and there would be economic and ecological benefits associated with using genetic resistance instead of fungicides to control CLS. Cb populations in Europe and North America have already shown their ability to evolve resistance to fungicides, but it is unknown how they will respond to deployment of CLS resistant cultivars.

Pathogen population genetic structure has proven to

be one of the best predictors of pathogen evolutionary potential. The core of this project is oriented around obtaining a detailed understanding of the population genetics of Cb to provide insight into the distribution of gene and genotype diversity within and among Cb populations sampled from different regions around the world. The results will enable quantitative assessments of the importance of sexual recombination, gene flow and effective population size, all of which affect a pathogen's evolutionary potential. This comprehensive population genetic analysis can be used to develop an overall risk assessment model for Cb that would consider both the evolution of virulence against resistance genes and the emergence of fungicide resistance. The analysis will also consider the potential for long-distance gene and genotype flow and the likely importance of sexual recombination.

In the first phase of the project, the student will obtain completely assembled PacBio genome sequences for 2 European strains of Cb and Illumina genome sequences for 10 additional strains of Cb. These genome sequences will be used to identify 20 robust SSR loci that can be assayed in ~1000 global strains of Cb, with 30-50 strains coming from each sugar beet field. The SSR data will be collected from all global strains and used to conduct detailed population genetic analyses.

In the second phase of the project, the student will identify ~150 global Cb strains to use in an FST/QST analysis. FST/QST analyses provide a powerful approach to identify quantitative traits that are under selection for local adaptation, as shown in our earlier work with three other fungal plant pathogens. In the framework of the FST/QST analysis, we will collect phenotypic data for a series of in vitro traits, including melanization, and growth rates at different temperatures, in the presence or absence of fungicides and in the presence or absence of reactive oxygen stress provided by hydrogen peroxide. For each trait, we will partition the phenotypic variance into components reflecting variance within field populations and between field populations (i.e. QST) and compare this to the distribution of neutral genetic variance for SNP markers (i.e. FST) distributed among the same populations. The SNP markers will be based on complete genome sequences obtained from each of the 150 strains used in the FST/QST analysis.

In the third phase of the project, the student will use the phenotype data collected in the FST/QST analysis and the SNP data obtained from the 150 genome sequences to conduct a genome-wide association study (GWAS) aiming towards determining the genetic architecture of each quantitative trait and identifying candidate genes underlying each trait.

Qualifications of the applicants: Applicants should have a masters degree in bioinformatics, biology, microbiology or a similar qualification. Previous experience in population genetics, evolutionary biology, plant pathology or mycology will offer an advantage. We seek individuals who possess good collaboration skills, can take their own initiative, and work independently.

Research fields covered by this project include: Plant pathology, Population genetics, Population genomics, Microbiology, Ecology, Evolutionary biology, Quantitative genetics

The Plant Pathology Group in the Institute of Integrative Biology at the ETH: Our major areas of research are population genetics and genomics, evolutionary biology, evolutionary ecology, experimental evolution, phylogeography and molecular biology. Our primary experimental

— / —

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>

---

## HIE Sydney AdaptiveCapacityToDrought

The Hawkesbury Institute for the Environment (HIE) is a research institute within Western Sydney University. HIE has rapidly become a research leader in environmental and ecological research, with a strong reputation for delivering research outcomes of the highest quality. HIE is home to a team of over 50 academic research scientists and more than 80 PhD students, with access to a unique suite of world-class research facilities. <https://www.westernsydney.edu.au/hie> We are looking for a highly motivated and qualified candidate for a 3-year PhD program of research commencing in 2019. This studentship is part of an exciting new research programme established under the NSW Office of Environment and Heritage 'Saving Our Species' initiative, investigating the adaptive capacity of threatened species and ecological communities to climate change. This project aims to quantify the genomic adaptation of woody plants to climate and droughts. Rare species are thought to have limited capacity to respond to climate change in part due to narrow climatic distributions. Given increasing documentation of drought impacts on natural forests, an understanding of the underlying genetic variation determining physiological tolerance to drought is urgently

needed for trees. The proposal will develop genomic predictions of drought tolerance in eucalypts through a comparative physiological and genomic approach. Importantly, this research will estimate the vulnerability of rare species to the increased frequency and intense of droughts under climate change. The outcomes will quantify adaptive capacity in rare trees to prioritise conservation efforts and improve adaptive management strategies.

The position is based at the Hawkesbury Campus of Western Sydney University, Richmond, NSW. The candidate will work in collaboration with the University of New England and the NSW Office of Environment and Heritage (Science Division and NPWS) to achieve key fundamental and applied outcomes in evolutionary ecology and conservation biology.

The HIE is situated in an agricultural landscape, near the historic towns of Richmond and Windsor NSW off the Hawkesbury River, at the base of the Blue Mountains with ample outdoor recreational activities. It is about 1.5 hours train to Sydney central station and all the things this amazing city has to offer from science and cultural institutions to the bridge and beaches.

Full details of the PhD scholarship can be found at [https://www.westernsydney.edu.au/-graduate\\_research\\_school/grs/scholarships/-current\\_scholarships/current\\_scholarships/-hie\\_saving\\_our\\_species\\_adaptive\\_capacity\\_to\\_climate\\_change](https://www.westernsydney.edu.au/-graduate_research_school/grs/scholarships/-current_scholarships/current_scholarships/-hie_saving_our_species_adaptive_capacity_to_climate_change)

Please do not hesitate to contact me if you have any questions.

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

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

technologies to study microbiome and host genotypes. The PhD will have extensive opportunities to interact with other lab members and collaborators and involve in different animal behavior and evolutionary and ecological genomics projects.

Duration: This is a four-year full-time PhD position.

Start Date: any time in 2019 or early-2020.

Qualifications and requirement: - BSc degree in biology or related fields (or will have completed a BSc before the position start); - High motivation and strong interest for behavioural ecology and evolutionary biology; - Proficiency in English; - Background in molecular genetics, behavioural ecology, chemical analysis, bioinformatics, genomics, evolutionary biology, or related disciplines is desirable; - Willingness to learn new skills in chemical analysis, molecular lab work, bioinformatics, etc.

Study Environment: The University of Hong Kong is an English-speaking institute and one of the most international universities in Asia. It has a rank of 36 according to the Times Higher Education World University Rankings 2019.

A Postgraduate Scholarship will be offered, in addition to annual leave and medical benefits

How to apply: Please send (1) a CV (including a list of publications), (2) motivation letter describing research interests and skills, and (3) contact details for 2-3 references to Dr. Simon Sin (sinyw@hku.hk). Review of applications will begin immediately and continue until the position is filled.

Simon Sin Assistant Professor School of Biological Sciences Kadoorie Biological Sciences Building The University of Hong Kong Pok Fu Lam Road, Hong Kong [www.simonywsin.com](http://www.simonywsin.com) <sinyw@hku.hk>

sinyw <sinyw@hku.hk>

---

## HongKongU AnimalCommunicationMicrobiome

\*\*\* A PhD position in Animal Communication, Chemical Ecology, and Microbiome \*\*\*

We are looking for a highly motivated candidate for a PhD position to work on animal communication on non-model species. A key focus of this project is to understand how body odor affects animal communication, and whether microbiome plays a role in it. The lab has several study systems and is routinely using genomic

---

## IntlMaxPlanck 5 EvolutionaryBiol

We advertise 5 doctoral position in chemical ecology, many of the 12 projects have evolutionary aspects, in particular projects 3,6, 8, 12.

Claudia Voelckel

5 PhD positions in Molecular and Chemical Ecology and Evolution International Max Planck Research School: "The Exploration of Ecological Interactions with Molecular and Chemical Techniques"

The International Max Planck Research School (IMPRS) “The Exploration of Ecological Interactions with Molecular and Chemical Techniques” in Jena, Germany, invites applications for 5 PhD positions beginning in October 2019 ’ January 2020. The overarching research topic is the use of molecular, chemical and neurobiological techniques to experimentally explore ecological interactions under natural conditions. The main focus is on the relationship between plants, microbes and herbivores, and their environment, as well as the evolutionary and behavioral consequences of these interactions. We offer 12 exciting projects focusing on different organisms and approaches. The complete list of projects offered including project descriptions is available on our website (<http://imprs.ice.mpg.de/ext/index.php?idB0#header.logo>). We are looking for enthusiastic PhD students with strong interests in the above-described central topic. Applicants should have or be about to obtain a Masters or equivalent degree in one of the following fields: entomology, neurobiology, molecular biology, biochemistry, analytical chemistry, plant physiology, genetics, ecology, evolutionary biology, bioinformatics, and mathematics and computer science. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds. The Research School is a joint initiative of the Max Planck Institute for Chemical Ecology and the Friedrich Schiller University. We offer state-of-the art equipment, an excellent research environment, supervision by a thesis committee and a structured training program including scientific courses, training in transferable and outreach skills and participation in research symposia. Successful candidates will receive a Max Planck support contract. There are no tuition fees and the working language is English. Application deadline is May 24th, 2019. For detailed information on the IMPRS, projects offered and application requirements, please visit our website: <http://imprs.ice.mpg.de/>. Please apply online from April 8, 2019, at: <https://imprs-reg.ice.mpg.de/>.

Projects offered in 2019

Please find below a list of projects we offer for this year’s recruitment. All projects are highly integrative and require the collaboration between different research groups. Applicants can identify up to three projects of interest. It is possible to change project preferences during the recruitment in Jena.

Project 1: Surfing the surface: Hydrophobins on fungal hyphae Supervisors: Prof. Dr. Erika Kothe, Institute for Microbiology, Friedrich Schiller University Jena; Prof. Dr. Jonathan Gershenzon, Department of Biochemistry, Max Planck Institute for Chemical Ecology; Dr. AleÅ SvatoÅ, Research Group Mass Spectrometry,

Max Planck Institute for Chemical Ecology

Project 2: Towards GC-MS: Adapting SIRIUS and CSI:FingerID for Electron Ionization fragmentation Supervisors: Prof. Dr. Sebastian Böcker, Chair of Bioinformatics, Friedrich Schiller University Jena; Prof. Dr. Georg Pohnert, Chair of Instrumental Analytics, Friedrich Schiller University Jena; Dr. AleÅ SvatoÅ, Research Group Mass Spectrometry, Max Planck Institute for Chemical Ecology

Project 3: Molecular basis of balanced color polymorphisms in grasshoppers Supervisors: Prof. Dr. Holger Schielzeth, Institute of Ecology and Evolution, Friedrich Schiller University Jena

Project 4: Communication in plant communities via a hyphal network connecting the roots of neighboring plants Supervisors: Prof. Dr. Ralf Oelmüller, Plant Physiology, Matthias Schleiden Institute, Friedrich Schiller University Jena; Priv. Doz. Dr. Axel Mithöfer, Department of Bioorganic Chemistry, Max Planck Institute for Chemical Ecology

Project 5: Tapping into signaling interactions between nematodes and aphids Supervisors: Prof. Dr. Nicole M. van Dam, Molecular Interaction Ecology, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig & Friedrich Schiller University Jena; Dr Grit Kunert, Chemical Communication in Plant-Aphid Interactions, Max Planck Institute for Chemical Ecology

Project 6: Convergent evolution of metabolic pathways: The biosynthesis of benzoxazinoids in dicotyledonous plants Supervisors: Prof. Dr. Sarah O’Connor, Department of Natural Product Biochemistry, Max Planck Institute for Chemical Ecology; Dr. Tobias

— / —

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>

## JagiellonianU AdaptiveEvolution

PhD-position on the effects of the environment on pace of life and microbiome of bank voles

We are seeking a highly motivated student for a PhD-position based at the Jagiellonian University in Krakow, Poland, as part of the project “The role of environmental factors in maintaining adaptive pace-of-life variation



in a mammal holobiont: an experimental evolution approach.”

Our aim is to investigate how environmental constraints experienced at different life stages influence the fitness of the mammal “holobiont”. According to the holobiont hypothesis an animal and its microbiome coevolve and should respond to the environment as a unit. To test this idea, we will study the effects of environmental manipulations on the life history and physiology of the individual animal and associated changes in its gut microbiome (the community of commensal microbes inhabiting the gut). We will test hypotheses about the role of the microbiome in influencing the fitness of the animal host through lab and field experiments with established bank vole (*Myodes glareolus*) selection lines.

The student will have an opportunity to conduct experiments with captive voles in Krakow and participate in field experiments conducted in large field enclosures in central Finland. The project offers opportunities to learn state-of-the-art methods and a range of transferable skills, including physiological measurements, genomic analyses of the gut microbiome and the associated bioinformatics and statistical analyses. The student will collect and analyse data and prepare publications in close collaboration with an international team of researchers at the Jagiellonian University, Poland (Dr Anni Hämäläinen, Prof Pawel Koteja) and the University of Jyväskylä, Finland (Prof Phillip Watts, Dr Tapio Mappes, Dr Esa Koskela).

The successful candidate will have an MSc degree in a relevant field by July 2019; evidence of good quantitative/computational skills; and strong English language, communication, organizational and collaboration skills. Previous experience with small mammals, microbial communities, bioinformatics, animal physiology and/or evolutionary biology are considered advantageous. The prospective student receives a generous stipend from the National Science Centre grant for 3 years, and a supplement to attend conferences and travel for field work. The official start date in the PhD program (graduate school) will be October 1st, 2019, but there may be a possibility for an interested student to begin earlier as a summer assistant.

Further information and application instructions available at: [https://wb.uj.edu.pl/en\\_GB/start](https://wb.uj.edu.pl/en_GB/start) -> “Job offers”

For informal inquiries, please contact the PI, Anni Hämäläinen (anni.m.hamalainen @ gmail.com).

Anni Hämäläinen <Anni.Hamalainen@oulu.fi>

---

## JagiellonianU Poland InsectSymbioses

The new Symbiosis Evolution research group ([www.symbioses.pl](http://www.symbioses.pl)) at the Institute of Environmental Sciences of Jagiellonian University in Kraków, Poland is seeking a motivated Ph.D. Student to join the project “The evolutionary dynamics of the symbioses of Auchenorrhyncha”, funded by the Polish National Science Centre (NCN) Sonata Bis 8 grant.

The project will comprehensively describe the evolutionary processes and patterns related to microbial symbioses of hemipteran insects from the suborder Auchenorrhyncha (cicadas, spittlebugs, leafhoppers, treehoppers, and planthoppers). These specialized microbes producing essential nutrients have been transmitted from mothers to offspring for a very long time – as much as 300 million years in some cases. But in many Auchenorrhyncha lineages, these ancient symbionts have become replaced or complemented by other microorganisms. We will describe the incidence and nature of these symbiont replacements, the origins of the replacing microbes, their genomic evolutionary patterns, their current biological roles, and the effects of the replacements on the ecology and evolution of hosts. Initially, we will conduct broad microbiome screens and reconstructions of the symbiont replacement patterns across the taxonomic diversity of Auchenorrhyncha. We will then follow up with phylogenomic, comparative genomic, and microscopy-based analyses of symbionts in clades that have experienced the replacements.

The Ph.D. Student will focus on bioinformatic reconstruction of the symbiont co-diversification and replacement patterns, and on phylogenomic analyses of the host and symbiont relationships. They will also have an opportunity to participate in international fieldwork, process the collected insects, conduct molecular work (automated DNA extraction, next-generation sequencing library preparation), and work on the reinterpretation of older, extensive microscopy data. They will be encouraged to work closely with project collaborators, including Gordon Bennett (University of California - Merced), Insect Biome Atlas consortium members in Sweden, and Anna Michalik (Jagiellonian University).

The successful candidate will have an M.Sc. degree in a relevant field by July 2019; a demonstrated interest in Evolution, Entomology, Microbiology, and/or Ge-

nomics; experience with, or a keen interest in learning, Bioinformatics, and Computational Biology; and strong English language, communication, and organizational skills. Previous experience with insect ecology, evolution and especially symbioses, molecular biology, microbiome surveys, phylogenomics and/or comparative genomics, as well as German language skills and willingness to travel, are advantageous.

The student will receive a generous 48-month tax-free stipend funded from the grant. Additional scholarships may be available through Ph.D. programs of Jagiellonian University. The official start date of the Ph.D. program is October 1st, 2019, but depending on the student's interest, there may be a possibility of an earlier start as a research assistant.

The candidates are asked to submit a cover letter, a CV, and contact details of two references to Dr. Piotr Ā ukasik (p.lukasik@gmail.com). The review of applications starts on 10th May 2019. The selected candidate or candidates will be assisted with the formal application to the Ph.D. program at Jagiellonian University.

For further information and informal inquiries, please contact Dr. Piotr Ā ukasik.

Piotr Lukasik <p.lukasik@gmail.com>

---

## JustusLiebigU ComparativeVenomic

### PhD Position in Comparative Venomics

In the interdisciplinary Animal Venomics group based at the Institute for Insect Biotechnology, Justus-Liebig-University Gießen, a PhD position is available as soon as possible for three years (Experience depending the salary band will be TV-H 13, 65%) within the German Science Foundation funded project:

Venom evolution in solitary and eusocial aculeate hymenopterans

Tasks - Working in the project that focuses on comparative venomics and toxin evolution of social and solitary bees and wasps. One aim is to understand better processes that drive toxin evolution in hymenopterans. Genomes will be complementary analyzed to proteomics and transcriptomics data to tackle this major aspect. - Proteomics is in parallel conducted via collaborations, depending on the results activity tests and assays are planned for some interesting toxin candidates. - The project-work allows to conduct a PhD within this

project.

Demanded skills and profile: - Applicants should hold a Diploma/Master degree in Biology or related natural sciences - Candidates should be highly motivated and should have a background in evolutionary biology, trait evolution and/or venomics - Proven background in transcriptomics and genomic work and analyses is necessary - Bioinformatics skills are important, experience in Perl or Python of advantage - Candidates should be self-organized but as well team players, good communication and English skills are important, the major tongue in the Animal Venomics group is English. - Fieldwork experience and taxonomic knowledge of hymenopterans is a further asset - Laboratory experience in RNA extraction, library reconstruction and/or HMW DNA extraction and general knowledge in proteomic work (HPLC, and MassSpec) is an advantage.

We offer a unique opportunity to grow and participate in an integrative environment within the new Animal Venomics group creating workflows comprising genomics, transcriptomics, proteomics, and protein characterization with evolutionary and applied perspectives. The main PI in this project is Dr. Björn M. von Reumont.

Gießen is a vibrant student town at the river Lahn in the green heart of the State Hessen, very central in Germany. Other, old university cities like Marburg or Wetzlar are located within 20 km. The metropolis Frankfurt with its large international airport is roughly 50 km away and its center can be reached from Gießen within 40 minutes by regional trains.

Please send applications without photograph and without date of birth as single PDF file including a CV (with two references), certificates, motivation letter (â1 page) with additionally a short summary of previous work and applied methods (â 1 page), and one reference letter to: Bjoern.Von-Reumont@agrar.uni-giessen.de.

The JLU Gießen promotes equal opportunities and diversity in its employment relations. Women are expressly encouraged to apply and given priority in accordance with the Equal Opportunities Act. We expressly welcome applications from individuals with severe disabilities or people of equivalent status. Severely disabled applicants of equal merit and qualifications will be given priority.

Application deadline is the 07.06.2019

Dr. Björn M. von Reumont

Research Associate LOEWE Center Translational Biodiversity Genomics University of Gießen & Fraunhofer IME Animal Venomics Winchesterstr 2 35394 Gießen Germany Tel +49 (0)641-99-39503

mob +49 (0) 151-61997924 www [http://-  
www.reumont.net](http://www.reumont.net) Björn Marcus von Reumont  
<bmvr@arcor.de>

---

## La Tremblade France Genomic Selection

Dear All,

I announce a PhD position in genomic selection to improve Pacific oyster quality to work at Ifremer in La Tremblade. The project is already funded. Please contact Pierre Boudry (Pierre.Boudry@ifremer.fr) and Jean-Baptiste Lamy (Jean.Baptiste.Lamy@ifremer.fr) for further information.

**Project description** Some phenotypic traits of the oyster are essential for adaptation to farming environment and also have an added commercial value, such as thickness of the oyster shell, strength of the adductor muscle, meat yield, resistance to viral and/or bacterial infection and biochemical composition. The measurements of those traits are destructive and hardly adapted to a large number of individuals (> 1000 individuals) as it is routinely done in various breeding programs of French hatcheries. Such phenotyping objectives require some technological and methodological developments. In addition, the recent progress and cost reduction of genotyping technologies allows the joint analysis of genetic and phenotypic dataset on a large number of individuals to explore the genomic determinism of such traits and test the effectiveness of genomic selection breeding schemes. This thesis aims to test and optimize the implementation of genomic selection methods, particularly for commercial traits as above-mentioned in Pacific oyster.

The founder populations will be genotyped on 20000 loci in order to have an initial image of their consanguinity and to follow its evolution. The thesis aims are to setup protocols, statistical pipelines and demonstrate the feasibility of such breeding scheme for the industry with an explicit control of the broodstock genetic diversity, mandatory for the genetic sustainability of the founder populations.

**Keywords:** Genomic selection, quantitative genetics, population genomics, high-throughput phenotyping, consanguinity, relatedness, traceability, sustainability.

Carole Blay <carole.blay@gmail.com>

---

## LeipzigU BiodiversityEcolEvol

Leipzig University (in Leipzig, Germany) is inviting applicants for the first cohort of MS students in our new international Master of Science in Biodiversity, Ecology, and Evolution program. The program will include: coursework covering the drivers and consequences of biodiversity change, biodiversity, conservation, and the evolutionary and ecological processes generating biodiversity as well as advanced statistics and modeling. Students will be embedded in the Leipzig University Institute of Biology and will have the opportunity to collaborate with many of the world-leading institutions in Leipzig including the German Centre for Integrative Biodiversity Research, the Helmholtz Center for Environmental Research, and the Max Planck Institute for Evolutionary Anthropology. Students will also have the ability to work at some of the unique research platforms available in Leipzig including our world-class Ecotron, the Global Change Experimental Facility, the Leipzig Canopy Crane, and several other large scale biodiversity experiments.

Applicants with a BSc in biology or related sciences and B2- level English (IELTS>5.5 or TOEFL >72 or degree from English-speaking institution) are invited to apply through the Uni Assist portal ( <https://www.uni-assist.de/en/how-to-apply/apply-online>). Applications must include a letter of motivation (max. 2 pages detailing the student's interest in the program and their relevant qualifications and research experience).

Admission will be based on: 1.) BSc grades, 2.) Overlap of coursework with the MS study course, 3.) Letter of motivation, and 4.) participation in extracurricular activities such as student administration/governance.

For more information - <http://bit.ly/MSBiodiversity> - Katie (Kathryn) Barry Postdoctoral Researcher

Community Assembly and the Functioning of Ecosystems German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Systematic Botany and Functional Biodiversity Institute of Biology Leipzig University

New paper out in Trends in Ecology and Evolution!: <http://bit.ly/TREE-Complementarity> Website: [www.katiebarryecology.com](http://www.katiebarryecology.com) Google Scholar: <http://bit.ly/KBarryGoogleScholar> Katie Barry <kathryn.barry@idiv.de>

---

## LinköpingU PhylogeneticComparativeMethods

At the Division of Statistics and Machine Learning, Department of Computer Science, Linköping University we have opened a PhD student in Statistics position that is related to phylogenetic comparative methods : <https://liu.se/en/work-at-liu/vacancies?rmpage=-job&rmjob890&rmlang=UK> [https://www.ida.liu.se/~krzba67/PhD\\_May2019.pdf](https://www.ida.liu.se/~krzba67/PhD_May2019.pdf) Please feel free to spread the word and of course apply if you are interested!

Thank you Krzysztof Bartoszek

Krzysztof Bartoszek <[krzysztof.bartoszek@liu.se](mailto:krzysztof.bartoszek@liu.se)>

---

## LundU SpeciationGenomics

We are very happy to announce a 4 year attractive PhD-position on speciation genomics at Lund University (<https://www.lunduniversity.lu.se>). The PhD-student will examine how the genome is shaped during the speciation process using host races of the peacock fly *Tephritis conura* that have specialised on different host plants as a model system. The position as a PhD-student in the Anna Runemark lab at the Department of Biology is open until May 15th. It is a full time position with a full salary including all social rights. The questions posed are related to how the genome develops during host plant specialisation and will be based on bioinformatics analysis of whole genome and transcriptome data. The exact project will be developed together with the selected candidate. The Department of Biology (<https://www.biology.lu.se/research>) is a highly international working place with a large community of researchers, post docs and more than 80 PhD-students from around the world. The Department has weekly seminars with invited speakers, well visited coffee breaks and Friday pubs, social activities such as floor hockey and has several journal clubs. The Runemark lab consists of a post doc, two MSc-students and two internship students and we collaborate closely with Magne Fribergs lab with more pre- and post graduate students and post docs to create

a friendly environment for scientific discussion and collaboration, see more about our projects on our joint website <https://www.biology.lu.se/research/research-groups/evolutionary-ecology-of-plant-insect-interactions>. Please find a link to the application and further information here <https://lu.mynetworkglobal.com/en/what:job/jobID:254869/type:job/where:4/apply:1> Contact [anna.runemark@biol.lu.se](mailto:anna.runemark@biol.lu.se) for inquiries.

Anna Runemark <[anna.runemark@biol.lu.se](mailto:anna.runemark@biol.lu.se)>

---

## MasarykU EvolMouseHybridSterility

A Ph.D. position is available at the Masaryk University in Brno, Institute of Zoology and Botany, Czech Republic

Application deadline: April 20, 2019 Starting date: October 2019

Title: Evolution of hybrid male sterility in the European house mouse

Supervisor: Jaroslav Piálek, CSc.

Subject: Two house mouse subspecies, *Mus m. musculus* and *M. m. domesticus*, that diverged between 0.5 MYR, undergo recipient speciation. Laboratory based crosses between the subspecies readily document the presence of F1 sterile males. This sterility is controlled by epistatic interaction between 2 loci, the *Prdm9* gene on chromosome 17 and X-linked gene(s) *Hstx1/2*, pleiotropically also controlling meiotic recombination. However, no laboratory borne sterility was reported from a natural hybrid zone between the subspecies. Here we address this incongruity by assessing variation of sterility in 648 intersubspecific crosses between 40 wild-derived strains from the Western Palearctic. Genotype-phenotype associations will be tested to the 2-locus model and, in those that differ, quantitative trait loci (QTL) will be mapped in the genome. Immunostaining of meiotic crossovers will search for geographic signal of within- and intersubspecific recombination rates. Finally, linking the QTL signal to mouse strain phylogeny, we will infer a general model of evolution of hybrid male sterility and genome-wide recombination in the house mouse. Experimental work will be realized in a breeding facility of the Institute of Vertebrate Biology, Czech Academy of Sciences, in Studenec (<https://www.ivb.cz/pracoviste/detasovane-pracoviste-studenec/>). The study is supported by the Czech Science Foundation in 2019'2021.

The successful applicant must hold a Master of Science (M.Sc.) in biology, have experience with methods in molecular methods and cytology, enthusiasm, reliability and good knowledge of written and spoken English.

If interested, please contact me at [jpialek@ivb.cz](mailto:jpialek@ivb.cz) and attach a PDF with your CV and contacts of two referees.

Jaroslav Piálek <[jpialek@ivb.cz](mailto:jpialek@ivb.cz)>

---

### MaxPlanckInst ShrewBrainSizeChanges

PhD student wanted for a project on reversible brain size changes in the common shrew.

In our long-term project on the evolution of reversible individual size changes in small high-metabolic mammals we have an open position for a 3-year PhD starting as soon as possible but hopefully before June this year. You would be working with captive shrews and study them as they go through the size changes in the brain using a combined approach of repeated state-of-the-art MRI imaging and behavioural assays of the same individuals. The MRIs will be done in the group of Dominik von Elverfeldt in Freiburg, where you will spend part of your time (<https://www.uniklinik-freiburg.de/mr-en/members/current/elverfeldt.html>).

This is a HSFP-funded collaborative project with Lilliana Davalos from Stony Brook University (looking at the molecular basis of this phenomenon) and John Nieland from Aalborg University (looking at the lipid metabolism) and their students.

What we are looking for:

If you are fascinated by evolution and questions such as how seasonal change affects animals, how the brain is shaped by evolutionary pressure, or how brain size is linked to behaviour and cognitive abilities this may be the right position for you. You need to be enthusiastic about working in a team and sharing data.

Ideal would be if you are a biologist with also a background in or inclination for physics or bioimaging as the MRI (which we will be the first to do with shrews) will be a large and important part of the project. Good English skills are also a requirement.

What you will find:

The Max Planck Institute for Ornithology is a thriving center for research on animal behaviour and our group

has been working on these shrews for years, working out many (but not all) of the potential kinks of working with the sensitive shrews. Our graduate school IMPRS for Organismal Biology provides added background where you can profit from a large spectrum of courses and support.

Interested? Please send your CV, a motivation letter and a research statement to [ddechmann@orn.mpg.de](mailto:ddechmann@orn.mpg.de) by May 15th.

more info on us and the project: <https://www.orn.mpg.de/641895/Sociality-and-Movement> Max Planck Institute für Ornithologie Am Obstberg 1 78315 Radolfzell Save

“Dechmann, Dina” <[ddechmann@orn.mpg.de](mailto:ddechmann@orn.mpg.de)>

---

### MemorialU Canada RarePlantConservation

MSc. student position in Rare Plant Conservation Genetics at Memorial University of Newfoundland-Canada

We are seeking a motivated MSc student to conduct research on the conservation genetics of endangered plant species of Newfoundland in Canada. Two species of Braya (Brassicaceae) and one species of Salix (Salicaceae) are endemic to the Limestone Barrens of Newfoundland ([www.limestonebarrens.ca](http://www.limestonebarrens.ca) for more information), and are endangered under the Canadian Species at Risk Act. We aim to elucidate the intraspecific genetic variation and population genetic structure for the conservation and management of these endangered species including the establishment of a genetically diverse seed bank, and the identification of stock for future reintroductions. We propose to use Genotyping-by-Sequencing (GBS), a cost-effective next generation sequencing method that permits the retrieval of millions of short DNA markers, and which we have successfully used in other plant projects at MUN Biology (Podocarpus, Vaccinium, Parajubaea). Other research questions of interest to the student are welcome within the framework of Conservation Biology or Genetics. The MSc student will work under the mentorship of three professors: Dr. Julissa Roncal (plant evolutionary biologist), Dr. Luise Hermanutz (conservation ecologist) and Dr. Lourdes Pena-Castillo (bioinformatician).

Student's qualifications: Â A BS degree with Honours in a related discipline (e.g. biology, botany, conservation, ecology, molecular biology, bioinformatics) Â Experi-

ence in organismic botany, ecology, conservation science, phylogenetic and/or population genetics analyses, and bioinformatic analysis of high-throughput sequencing data is highly desirable. • Excellent writing, analytical, organization and communication skills. Attention to detail. • Written and oral proficiency in English is mandatory for international students. TOEFL test required for admission to the university, but not the GRE tests.

Position characteristics: Project start date is September 2019. The MSc program comprises two years with an annual stipend of \$19,000. The student is expected to teach on average 10 hr/wk during the fall and winter semesters but not in the spring. The department of Biology at Memorial University has 29 faculty members and over 100 graduate students. Memorial University is Atlantic Canada's largest university offering a multicultural environment. Screening will begin immediately and will continue until the position is filled. Note this position is subject to funding.

How to apply: Interested applicants should send their CV, a one-page statement of research interests and career goals, transcripts, and contact information of 3 references (who have agreed to be contacted) in a single pdf or word file to Dr. Julissa Roncal at Email: jroncal@mun.ca. For more information on the research group visit: <http://www.mun.ca/biology/jroncal/> For instructions on how to apply to Memorial's graduate program visit: <http://www.mun.ca/become/graduate/-apply/index.php> Julissa Roncal <jroncal@mun.ca>

---

### Montpellier VaginalMicrobiotaDynamics

Dear all,

a PhD fellowship is opening in 2019 in Montpellier (France) to work with Dr Samuel Alizon (CNRS, Montpellier) and Prof Dr Vincent Foulongne (University Hospital Montpellier) to study the dynamics of circular viruses and plasmids in the vaginal microbiota of healthy young women followed longitudinally. These samples are collected in the context of the PAPCLEAR clinical study and the EVOLPROOF project: <http://alizon.ouvaton.org/EVOLPROOF.html>

Data will be generated during the PhD by applying existing methods to enrich samples in viruses (e.g. through ultra-centrifugation) and in circular DNA (e.g. RCA amplification). Funding is already available for

Illumina and/or nanopore sequencing. Further details about the PhD project can be found here: [https://www.adum.fr/as/ed/voirproposition.pl?langue=-fr&siteAS2&matricule\\_prop\\$865#version](https://www.adum.fr/as/ed/voirproposition.pl?langue=-fr&siteAS2&matricule_prop$865#version) The ideal candidate will have an MSc in bioinformatics or a research experience with analysing microbial data from high throughput sequencing. Skills in working in a wet-lab environment), in ecology & evolution and/or in biostatistics are a plus.

Applications should be sent before May 8 to the CBS2 doctoral school, who will be in charge of selecting the candidates: [https://edcbs2.umontpellier.fr/index.html?language=en&page=future\\_students&section=PhDcallapplications](https://edcbs2.umontpellier.fr/index.html?language=en&page=future_students&section=PhDcallapplications) Additional questions can be sent to [tosamuel.alizon@cnrs.fr](mailto:tosamuel.alizon@cnrs.fr)

Please do not hesitate to circulate this add.

– 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

Cell: +33 6 10 65 49 02

<http://alizon.ouvaton.org/> [Samuel.ALIZON@cnrs.fr](mailto:Samuel.ALIZON@cnrs.fr)

---

### NHM UOslo Norway EvolutionaryBiolOrnithology

For the following PhD (Jobbnorge ID: 167882), please apply at <https://www.jobbnorge.no/en/available-jobs/-job/167882/phd-research-fellowship-in-evolutionary-biology-ornithology> The deadline for applications is 30.04.2019.

Job advertisement: The University of Oslo is Norway's oldest and highest ranked educational and research institution, with 28 000 students and 7000 employees. With its broad range of academic disciplines and internationally recognised research communities, UiO is an important contributor to society. The Natural History Museum at the University of Oslo is Norway's most comprehensive natural history collection. For almost 200 years, preserved plant specimens, animal specimens, rocks, minerals and fossils have been collected, studied and preserved here. The museum is located at ?kern and in the beautiful Botanical Garden, which is not only popular for recreation, but is a scientific collection in

itself.

Natural History Museum PhD Research Fellowship in Evolutionary Biology/Ornithology

Job description A PhD fellowship (SKO 1017) is available at the Natural History Museum (NHM), University of Oslo. The position is placed in the 'Sex and Evolution Research Group' (SERG). The fellowship period is for 4 years, with 3 years in total devoted to carrying out a research project and one year (25%) of compulsory work load that will consist of teaching and supervision duties, collection work, outreach activities and research assistance. No one can be appointed for more than one PhD Research Fellowship period at the University of Oslo. Starting date no later than 01.10.2019.

More about the position The research themes in the SERG group are concentrated on the importance of sex, sex roles and sexual conflict in shaping evolutionary processes such as speciation, hybridization, diversification and adaptation. These processes are studied at different levels of organization, like genes, genomes, gametes, individuals, populations and species. Most projects use birds as their study systems. In recent years, the SERG group has mainly worked on these particular questions: 'Why are females promiscuous?', 'Why are sperm cells so diversified within and among species?' and 'What are the roles of pre- and postcopulatory sexual selection in reproductive isolation and speciation?' The research projects usually employ a combination of in-depth descriptive studies of morphology and behaviour, field experiments and comparative approaches. The research group has access to large museum collections in ornithology, including a DNA bank of more than 60 000 tissue samples, and a unique collection of formalin-preserved sperm cells from more than 500 species. Other available research infrastructures are a modern DNA laboratory, computer-assisted sperm analysis (CASA), microscopes with imaging software, and electron microscopes. Detailed population studies are usually carried out on target species around Oslo or at the NHM field station in 'vre Heimdalen, whereas fieldwork for comparative studies is usually carried out abroad and in collaboration with other institutions and research groups.

We invite a highly motivated and dedicated student to develop a PhD project within the framework of SERG's research themes as outlined above, and in close collaboration with the scientific staff in the group. We offer a specific project designed to understand how various forms of selection can affect variation in sperm size and function in passerine birds, though we assume that the successful candidate will actively contribute to the development of the specifics of the research plan.

Qualification requirements A Master's degree in ecology, evolution or molecular biology Skills in relevant laboratory practices, such a molecular techniques and microscopy Good computing skills Experience with ornithological field work and good knowledge in bird systematics Good communication skills (including written and spoken English)

Grade requirements for admission to the PhD program: The average grade point for courses included in the Bachelor's degree must correspond to C or better in the Norwegian educational system. The average grade point for courses included in the Master's degree must correspond to B or better in the Norwegian educational system. The Master's thesis must correspond to the grade B or better in the Norwegian educational system. The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD program at the Faculty of Mathematics and Natural Sciences. Appointment to a PhD research fellowship is conditional upon admission to the Faculty's research training program. A plan for the research training must be submitted no later than two months after

— / —

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

---

## NHM UOslo Norway EvolutionaryGenomicsZool

For the following PhD (Jobbnorge ID: 167875) please apply at <https://www.jobbnorge.no/en/available-jobs/-job/167875/phd-research-fellowship-in-evolutionary-genomics-and-zoology>. The deadline for the deadline is at 30.04.2019.

Job advertisement: The University of Oslo is Norway's oldest and highest ranked educational and research institution, with 28 000 students and 7000 employees. With its broad range of academic disciplines and internationally recognised research communities, UiO is an important contributor to society. The Natural History Museum at the University of Oslo is Norway's most comprehensive natural history collection. For almost 200 years, preserved plant specimens, animal specimens, rocks, minerals and fossils have been collected, studied

and preserved here. The museum is located at Åkern and in the beautiful Botanical Garden, which is not only popular for recreation, but is a scientific collection in itself.

#### Natural History Museum PhD Research Fellowship in Evolutionary Genomics and Zoology

Job description A PhD fellowship (SKO 1017) is available at the Natural History Museum (NHM), University of Oslo. The position is placed in the research group “Frontiers in Evolutionary Zoology”. The fellowship period is for 4 years, with 3 years in total devoted to carrying out a research project outlined below, and 1 year a compulsory work load (25 %) that will consist of teaching and supervision duties, collection work, outreach activities and research assistance. No one can be appointed for more than one PhD Research Fellowship period at the University of Oslo. Starting date no later than 01.10.2019.

More about the position The PhD project will address the foundations of speciation and dispersal in intertidal invertebrates characterized by seemingly no dispersal capacity. Many invertebrate species have very wide distribution ranges, but seemingly no or very low dispersal capacities. Some cases are known, for example, as the “Meiofauna paradox”. However, detailed studies of some traditionally recognized widespread species revealed complexes of cryptic species. Regardless of whether the distant populations are conspecific or belong to different cryptic species, two general questions can be asked: “Why are these taxa from distant areas so similar?” and “How can they have dispersed over long distances and occupied distant shores in the absence of propagative stages?”. The beetle genus *Aegialites* is widely distributed across the northern Pacific Ocean shores, both in Asia and North America where the beetles live on coastal rocks flooded at high tides or sprinkled by waves. These beetles are wingless and have no obvious adaptations to dispersal, yet they occur even on some distant islands that have never been connected to continents. The first aim of this project is to investigate the evolutionary history of this genus and to test if speciation is driven by vicariance or not. Second, the genome of an *Aegialites* species will be determined to allow genome re-sequencing approaches for the next hypotheses to be tested. Third, genome re-sequencing approaches will be applied to understand the dispersal capacity of *Aegialites* species at different geographical scales and, fourth, to test if hybridization between *Aegialites* species occurs possibly explaining their high morphological similarity. The results will contribute to answering the two more general questions above. Even though field work will be conducted to fill gaps in existing material, it will be necessary

to complement these with historical museum material. Therefore, in this project both classical zoological and population and evolutionary genomic approaches will be explored including the usage of historical museum material for molecular studies (often called museomics). The Natural History Museum has a modern DNA laboratory. The PhD will be associated with the research group “Frontiers in Evolutionary Zoology”, specifically Torsten Struck (Professor of Evolutionary Genomics) and Vladimir Gusarov (Associate Professor of Entomology).

Qualification requirements A Master’s degree or equivalent in biology or related disciplines like bioinformatics. Strong motivation for research in zoology and/or genomics. Skills in general molecular laboratory practices Experience with next-generation sequencing of genomes and working with small amounts of tissue material (i.e., whole genome amplification) is preferable. Computing skills and background in bioinformatics are expected for handling and analyzing large data sets emerging from next-generation sequencing approaches. Background in entomology, particularly knowledge of beetle morphology and systematics, will be an advantage. Communication skills (including written and spoken English)

Grade requirements for admission to the PhD program:

— / —

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>

---

## NortherArizonaU TreeClimateAdaptation

PhD position available in Landscape Genomics and Climate adaptation of tree species @ NAU

The School of Forestry at Northern Arizona University (NAU) is seeking one highly motivated PhD student to join Dr. De La Torres lab of Genomics and Evolution of Forest Tree Species. The position includes a stipend, tuition waiver, and full health benefits for 4 years. Outstanding candidates may qualify for the NAU Presidential Fellowship Program (<http://nau.edu/GradCol/-Financing/Presidential-Fellowship-Program/>). The student will use genomic tools to study phylogeography, migration rates, and the potential for adaptation to climate change in southwestern conifer species. The



research will include molecular lab work, greenhouse work, modelling and data analyses.

Qualifications:

- Master degree in Genetics, Forest Sciences, Biology, Plant Sciences, Evolutionary Biology, Bioinformatics or related fields of study.
- Proficiency in R, Perl or Python (familiarity with Linux is a plus)
- Willingness to work with big data sets in a computer cluster.
- Experience with GIS
- Availability to start by August 20th, 2019 (although a Jan2020 start date may be considered).

How to apply: Please send a 1-page statement of interest, CV, unofficial copy of transcripts, GRE scores, and TOEFL scores (international students), and the names and contact information of 3 references by April 26th, 2019. If found to be a good match for the position, you will be encouraged to apply to the graduate program at NAU.

Contact Information: Dr. De La Torre, Amanda.de-la-torre@nau.edu

Northern Arizona University is a 29,000 student-institution with its main campus in Flagstaff, a four-season community of about 70,000 at the base of the majestic San Francisco Peaks. Flagstaff has all-year easy access to the Arizona snowbowl ski resort and is located at 1-hour drive from the Grand Canyon.

School of Forestry- <http://nau.edu/forestry> SOF M.S. program- <http://nau.edu/CEFNS/Forestry/Degrees/-MS/> Amanda De La Torre, PhD Assistant Professor of Forest Genomics School of Forestry Northern Arizona University

Amanda De La Torre <Amanda.de-la-Torre@nau.edu>

---

## NTNU Trondheim AvianEvolutionaryEcol

PhD Position in Evolutionary Ecology: Dynamics of immigration, inbreeding and fitness in song sparrows

We have a fully-funded PhD position in Evolutionary Population Ecology available at the Centre for Biodiversity Dynamics, NTNU, Trondheim, Norway.

The Centre for Biodiversity Dynamics is a leading cross-

disciplinary Centre of Excellence, with primary interests in population ecology, evolutionary biology and community dynamics. It works at the interface between biology and mathematical sciences, and strives to apply cutting-edge theoretical and statistical frameworks to field data to resolve key questions in the context of both fundamental and applied science. Further information is available at <http://www.ntnu.edu/cbd> About the project Population and evolutionary dynamics depend critically on the outcomes of dispersal events among sub-populations, and resulting spatial movements of individuals and genes. Immigration and resulting genetic introgression can increase sub-population fitness by alleviating local inbreeding (i.e. 'genetic rescue'), but can also decrease sub-population fitness by introducing alleles that are locally maladaptive (i.e. 'immigration load'). Yet, it remains unclear how such effects can work together to increase or decrease the chance of local population persistence in the short-term and the longer-term.

This PhD project will use exceptional long-term data from free-living song sparrows (*Melospiza melodia*) to dissect the short-term and longer-term effects of immigrants on population genetic composition and local fitness. It will also aim to bring together strands of evolutionary theory to provide new insights into the compound evolutionary effects of immigration in fragmented populations with inbreeding and local adaptation.

The student will work with Professors Jane Reid and Henrik Jensen at NTNU, with strong collaborative links with Professor Peter Arcese and Dr Pirmin Nietlisbach (University of British Columbia, Canada), and Professor Lukas Keller (University of Zurich, Switzerland).

Job description The PhD project will involve sophisticated statistical analysis of existing long-term field data, and theory development using mathematical and/or simulation approaches. There will be opportunities to participate in fieldwork and further research training in Canada and Switzerland. The project would suit a highly motivated and numerate student with enthusiasm for confronting evolutionary theory with field data. Full training in key aspects of the project, and associated transferable skills, will be provided. The position provides an excellent opportunity for students who wish to qualify for future work in research positions.

Qualification requirements We seek candidates who have a strong academic record and interests in quantitative evolutionary ecology and/or population biology, of any nationality and country of educational origin. The working language will be English. The qualification requirement is completion of a master's degree or second degree (equivalent to 120 credits) in biology or equivalent edu-

cation, with a grade of B or better in terms of NTNU's grading scale < <https://innsida.ntnu.no/wiki/-/wiki-English/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.

General information about working at NTNU can be found here: [www.ntnu.edu/nirs](http://www.ntnu.edu/nirs) A good work environment is characterized by diversity. We encourage qualified candidates to apply, regardless of their gender, functional capacity or cultural background. Under the Freedom of Information Act (Offentleglova), information about the applicant may be made public even if the applicant has requested not to have their name entered on the list of applicants.

Informal enquiries about the position are very welcome, and can be directed to Prof. Jane Reid, e-mail [jane.reid@abdn.ac.uk](mailto:jane.reid@abdn.ac.uk)

About the application Please submit your application electronically via [jobbnorge.no](http://jobbnorge.no) with your CV, diplomas and certificates. Applicants invited for interview must include certified copies of transcripts and reference letters. Applicants from universities outside Norway are kindly requested to include a Diploma Supplement or a similar document, which describes in detail the study and grade system and the rights for further studies associated with the obtained degree.

— / —

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>

---

## PrincetonU EEBPreview Oct3-6

Princeton EEB Scholars Preview Weekend

The Department of Ecology and Evolutionary Biology at Princeton University is offering a special preview weekend - the EEB Scholars Program - this upcoming October 3-6, 2019 for students considering graduate school. The goal of this weekend is to invite competitive prospective graduate applicants to campus in order to showcase the department, demystify the graduate application process, and highlight participants' research

experience. We especially encourage students from underrepresented minority groups and those inhabiting other axes of underrepresentation in STEM to apply.

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

Please direct any questions to [EEB.Scholars@princeton.edu](mailto:EEB.Scholars@princeton.edu).

“Beth E. Leman” <[bl5@princeton.edu](mailto:bl5@princeton.edu)>

---

## Rennes PlantGenomeEvolution

Dear All,

I announce a PhD position in evolutionary genomics on recombination and plant genome evolution to work at the ECOBIO lab in Rennes (<https://ecobio.univ-rennes1.fr>). The project is already funded but the candidates will have to take the EGAAL doctoral school contest (<https://ed-egaal.u-bretagne.fr>) in June. The position will then start in October 2019. Please contact me for further information.

Sylvain

Project description Recombination is a central mechanism of eukaryotes life cycle. It allows genetic mixing during meiosis, which create new genetic combinations every generations, increasing genetic diversity and the efficacy of selection. Recombination also has local molecular consequences as the very chromosomal position where it occurs, as it involves DNA break and repair mechanisms. In many species, these repair mechanisms are biased towards G and C nucleotides, which leads to apparent selection for GC (aka GC-biased gene conversion, gBGC). gBGC enriches genome in G and C and can counteract natural selection. Characterizing recombination patterns and their consequences is thus crucial to understand genome evolution and how species respond to selection and adapt to their environment. Flowering plants offers a high variation in genomic characteristics: genome size, number of chromosomes, recombination rate, GC content. However, despite these striking variations, the study of base compositions is rather recent compared to animal species and recombination patterns

have been characterized in a handful of plant species only. The working hypothesis of the project is that variations in recombination patterns contribute to genomic diversity for genetic diversity, selection efficacy and base composition. More precisely: - Is GC content higher in highly recombining species and genomic regions? - Does recombination increase genetic diversity and the efficacy of selection? - Do these effects vary among species at the flowering plant scale? Comparative approach will be used in more than 50 species representing the major groups of flowering plant phylogeny using publically available data: full genome sequences, genetic maps, polymorphism data (from full genome re-sequencing data).

The project will require knowledge in molecular evolution/evolutionary genomics/population genetics, bioinformatics or skills in programming, and statistics.

Sylvain Glin Senior researcher / Chercheur CNRS UMR 6553 ECOBIO, Rennes <http://sylvain.glemin.pagesperso-orange.fr/sylvain-glemin/-Home.html> Glin Sylvain <sylvain.glemin@univ-rennes1.fr>

---

## RyersonU PlantPopulationBiology

### \*The Opportunity\*

The Campbell lab is recruiting graduate students (MSc and PhD) and a research technician! Our research links evolutionary and ecological processes in plant population biology. In particular, reproductive processes are highly labile in plants with immediate evolutionary, phenotypic, and demographic consequences. So, we study plant populations and their genetic systems (the reproductive machinery and processes that influence gamete quality and quantity, gamete dispersal, mating, fecundity and, ultimately, adaptive evolution). To accomplish this work we bring together folks with diverse skill sets and we're attempting to approach these topics with disruptive technologies. Thus, we're looking for folks with backgrounds in horticulture and plant science, public relations and citizen science, biochemistry, physics/computer science, and, of course, ecology or evolution. Current research projects ask questions around genetic and environmental control of quantitative genetic trait expression, plant mating and dispersal, and genotype-by-environment interactions, and all projects solve basic and applied questions in plant population biology. Positions start no later than September 1, 2019.

Located in downtown Toronto, Ryerson University is a distinctly urban, culturally diverse teaching and research institution offering more than 100 undergraduate and graduate programs, distinguished by a strong commitment to excellence in teaching, research and creative activities, to over 45,000 students. Ryerson is known for its culture of entrepreneurship and innovation and is recognized as a city builder, as it continues its growth through award-winning architecture and expansion of its campus. From our lab, trainees have found careers in academia (as professors and lab research technicians), scientists (horticultural managers, breeders, research directors, health care workers, municipal water scientists), and teachers (in both public outreach and high school science).

### \*Responsibilities\*

The successful candidate for the research technician position will engage in a combination of research, administrative and management duties. The candidate will be expected to carry out analytical chemical assessment of plant material (which will contribute to peer-reviewed research), potentially develop lab-specific protocols, as well as maintain standard operating protocols of the lab. The candidate will contribute to mentoring undergraduate and graduate students to facilitate junior scholars' research and education. Given that this candidate will be an integral part of many projects, we are looking for someone who is the 'social glue' in a group! The candidate will engage in maintaining an inclusive, equitable, and collegial work environment across all activities.

The successful candidates for the graduate student positions will engage in a combination of research (through paid RAships), teaching (through paid TAships), and service, as well as a typical classwork load. The candidate will be mentored through the process of developing and carrying out independent research projects within funded themes, applying for their own sources of funding, and publishing in peer-reviewed forums. We are seeking candidates for both MSc and PhD positions. We are looking for folks who are collegial, inclusive and promote equity in all that they do. We want a wonderful colleague and collaborator.

### \*Qualifications: \*

Candidates for the research technician position should have a MSc in analytical chemistry or closely related field by the appointment date. Note, that we will consider applicants with either a BSc in analytical chemistry AND practical experience in analytical chemistry industry positions with at least one publication (either peer-reviewed journal article or patent).

The successful candidate must present strong re-

search experience and provide strong endorsements/recommendations by referees on their abilities as an analytical chemist.

Evidence of, or potential for, excellence in mentoring and collaborative work must be provided through descriptions of mentoring and research collaboration accomplishments. Please demonstrate evidence of strong communication skills and a demonstrated ability to work with and potentially lead a team.

Candidates must have a commitment to our values of Equity, Diversity, and Inclusion (EDI) as it pertains to mentoring and scholarly research, including a demonstrated ability to make learning accessible and inclusive for the diverse student population that works in our lab.

\*Equity at Ryerson \*

At the intersection of mind and action, Ryerson is on a transformative path to become Canada's leading comprehensive innovation university. Integral to this path is the placement of equity, diversity and inclusion as fundamental to our institutional culture. Our current academic plan outlines each as core values and we work to embed them in all that we do. It is a central tenet of the Campbell lab.

— / —

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

## SLU Uppsala PlantGenomics

We are looking for a doctoral student for the project "New effective methods for the processing of timothy". Timothy is the most cultivated forage grass in Sweden, but climate change and altered cultivation conditions have accelerated the need for new, well-adapted timothy varieties to maintain high cultivation efficiency throughout Sweden. Swedish agriculture is therefore in great need of a more efficient domestic plant breeding of timothy. The aim of the project is to develop and introduce new, more efficient plant breeding methods, based on the latest achievements in plant genomics and genetics, in order to shorten the time and reduce the cost of breeding in Timothy.

The position is placed at the Department of Plant Biology at the Swedish University of Agricultural Sciences

(SLU), Uppsala, Sweden. The department conducts research on plant developmental biology, epigenetics, diversity and defence. The department is part of Uppsala BioCentre, which provides an excellent research environment combining competencies in plant biology, forest mycology and plant pathology, microbiology, food science, chemistry and biotechnology. The department is also part of the Linnean Center for Plant Biology in Uppsala, a platform for interactions between plant researchers at SLU and Uppsala University. Uppsala is also hosting a SciLifeLab node that provides national platforms for sequencing, proteomics and microscopy.

The candidate should have a suitable master's degree in biology, agronomy or an equivalent education. You will work closely with other researchers and graduate students in a creative and stimulating environment. Therefore, you should have an easy time working with others but also the ability to work independently with your own research topics. Creativity and drive are personal characteristics that are desirable due to the knowledge-driven aspect of the project. Excellent proficiency in English is required, as English is the working language in the research group. Documented experience of working with field trials and/or computational or statistical analyses of genetic data is highly desirable.

For more more information and to apply visit: <https://www.slu.se/en/about-slu/jobs-vacancies/?rmpage=job&rmjob!99&rmlang=UK> The Swedish University of Agricultural Sciences (SLU) develops the understanding and sustainable use and management of biological natural resources. The university ranks well internationally within its subject areas. SLU is a research-intensive university that also offers unique degree programmes in for example rural development and natural resource management, environmental economics, animal science and landscape architecture. SLU has just over 3,000 employees, 5,000 students and a turnover of SEK 3 billion. The university has invested heavily in a modern, attractive environment on its campuses in Alnarp, Umeå and Uppsala.

Pär K. Ingvarsson Professor, Plant genomics and breeding Department of Plant Biology Uppsala BioCenter Swedish University of Agricultural Sciences and Linnean Center for Plant Biology PO-Box 7080 SE-750 07 Uppsala, Sweden

Pär Ingvarsson <par.ingvarsson@slu.se>

---

## SouthDakotaStateU PlantPhylogenetics

One MS or PhD research assistant position is available (Aug 2019) in the Latvis Lab of the Department of Natural Resource Management for students interested in botany, biodiversity, phylogenetics, or plant conservation. We are particularly interested in recruiting students to work in either of the two areas: 1) systematics and diversification in the parasitic angiosperm family Orobanchaceae, or 2) community phylogenetics and biodiversity assessments of grasslands in the Northern Great Plains. Successful applicants will have a degree in Biology, Botany, or related field and a strong background natural history and plant evolution. Experience with plant identification, phylogenetic analyses, and data manipulation/analysis using R is desired. A willingness to learn new techniques is required. The graduate assistantships include a competitive stipend and tuition waiver.

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

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

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

“Latvis, Maribeth” <Maribeth.Latvis@sdstate.edu>

---

## ThunenInst Germany eDNA

Job offers of the Thunen Institute scientific assistant (f/m/d) (PhD student)

The Institute of Fishery Ecology at the Johann Heinrich von Thunen-Institute, Federal Research Institute for Rural Areas, Forestry and Fisheries, in Bremerhaven is offering a position for a

scientific assistant (f/m/d)

(PhD student)

with 65 % of the regular weekly working time. The position is filled until 13.12.2021 at the earliest opportunity.

The employment relationship shall be limited in time in accordance with section 2(1) sentence 1 of the Wissenschaftszeitvertragsgesetz. The call for applications is therefore directed at applicants who, in addition to their employment relationship, wish to pursue their own continuing academic education, in particular their doctorate. In this context, the Thunen Institute for Fishery Ecology cooperates with various universities.

Background of the project:

The aim is to determine the competitive potential of high-throughput sequencing methods in comparison to conventional fisheries surveys for the survey of fish stocks. At the Thunen Institute for Fishery Ecology, methods for the qualitative (meta barcoding) and quantitative analysis (RT-PCR/dPCR) of environmental DNA (eDNA) of important fish species from seawater samples will be developed and applied.

Tasks:

Literature research on the current status of eDNA analysis with a focus on marine fish stocks. Method development from sampling to sequence analysis (NGS) with special emphasis on avoiding contamination and methodological bias Development of bioinformatic evaluation strategies Multivariate data analysis and statistical modeling Writing scientific publications Presentation of the results

Technical requirements:

University degree (M.Sc./Univ.-Dipl.) in the field of molecular genetics, fisheries biology or related qualifying study courses practical laboratory experience with molecular genetic working methods basic knowledge of NGS methods and bioinformatics good knowledge of

statistical evaluation methods (preferably with R) very good knowledge of written and spoken English

Personal requirements:

Readiness for doctorate Willingness to participate in sea-going research trips High level of teamwork skills and ability to work independently Independent and structured way of working Ability to analyse complex issues

We offer you a highly interesting activity in applied research with a strong practical orientation at the interface between science and policy advice, the results of which also meet with considerable public interest.

The employment is governed by the Wage Agreement for Public Services (TVöD-Bund). The payment of remuneration is carried out according to tariff-category 13 TVöD.

The Thunen Institute promotes the professional equality of women and men and is thus especially interested in applications from women.

Severely disabled applicants with equal qualification will be given particular consideration. Only a minimum physical aptitude is expected from them.

For questions and additional information, please contact Dr. Erik Eschbach (Tel.: 0471/94460 278, E-Mail: erik.eschbach@thuenen.de).

Please send your application with your curriculum vitae in table form, a description of your training and professional career as well as copies of certificates, keyword 19-122-FI, by 28.04.2019, preferably electronically as one (1) pdf document, to:

fi-bewerbungen@thuenen.de

or in writing to the:

Johann Heinrich von Thunen-Institute

Institute for Fisheries Ecology

Herwigstrasse 31, 27570 Bremerhaven, Germany

Informations about Artikel 13 DSGVO: [www.thuenen.de/datenschutzinweis-bewerbungen](http://www.thuenen.de/datenschutzinweis-bewerbungen)  
Erik Eschbach <erik.eschbach@thuenen.de>

## U Aberdeen Beetle Expt Evolution

A fully-funded 4 years PhD position in experimental evolution is available at the School of Biological Science, University of Aberdeen, UK.

Title: Joint eco-evolutionary dynamics of dispersal and female multiple mating: empirical test. Supervisors: Dr. Greta Bocedi, Dr. Lesley Lancaster

This PhD project will use experimental evolution on the seed beetle model species, *Callosobruchus maculatus*, to study the joint eco-evolutionary dynamics of dispersal, mating system and inbreeding. We will test emerging theoretical predictions on how dispersal and mating system co-vary in space, how they jointly evolve, and the consequences for species' responses to changing environments. The ability of individuals to move (dispersal) to avoid the negative consequences of inbreeding (mating with self or relative), and the acquisition and choice of mates (mating system) are fundamental for species' persistence. Dispersal and mating system determine how genes are transmitted across generations and in space, and genetic variation ultimately determines a species' potential to adapt to new conditions. Additionally, although they have been studied largely separately, dispersal and mating system are tightly interconnected. Female multiple mating, in particular, is a component of the mating system that is now being shown to be widespread across organisms and to have far-reaching consequences for species evolution and potentially for species' responses to environmental changes<sup>1</sup>. As with dispersal<sup>2</sup>, female multiple mating is thought to evolve to allow inbreeding avoidance<sup>3,4</sup>. However, we still do not know how these two fascinating behaviours affect each other's evolution and feed back to the population inbreeding level, how environmental changes impact their evolution and what this means for species' persistence. We are developing theoretical predictions on how we should expect dispersal and female multiple mating to jointly evolve as a consequence of population structure and environmental changes, and to impact on species' survival. With this project the student will start testing this theory in the laboratory using a model species for the study of mating system and dispersal, the seed beetle<sup>5,6</sup>. The student will create microcosms with multiple populations of beetles where we will be able to test for joint evolution of dispersal, female multiple mating and level of inbreeding in both static environ-

ments and under range expansion conditions. Using next generation sequencing approaches, the student will be able to assess genetic variants and frequency shifts putatively involved in the evolution of dispersal and polyandry. This project will therefore provide a necessary step change in experimental study of dispersal and mating system by fully accounting and testing for their interactions and eco-evolutionary feed-backs, and thus start making headway in understanding how these two behaviours might jointly evolve in real organisms.

This project offers the student the opportunity to gain training in experimental evolution, quantitative genetics and genomic analyses. Further, the student will join a group that is strong in eco-evolutionary modelling and will have the opportunity of receiving excellent training on theory development and modelling. Candidates should have (or expected to achieve) a minimum of 2:1 Honours degree, ideally (but not required) an MSc in ecology, evolution or related, strong theoretical skills and passion and enthusiasm for developing experimental evolution studies.

The PhD is funded 100% by The Royal Society and the funding has already been secured. The studentship covers the registration fees (for UK/EU students), the student salary for 4 years, experimental costs and travel for training and conference attendance for the student.

Expected starting date is 1st October 2019.

Applications can be submitted by the 30th of April 2019, here: <https://www.abdn.ac.uk/study/-postgraduate-taught/apply.php> For enquiries please contact [greta.bocedi@abdn.ac.uk](mailto:greta.bocedi@abdn.ac.uk)

Dr Greta Bocedi Royal Society University Research Fellow School of Biological Science, University of Aberdeen Zoology Building, Tillydrone Avenue, AB24 2TZ Tel: +44 (0)1224 272392 [greta.bocedi@abdn.ac.uk](mailto:greta.bocedi@abdn.ac.uk)

“Bocedi, Greta” <[greta.bocedi@abdn.ac.uk](mailto:greta.bocedi@abdn.ac.uk)>

---

## UAlabama Huntsville EvolutionaryBiol

The Culumber Lab of Evolutionary Biology at the University of Alabama in Huntsville is currently seeking 2-3 students interested in pursuing an MSc or PhD to join our laboratory in Fall 2019 or Spring 2020. We are particularly interested in motivated students with an interest in integrating across disciplines including ecology, behavior, and physiology and incorporating ge-

nomonic approaches to address fundamental questions in evolutionary biology.

Potential projects include: (1) Examining the role of temperature in speciation and the maintenance of adaptive genetic variation, (2) the evolutionary consequences of indirect genetic effects, and (3) the underlying mechanisms and role of animal personality in biological diversification. Research in the laboratory focuses primarily on livebearing fishes as a model to understand broader evolutionary phenomena. However, highly-motivated students with interests in exploring other lines of research on evolutionary biology in any study system are encouraged to apply. Prior experience working with fish is not necessary, but prior research experience (either undergraduate or MSc) is highly preferred. The ideal candidate will have research experience with one or more of the following areas: molecular biology (DNA/RNA isolation, PCR, sequencing), bioinformatics, geographical information systems (GIS), animal behavior, or animal physiology.

Student support includes teaching assistantships, internal scholarships, and fellowships (internal and extramural).

If you are interested in joining the lab, please contact the PI at [zwc0001@uah.edu](mailto:zwc0001@uah.edu) and include a cover letter describing your research experience and interests, as well as a CV.

Zachary Culumber, PhD Assistant Professor Department of Biological Sciences University of Alabama in Huntsville

[Zachary.Culumber@uah.edu](mailto:Zachary.Culumber@uah.edu)

---

## UBasel 2 EvolutionRangeLimits

Two PhD Positions in Evolutionary Ecology, 100%

Working with Yvonne Willi in the Plant Ecology and Evolution group at the University of Basel, Switzerland. Positions are funded by the Swiss National Science Foundation (SNF) for a duration of 4 years. The goal is to understand the causes of geographic range limits? why evolution fails at the warm and cold end of species distribution. The research is fundamental to evolutionary biology, ecology, global change research and environmental stress research.

The evolutionary causes of geographic range limits are poorly known. Theory points to changes in the selection

regime and genetic limitations. The selection regime may be important if environmental gradients steepen at the edge of the distribution. Genetic limits may arise because of low genetic variation in individual environmental tolerances or because of genetic correlations antagonistic to the direction of selection.

Your Tasks Working with the plant *Arabidopsis lyrata*, the two students will perform crossing experiments and selection experiments in the field, assess performance under stressful conditions representative of distribution edges, and conduct whole-genome sequencing. Fieldwork will take place in eastern states of the US, in collaboration with local universities.

Your Profile Candidates should have an enthusiastic interest in plants and their evolution, and a strong background in quantitative thinking, experimental design, statistical analysis/bioinformatics, and rearing plants. Applicants must have a university degree in the natural sciences that allows entrance to a PhD program (ideally in evolutionary biology or ecology), and very good organizational, analytical, and scientific writing skills. Applicants should have a driver's license.

We offer The project is based at the Department of Environmental Sciences, University of Basel, Switzerland. The Department offers a stimulating environment, including a rich spectrum of research activities in life sciences (plant ecology, population genetics, evolutionary biology, plant physiology and molecular and cell biology). Students will be enrolled in the PhD program of the Zurich-Basel Plant Science Center. Basel is a mid-sized Swiss city, well connected and offering a broad range of cultural and recreational activities. Ideal starting date is October 2019 but is open to negotiation.

Contact For more information, contact Yvonne Willi (yvonne.willi@unibas.ch). Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) their CV, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information of two references (all as a \*\*\*single PDF\*\*\*) to: franziska.grob@unibas.ch. Applications are welcome until the position is filled and will be reviewed starting on May 6, 2019.

Yvonne Willi <yvonne.willi@unibas.ch>

---

## UBasel AlpineButterflyEvolution

PhD Student (100%) in Evolutionary Biology Start in July 2019

The prospective PhD student will be supervised by Kay Lucek and be part of the Plant Ecology and Evolution group at the University of Basel, Switzerland. The project is funded by the Swiss National Science Foundation (SNSF) for a duration of 3 years. The goal is to understand the role of chromosomal fusion and fission during speciation and secondary contact of closely related species. The project addresses fundamental questions in evolutionary biology both on a micro- and macroevolutionary scale and has significant implications for conservation.

Theory predicts chromosomal rearrangements to advance the process of speciation by acting as intrinsic barriers to gene flow yet empirical studies are lacking. This project aims to investigate role of chromosomal fusion and fission on i) the rate of speciation, ii) the degree and direction of interspecific gene flow and iii) reinforcement during secondary contact. Different types of data will be combined, including genomics, morphology and ecology and analysed using state-of-the-art phylogenomic, population genomic and statistic approaches. Our model system are *Erebia* butterflies, one of the most speciose butterfly genera in the temperate regions.

Your Tasks

The PhD candidate will conduct extensive fieldwork, collecting *Erebia* butterflies in the Swiss Alps. Collected species will be morphologically confirmed and subsequently sequenced. The genomic data will be used to conduct in-depth phylogenomic and population genomic analyses to identify the role of chromosomal rearrangement during speciation and secondary contact.

Your Profile

We are looking for a self-driven, highly motivated and dedicated candidate who is enthusiastic about evolutionary biology and brings strong conceptual thinking together with profound bioinformatic and/or statistical knowledge. Applicants must have a university degree in the natural sciences that allows entrance to a PhD program (ideally in evolutionary biology or ecology), and very good organizational, analytical, and scientific (English) writing skills. The candidate should be prepared to conduct sometimes strenuous fieldwork in the



Alps.

We offer you The research will be carried out within a 3-year project, starting July 2019. The project is based at the Department of Environmental Sciences, University of Basel, Switzerland. The Department offers a vibrant and interdisciplinary research environment, combining a broad spectrum of research activities in life sciences, including population genetics, evolutionary biology, evolutionary ecology and molecular and cell biology. Salary and social benefits are provided according to University of Basel rules. Finally, Basel is a mid-sized Swiss city, well connected and offering a broad range of cultural and recreational activities.

Contact For more information, contact Kay Lucek ([kay.lucek@unibas.ch](mailto:kay.lucek@unibas.ch)). Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) their CV, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information of two references (all as a **\*\*\*single PDF\*\*\***) to: [franziska.grob@unibas.ch](mailto:franziska.grob@unibas.ch). Applications are welcome until the position is filled and will be reviewed starting on May 6, 2019.

[kay.lucek@unibas.ch](mailto:kay.lucek@unibas.ch)

---

## UBasel PlantPhylogeneticsEvolution

PhD Position in Plant phylogenetics and evolution

100%, start July 2019 or upon agreement

The working group of Dr. Jurriaan de Vos (Department of Environmental Sciences, University of Basel, Switzerland; [ppe.duw.unibas.ch/en/devos/](http://ppe.duw.unibas.ch/en/devos/)) investigates the evolution and ecology of plant clades, with special emphasis on reproductive diversity. Our research primarily uses comparative phylogenetic approaches and aims at understanding the drivers of reproductive trait evolution and identifying the macro-evolutionary axes along which life diversifies. The open position is funded through the SNF project “Plant reproduction of the alpine zone: disentangling ecological drivers of trait evolution”, that investigates how plants adapt during major ecological transitions. The project addresses drivers of reproductive trait evolution in genera that radiated across elevational belts in multiple mountain systems. It addresses the extent to which species from different evolutionary backgrounds evolve similarly (convergently) along the same environmental gradients, helping us to understand whether studies of adaptation on few species

can be generalized.

Your Tasks The successful candidate will: improve phylogenies of multiple large plant genera using phylogenomic methods; assemble trait- and locality datasets based on field work (Alps, Andes) and herbarium specimens; use statistical phylogenetic methods to test how environmental factors drive trait evolution; disseminate results.

Profile We are looking for a dynamic, reliable and motivated PhD-student with a degree in biology or related discipline. The position requires a strong interest in plant evolution, the ability to work analytically with large datasets, the willingness to travel to remote, steep field sites and to herbaria abroad, and excellent spoken and written English language skills. Prior experience with statistical phylogenetics / comparative methods and next generation sequence data is highly desirable.

We Offer We offer a PhD position in an international and interdisciplinary research environment at the University of Basel, Switzerland. The project will benefit from the University’s excellent facilities, including the Herbaria and a fully equipped alpine research station ([www.alpfor.ch](http://www.alpfor.ch)). Salary and social benefits are provided according to University of Basel rules. Basel is a vibrant international city with a medieval old town, offering excellent quality of life.

Contact Please email your complete application in a single pdf file (containing your CV; a motivation letter that includes your career goals; and contact information of at least two references) to Mrs. Maura Ellenberger ([maura.ellenberger@unibas.ch](mailto:maura.ellenberger@unibas.ch)). Review of applications will start 1 May 2019 and continue until the position is filled. Further information can be obtained from Jurriaan de Vos ([jurriaan.devos@unibas.ch](mailto:jurriaan.devos@unibas.ch)).

Jurriaan de Vos <[jurriaan.devos@unibas.ch](mailto:jurriaan.devos@unibas.ch)>

---

## UBern FishEvolutionaryEcol

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, Department of Fish Ecology and Evolution (FishEc) has a vacancy for a PhD student in Fish Evolutionary Ecology.

Applicants should have or anticipate finishing an MSc or similar before the summer 2019 in a relevant field of biology, ecology, or environmental science and a strong interest in evolutionary ecology, life history variation, adaptive radiation and animal/fish migration.

Movement is a fundamental and ubiquitous feature of animals, and the movement of individual organisms is integral for many vital ecological and evolutionary processes. Migration is one of nature's most spectacular forms of animal movement and has a long and illuminating scientific history, with exciting new discoveries year after year. Centuries of research on animal migration have highlighted that migratory individuals most often show distinct adaptations to the migratory travel and profit from temporally changing relative benefits of alternative habitats. However, being migratory also means experiencing natural selection in at least two different habitats. Unfortunately, our knowledge on adaptation to a migratory life style is typically limited to adaptation to the migratory travel per se. Knowledge about all aspects of migratory versus non-migratory life history is crucially needed in order to understand the ecological dynamics of natural selection over space and time.

To enable strong empirical research on the ecological and evolutionary aspects of animal migration, replicate study systems are needed. This is for many of the classical migration study systems unfortunately not the case, e.g. for migration of large herbivores or for most bird migrations. However, migration of charr between streams and fjords in Southern Greenland offers an ideal study system with replication on individual-, on population level and on entire ecosystem level. Charr have after the last glaciation about 10'000 years ago colonized rivers and lakes and adapted to these habitats over time. The abundance of unoccupied niches appear to have caused the spectacular radiations that we have observed replicated in multiple drainage systems.

The current project focuses on fish migration and ecological diversification. Specifically, it will investigate how migratory charr (*Salvelinus alpinus*) diverge in their

migratory patterns and ecology in the resident and in the migratory habitat and additionally how this in turn affects divergence in the resident habitat. The fieldwork will be carried out in streams, lakes and fjords in Southern Greenland and the PhD-student will participate in two field expeditions to Southern Greenland of 1-2 months duration.

The position is funded for four years and will be hosted by the River Fish Ecology group, led by Dr. Jakob Brodersen (<http://www.eawag.ch/en/department/-fishec/main-focus/river-fish-ecology/>) within the FishEc Department (<http://www.eawag.ch/en/department/-fishec/>) and the Section of Aquatic Ecology at University of Bern (<http://www.aqua.iee.unibe.ch/>). The work will be carried out in close collaboration with the research groups of Dr. Blake Matthews, studying eco-evolutionary dynamics of sticklebacks in Greenlandic lakes and Dr. Ole Seehausen, studying biodiversity dynamics. Excellent communication and writing skills in English and ability to work in a team are essential.

The PhD-student will be enrolled at the Institute of Ecology and Evolution, University of Bern and in the West Swiss graduate school in ecology and evolution. The work place is at Eawag's Center for Ecology, Evolution and Biogeochemistry (CEEB) in Kastanienbaum, Lucerne, which besides the Fish Ecology and Evolution Department hosts research group from the Department Surface Waters ? Research & Management and offers a beautiful workplace at the shores of Lake Lucerne, a friendly international working climate and a strong cross-disciplinary research environment. Both departments within CEEB share a common interest in understanding the principles of the functioning of aquatic ecosystems and their susceptibility and adaptability to changing environments, and a common concern for sustainable management of ecosystems and biodiversity. Each department on its own aims at contributing cutting edge science to the development of theory in ecology, evolution and environmental sciences. Building on the synergies that emerge between these fields, the CEEB aspires to contribute to a future synthesis of evolutionary biology and ecosystem science.

Eawag offers a unique research and working environment and is committed to promoting equal opportunities and to support the compatibility of family and work. Applications from ethnic minorities and women are especially



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>

---

## UFlorida EvolutionaryEcol

Funding very recently became available for a Ph.D. student to start Fall 2019.

Research in my lab primarily focuses on sexual selection in insects, examining the evolutionary interplay of behavior and morphology. Ongoing projects in the lab include studies of trade-offs between sexually-selected weapons and testes; the effect of nutrition and social environments on female life history traits, male weapon structure, testes size, and male fighting behavior; and the role of phenotypic plasticity in the processes of invasion. We are currently reconstructing a phylogeny of the Coreidae to test hypotheses of weapon shape evolution.

The successful applicant for this position should have a M.S. or commensurate experience in evolution, behavior, or ecology. Prospective Ph.D. students are encouraged to immediately email Christine W. Miller at [cwmiller@ufl.edu](mailto:cwmiller@ufl.edu). In your email, please include a statement addressing: 1) the kinds of research questions that you would like to pursue, 2) how these fit in with current lab research, 3) a brief overview of your previous academic and research experiences. Also include: 4) CV or resume, 5) GRE scores, 6) unofficial transcripts.

Visit [www.millerlab.net](http://www.millerlab.net) to learn more about what we do.

One competitive applicant will be provided a tuition waiver and a competitive stipend for four years to complete a Ph.D.

Information about Gainesville, Florida:

Situated in the rolling countryside of north central Florida, Gainesville, is close to world-class fishing, snorkeling, canoeing, tubing and kayaking. On land, those so inclined may enjoy birding, hiking, biking, fishing and pretty much everything else under the sun. Home of the University of Florida, seat of Alachua County's government and the region's commercial hub, Gainesville is progressive, environmentally conscious and culturally diverse. The presence of many students and faculty from abroad among its 99,000-plus population adds a strong cross-cultural flavor to its historic small-town Southern roots. Its natural environment, temperate climate and civic amenities make Gainesville a beautiful, pleasant, and interesting place in which to learn and to live.

Christine W. Miller Associate Professor | Entomology & Nematology Department University of Florida, USA  
email: [cwmiller@ufl.edu](mailto:cwmiller@ufl.edu) phone: (352) 273-3917 web: [www.MillerLab.net](http://www.MillerLab.net) facebook: @bugweapons

"Miller, Christine W." <[cwmiller@ufl.edu](mailto:cwmiller@ufl.edu)>

---

## UHongKong BehaviouralEvolutionElephants

PhD Studentship Available

I have a position available for a student wishing to pursue a PhD in the School of Biological Sciences at the University of Hong Kong on the ecology of elephants.

Elephants are large-bodied, long-lived and socially complex mammals. One of my research areas is to understand how elephants make sense, particularly in relation to humans, be it through comparative studies of life history or ecology, or incorporating humans into studies to understand how elephants respond to their environment.

I have access to populations of captive elephants in Asia, and some opportunities for working with wild African elephants.

Projects on the following topics will be considered: Life histories Behavioural ecology and experimental approaches to behaviour Novel approaches to approaching human-wildlife interactions Applications linked to living in captivity and/or conservation of wild elephants

Essential requirements: An excellent academic track record, including undergraduate degree of at least a high upper second-class undergraduate degree, or GPA of 3.5 or over A passion for the general field and your specific topic The desire and drive to become an independent researcher

Desirable requirements: Field and/or lab experience clearly linked to the topic of your proposal Publishing experience Masters degree with a high grade

The position is available to start in September 2019 or as soon as possible thereafter. If you are interested in these topics, please contact me with a draft research plan and CV. Those applying by 30th April have the opportunity to apply for university scholarships. If selected I can develop a research proposal with you and guide you through the application process. Contact me on [hsmumby@hku.hk](mailto:hsmumby@hku.hk)

Dr Hannah S. Mumby Principal Investigator - The Bull

Elephant Network Project Assistant Professor - University of Hong Kong

Twitter: @hannahsmumby hannahsmumby.co.uk

hs.mumby@gmail.com

## UKiel Marine Evolutionary Genomics

The 'Helmholtz School for Marine Data Science' (MarDATA) invites applications for:

x2 PhD positions in computational evolutionary genomics

Application deadline is May 15, 2019.

PhD research topics:

1. Developing bioinformatic tools for detecting low-frequency genetic variants in large marine (meta)genomic data sets

Supervisors: Prof. Dr. Thorsten Reusch, GEOMAR Helmholtz Centre for Ocean Research Kiel, Marine Evolutionary Ecology, treusch@geomar.de

Prof. Dr. Tal Dagan, University of Kiel, Institute for Microbiology, tdagan@ifam.uni-kiel.de

Disciplines: bioinformatics, genomics, metagenomics, population genetics, evolutionary biology

Keywords: mutation, re-sequencing, next-generation sequencing, adaptive dynamics, unequal read coverage, genetic elements

Details: <https://www.mardata.de/topics/-bioinformatics-and-genomic-analyses/developing-bioinformatic-tools-for-detecting-low-frequency-genetic-variants-in-large-marine-metagenomic-data-sets/>

2. A machine-learning approach for detection of mobile replicons in metagenomics Supervisors: Prof. Dr. Ute Hentschel Humeida, GEOMAR Helmholtz Centre for Ocean Research Kiel, Marine Ecology, uhentschel@geomar.de Prof. Dr. Tal Dagan, University of Kiel, Genomic Microbiology, tdagan@ifam.uni-kiel.de

Disciplines: Bioinformatics, Machine-Learning, Marine Microbiology Key words: Metagenomes, Mobile replicons, Machine-learning, Marine sponges Details: <https://www.mardata.de/topics/bioinformatics-and-genomic-analyses/a-machine-learning-approach-for-detection-of-mobile-replicons-in-metagenomics/>

Doctoral candidates in the Helmholtz School for Marine Data Science (MarDATA) will be jointly supervised by

two professors, who have faculty recognition for doctoral supervision at one of the partner universities. This tandem consists of integrated knowledge and expertise represented by an expert located at GEOMAR, who will provide the marine research focus to the thesis, and a second expert located at a partner university (Kiel) who will lead the information & data science methodologies. Doctoral degrees will be awarded in the field of natural sciences (Dr. rer. nat.). After receiving a general introduction to marine sciences, block courses will focus on a range of information & data science methodologies: advanced scientific programming, statistics, data bases, machine learning, deep learning, computer vision and FAIR principles. A series of regular seminars and colloquia will ensure the continuous exchange among all partners. Summer schools will provide an in-depth exchange between information & data science topics and their application to marine research. The use of attractive (international) locations will ensure team-building efforts. Summer schools can be held at one of the research stations of GEOMAR (e.g., Ocean Science Center Mindelo, Cape Verdes), of AWI (e.g., Svalbard, Sylt, Helgoland), or on board a research vessel (e.g. RV Polarstern).

The language of the graduate school is English. Financial support is provided throughout the program.

Candidate qualifications: (1) Master of Science or Diploma degree in Molecular Evolution, Bioinformatics or related fields. (2) Knowledge and experience in the analysis of genomic data. Any of following expertise is an advantage: phylogenomics, genomics, transcriptomics, programming, biostatistics. (3) Good oral and written communication skills in English. (4) Skills and motivation to communicate and interact with other scientists.

To obtain further information about the PhD program and application details please visit our website at <https://www.mardata.de/>. The deadline for applications is May 15, 2019. The selection process will be held in June 2019. Project beginning is flexible between July-December 2019.

For enquiries regarding the positions and research topics please contact Prof. Tal Dagan: tdagan@ifam.uni-kiel.de

Applications may be submitted at: <https://www.mardata.de/apply/> (only online application possible),

Tal Dagan <tdagan@ifam.uni-kiel.de>

---

## UManitoba BeeSystematics

### GRADUATE STUDENT POSITION: BEE SYSTEMATICS

An MSc or PhD level position is available in the Department of Entomology, University of Manitoba (<http://umanitoba.ca/faculties/afs/dept/entomology/-index.html>). Students with interests in taxonomy, phylogenetics, or bee diversity are encouraged to apply. The successful applicant will lead a NSERC funded project studying the systematics of a group of bees. Taxonomic emphasis in the lab is on halictid bees, particularly *Lasioglossum*. Phylogenetic projects are expected to involve analysis of Ultra-Conserved Elements and may include collaborative studies with external partners. Students with an interest in revisionary taxonomy are also encouraged to apply.

The successful applicant will have a strong background in entomology, bee diversity and/or systematics. The student will be able to work closely with a team of melittologists at the University of Manitoba. Primary supervision will be in the Gibbs Lab in the Department of Entomology. The Gibbs Labs research focus is in wild bee systematics and biodiversity. There is opportunity to collaborate with additional lab members conducting taxonomic research on *Lasioglossum* or biodiversity surveys of bees in Manitoba. Students are required to take 6 credit hours of coursework (one semester courses are typically 3 credit hours).

The University of Manitoba hosts Canadas only Department of Entomology. Dr. Gibbs is an assistant professor and the curator of the J.B. Wallis-R.E Roughley Museum of Entomology, one of Canadas largest entomology collections. The Department has a well-equipped molecular facility for phylogenetics research. The Gibbs lab strives to be an open and supportive environment for students to thrive in their scholarly pursuits.

**Qualifications.** Masters degree in Entomology, Ecology, or related field for entry to the PhD. Direct entry from a Bachelors will be considered for students of exceptional academic ability and experience in systematics, bioinformatics, and/or bee identification. BSc for MSc position. Minimal GPA requirements are 3.0.

**Desirable traits:** Experience in phylogenetics, bioinformatics or taxonomy; strong writing; well-organized; drivers license and passport; willingness to travel; bilin-

gual.

ANTICIPATED START DATE: SEPTEMBER, 2019.

To apply: Applicants should send a letter of interest, curriculum vitae and contact information for three references to:

Dr. Jason Gibbs, [jason.gibbs@umanitoba.ca](mailto:jason.gibbs@umanitoba.ca)

PLEASE PUT SYSTEMATICS STUDENT IN THE SUBJECT LINE.

Applications will be considered until Apr. 30 or the position is filled.

The University of Manitoba is strongly committed to equity and diversity within its community and especially welcomes applications from women, racialized persons/persons of colour, Indigenous peoples, persons with disabilities, persons of all sexual orientations and genders, and others who may contribute to the further diversification of ideas. All qualified candidates are encouraged to apply; however, Canadian citizens and permanent residents will be given priority.

Jason Gibbs, PhD Assistant Professor Curator, J. B. Wallis / R. E. Roughley Museum of Entomology Department of Entomology University of Manitoba 12 Dafoe Road Entomology Bldg. Rm. 213 Winnipeg, MB, Canada R3T 2N2

Jason Gibbs <[dialictus@gmail.com](mailto:dialictus@gmail.com)>

---

## UmeaU ModelingEukaryoteOrigins

“A Ph.D. studentship in mathematics as related to modeling the evolution of endosymbiosis and the evolutionary origins of eukaryotes is available in the research group of Eric Libby at Umeå University in Sweden (<http://ericlibby.github.io/>). Candidates should have a quantitative background with an interest in building mathematical models of biological systems. The proposed work will feature interdisciplinary projects done in collaboration with Chris Kempes at the Santa Fe Institute.

**Background for the project:** A pivotal event for the evolution of life on earth was the endosymbiotic event in which two previously independent cells merged to give rise to what we now call mitochondria and eukaryotes. This event is thought to have occurred only once and account for the evolution of all large, complex life. Despite its importance, we do not understand the general princi-

ples that govern the probability or fitness consequences of an endosymbiotic event. The aim of this Swedish Research Council-funded PhD position is to address this significant knowledge gap by developing a theoretical framework based on mathematical models that can identify these principles. Useful modeling techniques include differential equations, network approaches, agent-based simulations, evolutionary analyses, probabilistic models, and allometric scaling analyses.

**Qualifications:** Candidates need to be skilled in both oral and written communication in English, and should be able to work independently as well as in collaboration with others. Certain coursework is needed in mathematics (contact Eric or see job posting for detailed information). Candidates need to have proficiency, but not necessarily documented, in working with computers and programming, e.g. in Matlab, Python, Julia, C++, or some other language. A good background in mathematics, differential equations, and/or programming is qualifying. Interest and knowledge of evolutionary biology, microbiology, and/or molecular biology is desirable but not necessary.

**Apply:** To apply see the official ad: [https://www.umu.se/en/work-with-us/open-positions/phd-position-in-mathematical-modeling\\_263754/](https://www.umu.se/en/work-with-us/open-positions/phd-position-in-mathematical-modeling_263754/) The deadline is May 15, 2019 with an anticipated start date in the fall of 2019.

**Questions:** If there are any questions please contact Eric Libby at: Eric Libby Umeå University [elibbyscience@gmail.com](mailto:elibbyscience@gmail.com) ”

Eric Libby <[elibbyscience@gmail.com](mailto:elibbyscience@gmail.com)>

---

## UMontpellier InvasiveInsectPopulationGenomics

Dear All,

We are recruiting a Ph.D. student, who will study invasive pest insects based on population genomics approaches. The student will perform field works for a few months as well.

We will select three candidates among all applicants, and these three will participate in the competition by GAIA Ecole doctoral school at the University of Montpellier ([https://www.adum.fr/as/ed/page.pl?site=gaia&pageAndidatures\\_modalites](https://www.adum.fr/as/ed/page.pl?site=gaia&pageAndidatures_modalites)). If you want to know more about this procedure, feel free to contact Kiwoong NAM ([ki-woong.nam@inra.fr](mailto:ki-woong.nam@inra.fr)).

**Project:** The detailed project is described at [https://www.adum.fr/as/ed/voirproposition.pl?langue=fr&site=gaia&matricule\\_prop\\$960](https://www.adum.fr/as/ed/voirproposition.pl?langue=fr&site=gaia&matricule_prop$960) It is written in French, but I will send an English version if you want.

The fall armyworm (*Spodoptera frugiperda*) is one of the most infamous pest insects against crops. This species was initially observed from North and South America. In 2016, this species invaded Africa and devastated crop fields. After fall armyworm was found in Yemen, India, and China and severe deleterious effects from this species are anticipated. These multiple intercontinental invasions imply a potential risk for this species to invade Europe. We generated the list of genes that are adaptively evolved to host-crops from original American fall armyworms using population genomics approaches. We also found that copy number variation is an important source of adaption to local geographical environment in Latin America. In this Ph.D., the student will study the path of invasion from the American continent to the African continent and potentially associated adaptation processes based on population genomics approaches. Then, the functional consequences of this adaptive evolution will be studied by reciprocal transplantation experiments, which estimate the relative fitness of original to alternative hosts from pre-determined traits of interest.

**Supervision:** There will be two supervisors; Kiwoong NAM (INRA) and Thierry Brevault (CIRAD). The thesis director is Emmanuelle d'Alencon. Kiwoong NAM will supervise population genetics analysis, and Thierry Brevault will supervise fieldworks.

**Candidates:** The student needs to have background on one or more fields among genetics, population genetics, molecular evolution, bioinformatics, evolutionary genetics, population genetics, entomology, and ecology. The candidate does not necessarily have to know how to perform computer-programming at the beginning. However, the candidate should like to work with a computer.

If you wish to apply, please email me a CV, letter of motivation, and a transcript during the master program. If the transcript does not indicate your rank (e.g., Xth among XX students), please provide us a document showing the rank from your coordinator with the signature.

**Deadline:** We accept the application until 29/04.

**Contact;** Kiwoong NAM ([ki-woong.nam@inra.fr](mailto:ki-woong.nam@inra.fr))

Ki-Woong Nam <[ki-woong.nam@inra.fr](mailto:ki-woong.nam@inra.fr)>

---

## UNorthernColorado PlantPopConservationGenetics

The McGlaughlin Lab at the University of Northern Colorado is recruiting a graduate student interested in plant population/conservation genetics. We currently have funding from the US Fish and Wildlife Service to examine the genetic structure of several plants that are candidates for listing under the Endangered Species Act. The research will focus on a detailed examination of a single species (MS Applicant) or multiple species (PhD Applicant) to answer specific management questions. The initial work will focus on *Mimulus gemmiparus* (*Erythranthe gemmipara*), an incredibly rare monkey flower endemic to the Colorado Rockies. All work in the McGlaughlin Lab is conducted in close communication with land management agencies (e.g. Fish and Wildlife Service, Bureau of Land Management, Forest Service) providing students with a strong foundation in land management needs and careers. The selected student could either study at the Masters, obtaining a MS in Biological Sciences, or PhD level, obtaining a Doctorate in Biological Education. PhD applicants must have an interest in learning about pedagogy, as this is a central component of the doctoral program. Support will include serving at a Teaching Assistant, Research Assistant, or Herbarium aid during the 9-month academic year, with additional grant based summer support. All expenses associated with genetic research questions are covered by existing grant funding, with the opportunity for students to develop novel components of their research project.

**Qualifications.** BS/BA in Biology, Botany, or related field. Previous botanical skills/knowledge. Genetic lab skills are a plus, but not required. Willingness to conduct fieldwork in isolated locations. All candidates must have a willingness to learn bioinformatic skills to analyze large genetic datasets. All candidates must be able to establish residency in Colorado within 1 year of starting the graduate program.

Initial inquiries should be sent to Dr. Mit McGlaughlin [MITCHELL.MCGLAUGHLIN@UNCO.EDU](mailto:MITCHELL.MCGLAUGHLIN@UNCO.EDU) including a letter of interest, unofficial transcripts, and CV. Full applicants will need to submit transcripts, CV, letter of intent, GRE scores, and 3 letters of reference to the UNC graduate school.

Mitchell McGlaughlin, Ph.D. Professor, Associate

Director School of Biological Sciences Ross Hall  
1560 | Campus Box 92 | Greeley, CO 80639 O:  
970-351-2139 | [MITCHELL.MCGLAUGHLIN@UNCO.EDU](mailto:MITCHELL.MCGLAUGHLIN@UNCO.EDU)  
<[applewebdata://1355773E-072B-4B88-95F1-0CF2A8C6349D/Mitchell.McGlaughlin@unco.edu](https://applewebdata://1355773E-072B-4B88-95F1-0CF2A8C6349D/Mitchell.McGlaughlin@unco.edu)>

“McGlaughlin, Mitchell”  
<[MITCHELL.MCGLAUGHLIN@UNCO.EDU](mailto:MITCHELL.MCGLAUGHLIN@UNCO.EDU)>

---

## UPorto FishPopulationGenomics

We are currently accepting applications to fill a 36 months contract for a PhD researcher on the topic of Population Genomics of the European sardine *\*Sardina pilchardus\**, at Faculty of Sciences - University of Porto, Portugal. The position is part of a 3-year research project entitled “SARDINOMICS - Developing molecular tools to improve the knowledge and management of Sardine stocks” funded by Mar2020 programme. Other partner institutions are the Portuguese Marine and Atmospheric Institute (Instituto Português do Mar e da Atmosfera, IPMA), CIBIO - Research Centre in Biodiversity and Genetic Resources, and CCMAR - Centre of Marine Sciences.

Preferred candidates must possess a PhD, 3 or more years of post-doctoral experience, and:

1. Experience in population genomic data analyses, including bioinformatic skills (i.e. experience in linux, programming language, e.g. python, R) and experience in using relevant data analyses software;
2. Successful publication of peer-reviewed papers on population genetics/genomics topics, in which the focus on teleost fish species will be valued;
3. Participation in research projects, as well as scientific outreach and dissemination events.

Please see more details using the link: <http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=112415> \*Deadline for application submission is April 18th, 2019\*.

– Ana Veríssimo, PhD Researcher

CIBIO - Research Centre in Biodiversity and Genetic Resources Campus Agrário de Vairão, Rua Padre Armando Quintas 4485-661 Vairão, Portugal

<http://orcid.org/0000-0003-3396-9822> Ana Verissimo  
<[verissimoac@gmail.com](mailto:verissimoac@gmail.com)>

---

## UppsalaU AvianGeneRegulatoryEvol

A PhD student position in molecular evolution is available at the Department of Ecology and Genetics, Uppsala University, Sweden

Supervisors: Dr. Carina Farah Mugal, Prof. Hans Ellegren  
Title: The role of gene regulatory evolution in speciation and adaptation of flycatchers

The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see [www.ieg.uu.se](http://www.ieg.uu.se). The PhD project will focus on understanding the molecular basis and mechanisms of phenotypic variation and differentiation between species. Two classical candidates underlying phenotypic change are protein coding sequences and functional sequences that regulate gene expression. Here, changes of the DNA sequence itself or epigenetic modifications can influence the phenotype. However, the relative importance of these two sequence classes and the role of epigenetic modifications is still unclear. Flycatchers provide a good model system to study this question. Collared flycatcher (*Ficedula albicollis*) and pied flycatcher (*Ficedula hypoleuca*) have been a model of speciation research for decades, and a rich source of genomic, transcriptomic and epigenomic data have become available. In particular, data on naturally occurring hybrids provides the opportunity to study the molecular basis and mechanisms of reproductive isolation in an ecologically relevant setting. Moreover, genomic data of the more distantly related Taiga flycatcher (*Ficedula albicilla*) permits studying molecular evolution also at larger time-scales. The initial work will focus on the identification and characterization of gene regulatory elements in the collared flycatcher genome. In addition, you will establish associations between regulatory elements and their target genes. This exploration will form the background for all subsequent analysis. You will then perform comparative analysis between flycatcher populations, in the context of speciation research as well as on larger evolutionary time-scales. The ultimate goal of the project is to gain a conceptual understanding of the role of molecular evolution and adaptation at different evolutionary time-scales and levels. This applies to genetic and epigenetic changes in protein coding se-

quences, regulatory elements and transposable elements. You will acquire cutting-edge skills in bioinformatics and statistical analysis, which are essential for modern biology research. In addition, the project will involve mathematical modelling.

To be eligible for a PhD-student position the applicant must hold a master degree (or equivalent) in mathematics, bioinformatics or biology, at the time of appointment. The applicant with a mathematics background must have an interest in molecular evolution and population genetics, and a readiness to acquire relevant skills in bioinformatics. The applicant with a bioinformatics or biology background must have a readiness to acquire relevant skills in computer science, statistics and mathematics. Candidates must be able to express themselves fluently in spoken as well as written English. In addition, the applicant must be able to work independently, have good collaborative skills and be able to communicate (both spoken as well as written). The applicant must have integrity and personal maturity, be able to take initiative and handle setbacks.

The expected starting date is from October 2019.

Further information about the position and details about application are available at: <http://www.uu.se/en/about-uu/join-us/details/?positionId&3056> You are welcome to submit your application no later than 2019-05-13.

For inquiries please contact: Carina Farah Mugal, [carina.mugal@ebc.uu.se](mailto:carina.mugal@ebc.uu.se)

Carina Farah Mugal, Ph.D. Department of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

<http://katalog.uu.se/profile/?id=N8-1504> Carina Farah Mugal <[carina.mugal@ebc.uu.se](mailto:carina.mugal@ebc.uu.se)>

---

## UQueensland UExeter SexualConflict

The University of Queensland (UQ) and the University of Exeter are seeking an exceptional student for a PhD Scholarship on Sexual conflict and aging as part of the QUEX Institute < <https://global-engagement.uq.edu.au/quex> >. This joint PhD scholarship provides a fantastic opportunity for a talented doctoral student to work closely with a world class research group and benefit from the combined expertise and facilities offered at the two institutions. The success-



ful applicant will have the chance to study in Australia and the UK, and will graduate with a joint degree from The University of Queensland and the University of Exeter.

The PhD will be supervised by Dr Katrina McGuigan (Queensland) and co-supervised by Dr David Hosken (Exeter) in conjunction with Dr Ruth Archer (University of Ulm). Unofficial enquiries should be sent to k.mcguigan1@uq.edu.au.

For further detail and to apply please see

<https://graduate-school.uq.edu.au/quex-mcguigan>  
"Hosken, David" <D.J.Hosken@exeter.ac.uk>

---

## Vienna Population Genetics

Call for PhD students in Population Genetics is open: apply by May 13, 2019

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

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

Topics include:

- Complex trait dissection in conifers. - Efficient detection of variants of polygenic adaptation in *Drosophila* experimental evolution. - Evolution of gene expression. - Functional characterization of beneficial alleles in *Drosophila*. - Genomic architecture of reverse selection. - Incipient speciation during adaptation to a new environment. - Inference of selection parameters using whole genome data. - Long-term dynamics of adaptive alleles. - Microbiome evolution in *Drosophila*.
- Multi-measurement experimental evolution: How to combine evidence from different sources? - Polygenic adaptation: The roles of pleiotropy and epistasis. - Population genomic footprints and drivers of repeated trait shifts during adaptive radiation. - The genetics of local adaptation in *Arabidopsis thaliana*. - The role of a nascent sex chromosome on interspecific patterns of

allele sharing. - Transposon polymorphism in *Arabidopsis thaliana*. - Within-species consequences of genomic interactions in ecologically important species.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 13, 2019 will be considered. Two letters of recommendation need to be sent directly by the referees. Accepted PhD students will receive a monthly salary based on currently EUR 2.162,40 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at [www.popgen-vienna.at](http://www.popgen-vienna.at) Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

---

## VLIZ Belgium 2 Marine Biodiversity

The Flanders Marine Institute (VLIZ) in Ostend, Belgium, has a vacancy for a researcher. Through collaboration with academic research groups, the research is intended to lead to a PhD at a Flemish University. Employment can start immediately after the selection procedure and ideally not later than 1st of October 2019. Deadline for applications is 15th of May. Read the full job posting here: <http://www.vliz.be/en/vacancy/14-new-research-positions-2019> Project description: Marine viruses play a key role in the functioning of the global ocean. Viruses are the most abundant biological entity in the ocean, and harbour the single largest pool of unexplored genetic diversity on Earth. In addition to their keyrole in causing illness or even death in a wide range of marine organisms, viruses also influence the evolutionary dynamics and biogeochemical cycles by infecting and lysing bacteria and protists. There is, however, still limited knowledge about virus community structure and the quantitative influence of viruses on regional ecosystems.

VLIZ will initiate a research project that investigates the presence and diversity of marine viruses in the Southern Bight of the North Sea. Throughout this project, we will seek to answer some of the following research questions: 1) What is the viral diversity in the Southern North Sea? 2) What is the natural variability on the abundance and diversity of viruses within this ecosystem? 3) What are the biotic and abiotic factors that determine the presence of marine viruses; can we find causal links between the diversity of viruses and the diversity of

phytoplankton and bacteria? 4) Can we get an idea on the importance of viruses in the North Sea ecosystem based on the viral traits (speed of infection, production, lysis and decay) of the most common viruses from the Southern North Sea?

This project will be performed in collaboration with one or more Flemish university research groups and with the NIOZ Royal Netherlands Institute for Sea Research. The project will be largely based on field samples taken from the Belgian and Dutch coast. It will focus on metagenomic analysis of the marine virus community and virally induced mortality rate measurements of the marine microbial host community.

For questions, please contact Maarten De Rijcke, head of the research unit Life's Roots & Rates, maarten.derijcke@vliz.be, +32 (0)59 34 14 15

The Flanders Marine Institute (VLIZ) in Ostend, Belgium, has a vacancy for a researcher. Through collaboration with academic research groups, the research is intended to lead to a PhD at a Flemish University. Employment can start immediately after the selection procedure and ideally not later than 1st of October 2019. Deadline for applications is 15th of May. Read full job posting here: <http://www.vliz.be/en/vacancy/14-new-research-positions-2019> Project description: Natural ecosystems are often too complex to study them under controlled laboratory conditions. Organisms interact with their environment in multifaceted ways. Our understanding of how species traits, species interactions and evolution of individual species contribute to ecosystem functions is therefore still very fragmentary. Nevertheless, we urgently need better insights in the functioning of ecosystems to predict how they will change under anthropogenic pressures such as global warming or ocean acidification.

In this research line, VLIZ aims to unravel important processes in natural plankton communities such as ecosystem functions, and mutualist and antagonistic interactions among different species using an ecosystems biology approach. Specifically, VLIZ wants to use high throughput sequencing to describe the composition (metagenomics) and functions (meta-transcriptomics) of plankton communities. This information will be used to model relevant ecosystem processes such as biogeochemical cycling. VLIZ is furthermore interested to investigate how such processes will alter under various scenarios of global change.

The study area is primarily the southern North Sea, where field surveys can readily be conducted to cover seasonal and spatial dynamics of plankton communities.

Next to the regional focus, we will encourage collaboration in international consortia to work on global datasets. Within this context, VLIZ wants to address the following research questions: 1) How are plankton communities composed and which factors define their spatial and temporal dynamics? 2) Which key species and key traits can we identify using gene expression profiles? 3) How can we use meta-transcriptomics data in ecosystem models (e.g. to investigate biogeochemical processes)? 4) Can we use these models to predict the effect of anthropogenic change (e.g. global warming or ocean acidification)?

— / —

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>

## WesternConnecticutStateU WildlifeDiversity

Graduate Position: Western Connecticut State University

The Pinou Lab, in collaboration CT DEEP Wildlife Division, Connecticut DOT, and the Norwalk Aquarium is looking for a student interested in pursuing a MS to join our Terrapin Tracking Team to collect data on Diamondback Terrapins in Connecticut. We are particularly interested in motivated students with an interest in integrating land use ecology with citizen science research. The project is part of a larger effort to map wildlife mortality on Connecticut roads. The student will be responsible for responding to hotline calls and managing all spatial and temporal data, as well as for working with citizen scientists to conduct surveys. The project will provide the student experience in geographic information systems (GIS) and in implementing citizen science initiatives. This project can be applied towards the stewardship requirement for the MS degree and can be used to develop a research thesis that explores frameworks in wildlife conservation, landscape and urban ecology, the reliability of citizen science data, and the intersection between citizen science outreach and policy. Student support includes university assistantships, internal scholarships, and fellowships (internal and external). Interested students should contact the PI at pinout@wcsu.edu and include a cover

letter describing your research experience and interests, as well as a CV by May 15th. All interested students must hold a drivers license and be accepted into the MS in Integrated Biological Diversity program (<http://wcsu.edu/biology-msbiodiversity/how-to-apply/>).

Theodora Pinou, Professor of Biology MS in Integrative Biological Diversity CSCU Program Coordinator, & WCSU program liaison H. G. Dowling Herpetological

Collection Faculty Curator

Department of Biological and Environmental Sciences  
Western Connecticut State University 181 White Street,  
Danbury CT 06810 E-mail: Pinout@wcsu.edu

Phone: 203-837-8793 Fax: 203-837-8875

<https://sites.wcsu.edu/pinou/>

Theodora Pinou <PinouT@wcsu.edu>

---

## Jobs

AarhusU Bioinformatics .....	51	SouthAfrica ResAssist BuzzPollination .....	63
AarhusU CancerEvolutionGenomics .....	52	StirlingU LabResAsst EvolBiocontrolResistance ...	64
AarhusU StatisticalGenetics .....	53	StMarysC Maryland 1yr EvolutionaryCoastalBiologist	65
DesertBotanicalGarden Arizona NewWorldSucculents	53	UAberdeen 14 EvolutionaryBiology .....	66
Frankfurt Bioinformatics .....	54	UBristol PhylogeneticsCulturalEvolution .....	66
ImperialC London Tech MolecularEcologyRotifers .	55	UCollege London CancerEvolution .....	67
JGutenbergU LabManager SocialInsectEvolution ..	56	UCollege London EvolutionaryBiol .....	68
NatureCommunications EvolutionEditor .....	57	ULiverpool ResFellow 35mnths EvolutionaryBiol ..	68
NewYork ComputationalBiology .....	57	UMichigan SummerFieldTech PlantEvol .....	69
NorthCarolinaZoo ResearchCurator .....	58	UNewMexico Albuquerque FishCollectionsManager	69
PennState LabManager EvolutionaryGenomics ....	59	UOslo SystematicMycology .....	70
Rennes Bioinformatician GenomeAssembly .....	60	UVirginia ResAssist SocialNetworkEvolution .....	71
Rennes GeneticSelectionOfAquacultureSpecies ....	60	UZurich SystematicBotany .....	71
SangerInst CancerEvolutionBioinformatics .....	61	Vienna Bioinformatics .....	72
Seattle FishPopGenetics .....	61	Wageningen EvolutionaryEcol .....	72
SouthAfrica FieldManager StripedMouseProject ...	62		

---

### AarhusU Bioinformatics

A position as Professor in Bioinformatics is available from October 1, 2019 at the Bioinformatics Research Centre (BiRC), Aarhus University (birc.au.dk), Den-

mark. The deadline for receipt of all applications is June 1, 2019.

<http://scitech.au.dk/en/about-science-and-technology/-vacant-positions/job/professor-in-bioinformatics-at-aarhus-university-denmark/> A Tenure Track position or an Associate Professorship in Bioinformatics is available from October 1, 2019 at the Bioinformatics Research Centre (BiRC), Aarhus University (birc.au.dk),

Denmark. The deadline for receipt of all applications is June 1, 2019.

<http://scitech.au.dk/en/about-science-and-technology/vacant-positions/job/tenure-track-position-associate-professorship-in-bioinformatics-at-aarhus-university-denmark/> Best regards, Kasper Munch

Associate professor Bioinformatics Research Centre Aarhus University phone: 8715 6536

Kasper Munch Terkelsen <kaspermunch@birc.au.dk>

## AarhusU CancerEvolutionGenomics

I have three open bioinformatic post doc positions in cancer genomics and big data analysis at Department of Molecular Medicine, Aarhus University. I'm looking for candidates with interests in a combination of cancer evolution, gene regulation, analysis of large genomics data sets, and quantitative modelling.

Job call: <https://www.au.dk/om/stillinger/job/postdocs-in-cancer-genomics-and-medical-big-data-analysis/> . The application deadline is May 7, 2019.

' Further details:

The Department of Molecular Medicine (MOMA), Department of Clinical Medicine at Faculty of Health at Aarhus University invites applications for three positions as Postdoc in the field of bioinformatics, as per 1 July 2019 or as soon as possible thereafter. The positions are full-time positions for up to 24-36 months.

The Department of MOMA MOMA (<https://moma.dk/>) offers a vibrant and unique interdisciplinary research environment with more than 20 years' experience in genomics, transcriptomics, and translational cancer research. The department houses state-of-the-art laboratory facilities, comprehensive cancer biobanks, an extensive next-generation sequencing facility, access to a large HPC facility, and extensive genomics data infrastructure. The department also plays a central role in the recently established Danish National Genome Center and will house genome sequencing.

About the research group Jakob Skou Pedersen's research group (<https://moma.dk/bioinf-2/pedersen-group>) studies cancer evolution and gene regulation. The research is primarily based on computational analysis of local and third-party large cancer genomics data sets, typically with thousands of samples. Projects may

include statistical modelling and methods development. They may be supplemented by collaborative experimental hypothesis evaluation. There are close collaborations with local groups in statistics, bioinformatics, molecular biology, and clinical oncology as well as numerous international collaborations, including participation in the International Cancer Genome Consortium (ICGC) and the Pan-Cancer Analysis of Whole Genomes Project (PCAWG). Jakob has a dual affiliation at the Bioinformatics Research Center (BiRC), Faculty of Science and Technology, where part of the research projects may be carried out.

Your job responsibilities As a Postdoc in bioinformatics, your position is primarily research-based. You will contribute to the development of the department through research of high international quality. In your daily work, you will work closely with colleagues on your project, where you will receive supervision and guidance.

You will be joining one of the following research projects:

A) Cancer evolution (1-2 positions): Explore the mutational processes underlying cancer development and progression. A key question will be how repair deficiencies shape mutational patterns. The analysis will involve thousands of whole cancer genomes and rely on integration of somatic mutations at both the single nucleotide and structural level, germline variants, expression data, epigenetic data, layers of genomics annotation, etc. Depending on your background, the analysis may rely on existing tools and methods or involve statistical modelling and method development. Concrete hypotheses may be sought validated in local patient cohorts or in wet-lab experiments through ongoing local collaborations.

B) Gene regulation and non-coding RNAs (1-2 positions): Explore tens of thousands of gene expression data sets to learn about non-coding RNAs and post-transcriptional regulation in cancer. One of your possible aims is to characterise intronic RNAs in cancer from large local and third-party total RNAseq data sets. Another possible aim is to use statistical modelling to identify and characterise non-coding RNAs and RNA binding proteins that affect post-transcriptional regulation in cancer, by correlating gene expression patterns with presence of binding sites across large sample cohorts. Functional hypotheses may be sought experimentally evaluated through local collaborations.

You must indicate which positions you would like to be considered for.

Your competences You have academic qualifications at PhD level, preferably within bioinformatics, statis-

tics, computer science or a related discipline. You have a strong relevant publication track-record, with first-author publications in peer-reviewed articles in international recognized journals. Proficiency in statistical data analysis and scientific computing is required. Experience with genomics data analysis, software development and experience with R or Python programming languages is advantageous. Knowledge of cancer biology, mutational processes, 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>

## AarhusU StatisticalGenetics

We are currently searching for candidates to fill a professor position within the field of Statistical Genetics. If you have a strong scientific background in this field and have an interest in developing statistical genetic tools for animal/plant breeding, personalized medicine, or understanding regulation of complex traits, you may be the candidate we are looking for. The successful candidate will be an important contributor to further develop the research area within the internationally recognized Center for Quantitative Genetics and Genomics (QGG) at Aarhus University in Denmark. For more details on QGG, please go to our webpage: <http://mbg.au.dk/forskning/forskningscentre/-center-for-quantitative-genetics-and-genomics/> .

If you are interested, please go to our webpage to see more details on the position and how to apply;

<http://mbg.au.dk/en/news-and-events/vacancies/job/-professor-in-statistical-genetics/> You are more than welcome to contact Mogens Sandø Lund directly for any further information regarding the position.

Mogens Sandø Lund Professor, Center director Tel.: +45 8715 8024 Mobile: +45 2075 1222 Email: Mogens.Lund@mbg.au.dk QGG Dept. of Molecular Biology and Genetics, Aarhus University Blichers Allé 20, Postboks 50 DK-8830 Tjele

Kind Regards

Johanna Höglund (PhD) Scientific Coordinator

Dept. of Molecular Biology and Genetics Aarhus University Blichers Allé 20, Postboks 50 DK-8830 Tjele

Tel.: +45 87157779 Mob:+4522825356 Email: johanna.hoglund@mbg.au.dk

Tel: +45 871 56000 Web: [www.au.dk](http://www.au.dk) Johanna Höglund <johanna.hoglund@mbg.au.dk>

## DesertBotanicalGarden Arizona NewWorldSucculents

Desert Botanical Garden has opened a search for a Research Scientist-New World Succulents: <https://www.dbg.org/join-our-team/> Desert Botanical Garden, one of the world's major botanical gardens specializing in desert plant taxa, seeks a Research Scientist to join the Garden's Research, Conservation and Collections team. The Research Scientist will contribute to the Garden's mission to advance excellence in education, research, exhibition and conservation of desert plants of the world.

Areas of specialization may include any aspect of the biology and conservation of New World succulent plants, with special emphasis on cactus and agaves. We are particularly interested in applicants with expertise in one or more of the following: taxonomy and systematics, evolutionary biology, ecology, conservation biology, or physiology. Individuals with emphasis on linking research outcomes to conservation are especially sought, as well as applicants using novel approaches involving molecular genetics techniques. The successful applicant is expected to develop an internationally recognized research program focused on members of the cactus and/or agave families.

Responsibilities include: conducting original research, seeking extramural funding, advising students, serving on the IUCN Cactus and Succulent Specialist Group (CSSG), and cooperating with other Garden departments in the development of exhibits and educational programs.

Qualifications: Ph.D. in relevant plant focused field is required.

The Desert Botanical Garden (DBG) was established in 1939 with a mission focused on research, education, conservation, and exhibition of desert plants of the world, with special emphasis on the Sonoran Desert ([www.dbg.org](http://www.dbg.org)). The Garden's scientifically documented, living collections of Cactaceae and Agavaceae are taxonomically diverse and among the world's largest and are designated as National Collections by the Plant Col-

lections Network of the American Public Gardens Association. The institution also maintains a particularly strong herbarium collection of cacti and agaves. DBG serves as host institute for IUCN's CSSG. The successful applicant will join a strong multidisciplinary team in the Department of Research, Conservation, and Collections (RCC Staff) and will be eligible to obtain adjunct faculty status in the School of Life Sciences, Arizona State University. In addition to living and herbarium collections, facilities include a newly constructed Desert Conservation Laboratory building (housing herbarium prep space, seed conservation lab, and soil ecology lab), 1200 sq. ft. molecular genetics laboratory, library, and state-of-the-art greenhouses.

Put your passion for the desert to work! To apply, send letter of application, C.V., a concise, 1-page description of research approaches, goals, and conservation synergies, and names and contact information of three references to [hr@dbg.org](mailto:hr@dbg.org), or mail to:

Human Resources Desert Botanical Garden 1201 N. Galvin Parkway Phoenix, AZ 85008

Review of applications will begin April 15, 2019

Desert Botanical Garden is an Equal Opportunity Employer and considers all applicants without regard to race, religion, color, sex, gender identity and/or expression, sexual orientation, marital or parental status, age, national origin, veteran status, disability, or any other status protected by law.

The Garden fosters and supports workplace diversity, equity and inclusion to honor the unique perspectives, experiences and contributions of all, to celebrate successes, and to cultivate individual and institutional excellence.

The benefits of regular employment at the Desert Botanical Garden include a stunning environment, competitive benefits package, complimentary family membership, employee cultural exchange, wellness initiatives and discounts.

Shannon Fehlberg <[sfehlberg@dbg.org](mailto:sfehlberg@dbg.org)>

---

## Frankfurt Bioinformatics

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE-TBG invite applications for a

Lead Bioinformatician (m/f/d) for high-throughput genome assembly and annotation (100%)

Your tasks:

- \* Lead a team of bioinformaticians to develop, maintain and run high-throughput pipelines for the assembly and annotation of de novo genomes from diverse eukaryotes
- \* Implementing and documenting the work-flow from receiving data, issue assembled genomes to users and archiving data in public databases
- \* Communication with user groups, service providers and external database managers

Your profile:

- \* PhD in Bioinformatics or related subjects
- \* Experience with de novo genome assembly of non-model organisms and developing large scale, high-throughput procedures for de novo genome assembly and annotation
- \* Proven understanding of comparative genomics or evolutionary biology research preferably in non-model organisms
- \* Familiarity in leading a service orientated unit and excellent communication skills

What is awaiting you?

- \* A central role in an innovative large-scale genomics project
- \* A motivated and dynamic team of international researchers at an internationally recognized biodiversity research institution
- \* An opportunity to build a central research and service unit within LOEWE-TBG and Senckenberg
- \* Excellent opportunities to expand

your scientific network across disciplines \* Flexible working hours ' annual special payment ' company pension scheme ' 30 days holidays

Salary and benefits are according to a full time public service position in Germany (TV-H E14/15) according to qualification and experience). The contract should start as soon as possible and will initially be limited to December 31th, 2021. The Senckenberg Gesellschaft für Naturforschung support equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application, mentioning the reference of this job offer ( ref. #12-19002) before April 17th, 2019 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your certification to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

Maria Di Biase <[recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)>

---

## ImperialC London Tech MolecularEcologyRotifers

Applications are invited for a Research Technician who will join an exciting new project to study how microscopic rotifers adapt to resist diseases. The role is based at the Silwood Park Campus of Imperial College London and is a part-time position for a fixed term of 33 months.

We are looking for candidates who bring enthusiasm, curiosity, flexibility, practicality and excellent organisational skills, as well as previous research experience in microbiology, molecular biology or related areas. You will help to run a dedicated laboratory customised for this project, where you will use experimental, molecular and microscopic techniques to study how freshwater rotifers respond to attack by virulent pathogenic fungi. This will involve isolating animals and fungi from moss, growing and maintaining lines in culture, extracting DNA and RNA and helping to process and analyse data.

We will provide training and support in research techniques that are specific to this system. As the project progresses, you will have a chance to get involved in study design, data analysis (including the option to learn bioinformatic skills) and presentation of results. The role will involve laboratory work, local fieldwork, organisational tasks and computing. You will be working approximately 21 hours per week (0.6 FTE), with considerable scope for flexibility as to working days and times.

You will have a BSc (or equivalent) in Biology or a closely related discipline, or equivalent research or industrial experience. We would be open to discussing possibilities for you to pursue a part-time Masters-level research degree at Imperial during the contracted period.

For full details and to apply, please visit: <https://www.imperial.ac.uk/jobs/description/NAT00435/-research-technician-molecular-ecology-rotifers> Salary: £31,770 - £36,009 (pro rata) plus benefits

Closing date: 6th May 2019

Informal enquiries are encouraged, and should be directed to Dr. Chris Wilson ([chris.wilson@imperial.ac.uk](mailto:chris.wilson@imperial.ac.uk))

<https://www.imperial.ac.uk/people/chris.wilson> <http://barralab.bio.ic.ac.uk/what-we-do/bdelloids.html> Imperial College London is the UK's only university focussed entirely on science, engineering, medicine and business and we are consistently rated in the top 10 universities in the world. We work in a multidisciplinary and diverse community for education, research, translation and commercialisation, harnessing science and innovation to tackle the big global challenges our complex world faces. We are committed to equality of opportunity, to eliminating discrimination and to creating an inclusive working environment. We are an Athena SWAN Silver award winner, a Stonewall Diversity Champion, a Disability Confident Employer and work in partnership with GIREs to promote respect for trans people.

Silwood Park is a postgraduate campus, located 25 miles west of central London in the village of Sunninghill near Ascot. A global centre for research and teaching in ecology, evolution, and conservation, Silwood provides modern academic buildings, laboratories and greenhouses, set in 100 hectares of parkland where long-term ecological field experiments are conducted.

[chris.wilson@imperial.ac.uk](mailto:chris.wilson@imperial.ac.uk)

---

## JGutenbergU LabManager SocialInsectEvolution

The faculty of Biology - Institute of Organismic and Molecular Evolution - research group Behavioral Ecology and Social Evolution of the Johannes Gutenberg-University Mainz is looking from 01.07.2019 onwards for a

Biological Technician / Lab manager (m/f/d) (pay scale EG 9 TV-L) Position number: 5519-10-ml

- Full time -

on a permanent position. The applicant will support the research group with a focus on Evolution, Behavior and Ecology of Social Insects (<https://evo.bio.uni-mainz.de>) in research and teaching.

Responsibilities:

- Development, application and teaching of methods in molecular biology, behavioral and chemical ecology for the research and teaching programme on the evolution of ants and bees. - Support of scientific projects, including conducting independently subprojects and supporting the preparation of manuscripts and research grants (e.g. compiling and visualisation of research results, budget calculations). - Laboratory management (ordering of laboratory materials, support and care of laboratory instruments, laboratory hygiene and safety). - Preparation of teaching courses and excursions. - Laboratory maintenance of social insect colonies.

Conditions of employment:

- Training as a biological technician or similar proficiencies and experiences - Extensive Research experience is an advantage - Very good skills in written and oral English - Very good knowledge of techniques in molecular biology and behavioral and chemical ecology - Familiarity with statistical and bioinformatic analyses is an advantage - Good Skills in - Organisation of a modern, methodological diverse laboratory - MS-Office and reference manager software - the scientific approach and terms

Expected in addition: - Interest in the research and work with social insects - Ability and enthusiasm to work in an international team - Work independence and effective organisation of work - Development and training of new laboratory techniques - Participation in seminars and meetings of the research group

We invite candidates without an official training as a biological technician to apply. However, we have to mention in this context, that they will be grouped into EG 9 with longer times in pay levels, resulting in a slower pay increase over time (The level 3 will be reached after 5 years in level 2, level 4 will be reached after 9 years in level 3, there are no levels 5 and 6).

We offer:

An interesting and diverse position in an international team with many opportunities for individual development in research and university teaching. Independent conduct of research projects and participation in national and international research trips and excursions if desired. Excellent, brand new laboratories within the new bio center I of the Johannes Gutenberg-University Mainz.

Next to the security of an employment in the public service, we offer additional social benefits e.g. extra retirement benefits in the public service via VBL, the possibility to buy a job ticket for public transportation and participation in training courses.

The Johannes Gutenberg-University Mainz supports the compatibility of family and career. Family-friendly conditions include flexible working hours.

\*\*\*\*

Applications of elderly candidates will be equally considered.

Applications of seriously disabled < <https://dict.leo.org/englisch-deutsch/disabled> > person < <https://dict.leo.org/englisch-deutsch/person> >s with similar qualifications will be prioritised.

Questions regarding the position and research of the group please contact Prof. Susanne Foitzik foitzik@uni-mainz.de.

Please submit your electronic application with the usual documents and under the position number: 5519-10-ml until 29.04.2019 to

beruf@uni-mainz.de

Prof. Dr. Susanne Foitzik Evolutionsbiologie Institut für Zoologie Johannes Gutenberg Universität Mainz Johannes von Muller Weg 6 55099 Mainz

Tel: +49 (0) 6131 39 27 840 Fax: +49 (0)6131 39 27 850 Email: foitzik@uni-mainz.de

“Foitzik, Susanne” <foitzik@uni-mainz.de>



---

## NatureCommunications EvolutionEditor

Job title: Associate or Senior Editor (Evolution)

Department: Nature Communications

Location: London / New York / Berlin / Shanghai

Do you love science but feel that a career at the bench isn't enough to sate your desire to learn more about the natural world? Do you enjoy reading papers outside your chosen area of research? If the answer is 'yes' to any or all of these questions, you could be the person we're looking for to join the editorial team of Nature Communications.

Nature Communications is the world's leading multidisciplinary Open Access journal, publishing high-quality research from across the natural sciences. To help us to build on the success of this journal, we're seeking an evolutionary biologist who has a critical eye, a deep understanding of their subject and interests beyond, and who can think on their feet.

To be considered for the position, you will have:

A PhD (or equivalent) in a field related to evolution and significant research experience. Candidates with expertise in using molecular data to investigate evolutionary questions are particularly encouraged to apply.

Editorial experience is not required, although applicants with significant editorial experience are encouraged to apply and will potentially be considered for a Senior Editor position. A thorough understanding of recent trends and developments in the field is essential. A passion for science and a thirst to learn more. You must be able to demonstrate the breadth of your interest in scientific research, both within and beyond your speciality. Excellent communication and interpersonal skills and be fluent in English (written and spoken). The ability to read and assess the novelty, context and implications of research submitted to the journal from different areas of this discipline. Be eager to travel and meet scientists worldwide, learn more about them and their research, and help them learn more about us and what we are looking for in the papers we seek to publish. The successful candidates will report to a team manager in the life sciences, and play an important role in determining the representation of their subject in the journal. They will handle original research papers, and work

closely with other editors on all aspects of the editorial process, including manuscript selection and overseeing peer review. The ability to recommend well-reasoned editorial decisions on submitted manuscripts in the light of expert advice is crucial. They will liaise extensively with editors at other journals in the Nature family and experts in the international scientific community.

The position is available on a full-time, permanent basis and may be located either in our New York, London, Shanghai or Berlin office.

Applicants should include a CV, a covering letter explaining their interest in the post and their preferred office of employment, and a Research Highlight in the style of Nature Cell Biology (of around 300 words) on a recent evolution paper from the literature.

Closing date: 30th April 2019 <https://www.nature.com/naturecareers/job?idh5405> Emily Jones <Emily.Jones@us.nature.com>

---

## NewYork ComputationalBiology

Department of Systems and Computational Biology  
Tenure Track Faculty Position

The Albert Einstein College of Medicine, one of the leading medical schools, located in New York City, is seeking to fill multiple tenure track faculty positions in the Department of Systems and Computational Biology. The major goal of the department is to advance our understanding of living systems by developing theoretical, computational and experimental approaches to study complex biological systems.

The College has 711 medical students, 160 Ph.D. students and 107 M.D./Ph.D. students, 265 postdoctoral research fellows in training and boasts a strong research faculty covering broad areas of experimental biology. The College of Medicine has more than 1,800 full-time faculty members located on the main campus and at its clinical affiliates. The 200,000 square foot Center for Genetic and Translational Medicine at Einstein locates computational, systems and experimental scientists in physical proximity to foster interdisciplinary communication and collaboration. Highly competitive start-up packages are available.

We seek outstanding scientists with broad experience and demonstrated collaborative interactions with experimental or clinical investigators. Candidates should have strength in a physical, mathematical or computational

field at the Ph.D. or equivalent level. Experience applying these skills to a biological or biomedical area (demonstrated through publications or support) is also desirable. Areas of interest include, but are not limited to: Modeling cellular processes; Evolutionary medicine; Evolution of structure and function; Biological networks analysis; Microbiome; Computational neuroscience; Mathematical and computational modeling of high-dimensional data related to complex traits; Evolutionary biology.

Applicants should send a letter of interest, C.V., statement of research and teaching interests, and names of three referees, in electronic format to:

Systems and Computational Biology Search Committee  
Albert Einstein College of Medicine Jack and Pearl Resnick Campus  
1300 Morris Park Ave. Price Center, Rm. 153  
Bronx, New York 10461  
E-mail Address: SysBio@einstein.yu.edu  
Subject line should be: SCB Faculty Search

The Albert Einstein College of Medicine is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, protected veteran or disabled status, or genetic information.

Lane Saucier Administrator Systems and Computational Biology  
Price Center Room 153 Phone 718-678-1115 Fax 718-678-1018  
lane.saucier@einstein.yu.edu

Lane T Saucier <lane.saucier@einstein.yu.edu>

---

## North Carolina Zoo Research Curator

STATE OF NORTH CAROLINA invites applications for the position of: Associate Curator of Research

JOB CLASS TITLE: Natural Science Research Curator I

POSITION NUMBER: 60033432

DEPARTMENT: Dept of Natural and Cultural Resources

DIVISION/SECTION: NC Zoo

SALARY RANGE:

\$35,474.00 - \$57,292.00 Annually

RECRUITMENT RANGE: \$42,780 - \$52,000

SALARY GRADE / SALARY GRADE EQUIVALENT:  
GN11

COMPETENCY LEVEL: Not Applicable

APPOINTMENT TYPE: Permanent Full-Time

WORK LOCATION: Randolph County

OPENING DATE: 04/10/19

CLOSING DATE: 05/07/19 5:00 PM Eastern Time

DESCRIPTION OF WORK:

\*\*\*Pay Grade - GN11, Recruitment Range - \$42,780 - \$52,000\*\*\*

Department Information: The Department of Natural and Cultural Resources' (DNCR) vision is to be the leader in using the state's natural and cultural resources to build the social, cultural, educational and economic future of North Carolina. Our mission is to improve quality of life by creating opportunities to experience excellence in the arts, history, libraries and nature throughout North Carolina. The Department works to stimulate learning, inspire creativity, preserve the state's history, conserve the state's natural heritage, encourage recreation and cultural tourism, and promote economic development. Our goal is to promote equity and inclusion among our employees and our programming to reflect and celebrate our state's diverse population, culture, and history by expanding engagement with diverse individuals and communities. We encourage you to apply to become a part of our team.

Primary Purpose of the Organizational Unit: The North Carolina Zoo exists for the enjoyment, education and inspiration of all of North Carolina's citizens and visitors to the zoo. The mission of the zoo is to encourage the understanding of and commitment to the conservation of the world's wildlife and wild places through the recognition of the interdependence of people and nature. The Zoo displays, conserves and protects representative examples of natural beauty, plant and animal species and ecological features of the North American and African regions of the world through the presentation of live animal exhibits from these regions.

Primary Purpose of the Section Responsible for scientific research and field conservation programs. Conducts and develops on-site research on animal health and behavior, visitor experience, and education, including oversight of research by outside institutions and agencies. Initiates and participates in multi-institutional science, conservation, management and research programs. Promotes the zoo's conservation mission by actively engaging in field conservation programs in North Carolina and internationally independently and in partnership with other organizations. Serves as institutional liaison with the Association of Zoos and Aquariums (AZA) conservation and science programs, international conservation

organizations.

Primary Purpose of the Position: The North Carolina Zoo seeks a dynamic, motivated and progressive individual to oversee zoo-based research activities as part of the Conservation, Education and Science Department. The position has responsibility for coordinating zoo animal welfare research and monitoring, conducting original research at the zoo, for coordinating and tracking the work of outside researchers, overseeing the zoo's Research Committee, administering the zoo's research internship program in collaboration with North Carolina State University, working with undergraduate and graduate students, and for communicating the NC Zoo's research work both internally and to a wide range of external audiences. Research at the zoo requires partnering with staff from across the institution on topics including (but not limited to) animal welfare, evaluation of behavioral enrichment, visitor studies, effectiveness of marketing strategies, evaluation of education programs, and others. The Associate Curator of Research works closely with the Curator of Conservation and Research to ensure that research conducted at the zoo meets accepted scientific standards and that research outcomes can inform zoo operations and support the zoo's mission. The position also works closely with the zoo's Curator of Animal Welfare and Behavioral Management to develop a comprehensive, science-based program to assess and adaptively improve animal management. The position is responsible for fundraising to support research at the zoo (both through grant applications and working with the North Carolina Zoological Society), broadly communicating findings both internally and externally through written articles, social media, and outreach, and assisting with education programming related to research. The position requires regular contact with other sections of the zoo, the Zoological Society, research staff at other zoos, and students and researchers from universities. Work is performed with considerable independence under the general guidance

— / —

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>

---

## PennState LabManager Evolutionary Genomics

The Toews Lab at The Pennsylvania State University is seeking to hire a Research Technologist / Lab Manager. The person will generate and analyze high-throughput DNA sequencing data to address several evolutionary and ecological questions regarding the diversification of wood warblers. Two active projects the technologist will help manage: comparative genomics amongst several species of wood warblers from whole-genome resequencing data and using fecal metabarcoding data to understand the diets of insectivorous birds in diverse forest communities. The candidate will coordinate data collection and sample storage. They will also assist in helping develop and apply new molecular and analytical tools to these projects, and independently assess the feasibility and cost effectiveness of these new methods. The candidate will be responsible for helping train students and postdocs with laboratory methods as well as some specialized equipment. The candidate will also help foster a safe, productive, and collegial lab environment. The candidate will work with the PI (Toews) on effective communication of the data and will hopefully co-author subsequent publications. Interested applicants should submit a cover letter describing their research interests, a current CV, and contact information for three references. Review of applications will begin immediately and continue until the position is filled. Typically requires a Bachelor's degree or higher (Master's degree preferred) or higher plus seven years of related experience, or an equivalent combination of education and experience. A MSc or a Ph.D. degree in biology, evolutionary biology, bioinformatics, genomics, or a related field is preferred, and/or experience from biotech or informatics positions. Comprehensive knowledge of high-throughput sequencing library preparation, and bioinformatics analysis is highly preferred. This is a fixed-term appointment funded for one year from date of hire with possibility of re-funding.

<https://psu.jobs/job/86206> David Toews, PhD. Assistant Professor Department of Biology Pennsylvania State University 619 Mueller Lab, University Park State College, PA [toews@psu.edu](mailto:toews@psu.edu) (814) 863-0848 <http://www.davetoews.com> David Toews <[toews@psu.edu](mailto:toews@psu.edu)>

---

## Rennes Bioinformatician GenomeAssembly

### WHAT

<https://team.inria.fr/genscale/job-offers/assembly-of-heterozygous-genomes/> Context:

\* INRA contract in the ITN Ignite < [http://www.itn-ignite.eu/show/about\\_11570/](http://www.itn-ignite.eu/show/about_11570/) > network. Located at Inria, GenScale team \* Marie Sklodowska-Curie grant

### Supervision:

Â Supervisor: Denis Tagu (INRA Rennes), Â Co-supervisor Fabrice Legeai (INRA Rennes) / Pierre Peterlongo (IRISA, Rennes)

### Context & Objectives:

Assembly of complex, very large, and highly heterozygous genomes remains nowadays a complex task for which no tool performs well. This is particularly true for insect genomes, despite countless initiatives such as i5K. The ITN Ignite aims among other things to propose new methods for assembling such non-model invertebrates. New sequencing strategies using both short (Illumina), long reads (Oxford Nanopore/PacBio), linked reads (Chromium 10X), as well as approaches based on chromosome conformation capture (3C) are being used to alleviate these problems. This project will aim to develop new algorithms and tools for increasing the quality and the assembly of large and complex heterozygous genomes, while integrating data from diverse technologies (NGS, long reads, 3C/HiC, 10X), create new references structure (e.g. haplotypes in genome graphs) and further applications.

The applicant will be located at the INRIA/IRISA laboratory in the GenScale bioinformatics research team that focuses on methodological research at the interface between computer science and genomics. The main objective of this group is the design of scalable, optimized and parallel algorithms for processing genomic data generated by the recent advances of biotechnologies. This work will be based on the usage and development of GATB, a C++ library and software suite developed by the team. And, this project will benefit from the INRA IGEPP laboratory and their collaborators for evaluating these new strategies on various species with the aim to infer different traits (host recognition, reproduction) involved in the adaptation of target insect species to

their environment.

### Skills

The candidate should have strong algorithmic and C++ development expertise. An important biological background and motivation is highly recommended.

### Working conditions

The recruited engineer will belong to the ETN Ignite project. Hence she/he will benefit from an annual workshop, from the whole ETN network and within planned secondments she/he will work partly abroad in the lab of "Jean-François Flot" (Bruxelles).

### Recruitment conditions

Â The candidate should not have a PhD degree

Â The candidate must have a master degree for four years or less

Â The candidate can be of any nationality. However, candidate's residence or main activity during the 3 years prior to its recruitment should not be France.

### Practical aspects:

Â Start: 01/05/2019 ' End: 31/07/2021

### WHERE

Irisa, Rennes, France.

### Contacts

denis.tagu@inra.fr

fabrice.legeai@inra.fr

pierre.peterlongo@inria.fr

Pierre Peterlongo <pierre.peterlongo@inria.fr>

---

## Rennes GeneticSelectionOfAquacultureSpecies

PROPOSAL FOR A PERMANENT POSITION (Location: Rennes, France) Closing date for candidature: 30/04/2019 \*"Genetic advisor in genetic selection of aquaculture species"\*

\*SYSAAF:\* SYSAAF is a non-profit and specialised organisation to advice poultry and aquaculture breeding companies in genetic and genomic selection ([www.sysaaf.fr](http://www.sysaaf.fr)). SYSAAF employs presently 14 scientists among which a majority of geneticist and hire 3 PhD students at the interface between mainly French research organisms (INRA, Ifremer, ANSES, etc.) and around 40 breeding companies (mostly located in France)

selecting more than 20 different species. SYSAAF activity is recognised by the French Law and follows the recommendation of the National Commission for Animal Genetic Improvement (CNAG), placed under the French Ministry of Agriculture authority.

\*The position:\* The candidate recruited will advise aquaculture breeding companies to develop or improve their selection programs and will collaborate to the development of genomic tools in order to implement genomic selection.

He, or she, will: (1) Advise the French breeding companies and oversea to collect performances and pedigree information in different type of breeding programs (from mass to genomic selection) for approximately 50 % of his/her working time. (2) Participate to the development of specific genomic tools for DNA parentage assignment (SNP markers panels) and genomic selection arrays (LD to HD arrays) collaborating with different genotyping laboratories. (3) Participate to R&D projects in the aim to contribute to the improve of the breeding programs efficiency.

This position request to be autonomous but also high capacities to work with collaborators, R&D partners and genotyping companies for the breeding companies in France and abroad.

Requirements: Master level minimum, preferably PhD. Competencies in quantitative genetic and genomic selection (statistics) are required, but also in bio-informatics and genomic to support breeding companies in developing genomic tools. Language competence in French and English would be appreciated. A specific interest in knowledge transfer and contact with the industry is also prerequisite.

Localisation: SYSAAF, LPGP Research unit - INRA, Campus de Beaulieu ' 35042 Rennes, France.

Contact: Mr. Pierrick Haffray (+ 33 6 66 86 08 55, pier-[rick.haffray@inra.fr](mailto:pier-ric.haffray@inra.fr)) or Mr Daniel Guémené (SYSAAF Director) (+33 2 47 42 76 43/+ 33 6 62 69 19 58, [daniel.guemene@inra.fr](mailto:daniel.guemene@inra.fr))

§Mail address to be candidate (letter + CV) : [pier-ric.haffray@inra.fr](mailto:pier-ric.haffray@inra.fr) & [daniel.guemene@inra.fr](mailto:daniel.guemene@inra.fr) §Website: [www.sysaaf.fr](http://www.sysaaf.fr) Carole Blay <[carole.blay@gmail.com](mailto:carole.blay@gmail.com)>

---

## SangerInst CancerEvolutionBioinformatics

We are looking for a senior Bioinformatician in cancer evolution and center predisposition.

An exciting statistical analysis and development opportunity has become available within our team in the Cancer, Ageing and Somatic Mutation Department (CASM). The successful candidate will be embedded in a large multidisciplinary team and will be tasked with further developing our cancer analysis algorithms specifically for cancer predisposition and cancer evolution.

The role involves working closely with scientific/IT staff within CASM to develop novel analysis strategies and actively contribute to the statistical modelling and data analysis of this important study. In addition, the role will also involve improving existing algorithms and developing new software when required as well as analysing whole genome sequencing and single cell data.

The position would suit a Bioinformatician/Statistician who enjoys developing algorithms and statistical modelling to analyse complex NGS biological data sets. We are looking for an individual who enjoys working in a multi-disciplinary team environment, to help solve complex IT issues, which will ultimately aid our analysis of cancer related datasets.

For more details please check: [https://jobs.sanger.ac.uk/wd/plsql/-wd\\_portal.show\\_job?p\\_web\\_site\\_id64&p\\_web\\_page\\_id84154](https://jobs.sanger.ac.uk/wd/plsql/-wd_portal.show_job?p_web_site_id64&p_web_page_id84154)  
Raheleh Rahbari, PhD Cancer Research Career Development Fellow The Wellcome Sanger Institute Genome Campus Hinxton, Cambridge, CB10 1SA, UK <https://-www.sanger.ac.uk/people/directory/rahbari-rahelehrr11@sanger.ac.uk>

---

## Seattle FishPopGenetics

This job is to be posted to USAJobs tomorrow, April 5th and will remain open for 14 days. As a federal position, it is open to US citizens.

Jeff Hard

RESEARCH GENETICIST (MOLECULAR) GS-0440-ZP-3

(Full time, Permanent)

The National Marine Fisheries Service seeks a full time, permanent Research Molecular Geneticist with experience in population genetics and genomics, bioinformatics, and analyses of mixed stock fisheries. Our research group is located in the Conservation Biology Division at the Northwest Fisheries Science Center in Seattle, Washington. Our group focuses on applying empirical genetics/genomics data to address questions related to the conservation and management of a variety of marine and anadromous species, including fishes, marine mammals, and marine invertebrates. The position is classified at ZP-3 with promotion potential to ZP-4, with salary ranging from USD \$66,386 to \$103,441, depending upon qualifications and experience. Direct questions about the position to Dr. Jeff Hard (jeff.hard@noaa.gov; 206-860-3275) or Dr. Linda Park (linda.park@noaa.gov; 206-860-3241).

The successful candidate will serve as a population geneticist working primarily in the Pacific Northwest on issues related to management and conservation of marine and anadromous species. The candidate will focus on collecting samples and data from anadromous and marine fishes and organisms, conducting studies on the population genetics and genomics of these species along the Pacific coast, and providing technical support for management and conservation. Responsibilities include field work, lab work, data analysis, management of sample inventories, and communication of results to scientists, managers, and the public.

Experience should include two years or more analyzing population genetic data involving DNA markers such as DNA microsatellites, single nucleotide polymorphisms (SNPs), and restriction site associated DNA (RAD) markers; conducting genome-wide association studies and genome mapping; and analyzing genomic data using bioinformatics. Familiarity with the use of environmental DNA (eDNA)-based metabarcoding for monitoring of biodiversity and abundance of aquatic organisms is desirable. Familiarity with programming languages such as Unix, Perl, Python, C++, and R, and with multivariate statistical methods (in both likelihood and Bayesian frameworks) is expected. Applicants should be able to demonstrate success in securing funding for research projects.

Jeffrey J. Hard

\*Supervisory Research Fishery Biologist\*

\*NOAA Fisheries, Northwest Fisheries Science Center\*

\*Conservation Biology Division, Genetics & Evolution Program 2725 Montlake Boulevard East-Seattle, WA 98112\*Office: 206.860.3275 Fax: 206.860.3335 jeff.hard@noaa.gov <first.last@noaa.gov> www.nwfsc.noaa.gov < <http://www.nmfs.noaa.gov> > jeff.hard@noaa.gov

---

### 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 fasci-

nated 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>

---

## SouthAfrica ResAssist BuzzPollination

Volunteer field assistant: buzz pollination in South Africa

The Plant Evolution group at the University of Stirling (UK) is seeking a highly motivated, detail-oriented assistant for fieldwork in the Cape mountains (South Africa)

during austral Spring 2019 (September/October).

**PROJECT:** Many plant species use pollen as reward for pollinators. Some species have evolved a complex mechanism where pollen is contained within closed (i.e. poricidal) anthers, and bees need to vibrate the anthers at particular frequencies for the pollen to be released. This buzz pollination syndrome has been recorded in 6-8% of all plant species. However, in the hyperdiverse Cape Floristic Region (CFR), this syndrome is markedly underrepresented (0.003% of plant species), despite the presence of some buzz pollinated plants that are endemic to the CFR. We will be conducting the first quantitative study on buzz pollination interactions in the CFR. Particularly, we will construct plant-pollinator interaction networks, measure various plant traits, and record the vibrations of sonicating bees.

**LOCATION:** Cape Town, South Africa. The field sites will mostly be located in the Cederberg mountains and around Nieuwoudtville. During Spring, these areas are transformed into carpets of colour when the world's most predictable mass flowering display occurs. Nieuwoudtville also boasts the highest diversity of geophytes (including Orchidaceae and Iridaceae) in the world, and it is an excellent place for botanising, hiking, and birding. We will be staying in small cabins or camping, and we will regularly move between field sites. The work will involve hiking and long hours in the field, as well as processing samples in the evenings.

**DUTIES:** The successful applicant will be expected to assist with pollinator observations, trait measurements, data entry, and collecting flowers and pollinators in the field.

**QUALIFICATIONS:** Suitable candidates should be hardworking, organized, and independent. Experience in identifying plants and pollinators, recording pollinator visitation rates, and experience with field-based projects is preferred. Temperatures in this region can be quite high (30C), and candidates should be prepared to spend a lot of time in the sun.

**WE OFFER** food, accommodation and travel within South Africa. However, we unfortunately cannot offer a further stipend.

**PERIOD:** mid-September to mid-October 2019

Please send your questions and applications asap to Dr Jurene Kemp (jurene.kemp@stir.ac.uk). To apply, send a cover letter (that includes your background and interests) and your CV. References will be requested at a later stage. ?

– The University achieved an overall 5 stars in the QS World University Rankings 2018 The University of Stir-

ling is a charity registered in Scotland, number SC 011159.

Jurene Kemp <jurene.kemp@stir.ac.uk>

---

## StirlingU LabResAsst EvolBiocontrolResistance

Research Laboratory Assistant (Sustainable Insect Control)

We are seeking a full time Research Assistant to join a large cross disciplinary research team investigating host-pathogen interactions to achieve sustainable insect agricultural pest control. This is a fixed term contract for 20 months. The appointment is expected to be effective from the 1st June 2019 and a start date in early June is highly desirable.

As the global human population continues to grow, we will need to produce 56% more food by 2050 without using any additional land. This is going to require radical agricultural innovation, particularly in the area of crop protection. The availability of effective pest control strategies has steadily declined due to emerging legislation protecting human health and the environment, as well as the mismanagement and widespread overuse of pesticides leading to the evolution of resistance in many pest species. As a result, there is an urgent need for new technologies that minimise damage to our natural environments while sustainably safeguarding our ability to protect crops. To address this problem we are examining how heterogeneous environments produced by crop and fungal biopesticide combinations can delay or prevent the evolution of resistance. The appointee will help manage a large selection experiment manipulating the infection status and diet of moth larvae of the species *Helicoverpa armigera*, and monitor responses to infection. The work is part of a Newton Funded international partnership featuring scientists in the UK and Brazil, and includes a partnership between academic scientists and the global NGO CAB international. Collaboration and joint training with other researchers (including 3 UK and 1 Brazilian post-doctoral researchers) will be encouraged and facilitated. The ability to travel to Brazil to assist with fieldwork is desirable.

The research will be conducted using the Stirling University's state-of-the-art Controlled Environment Facility and University Gardens. The appointee will be part of a thriving research environment within Biological and Environmental Sciences (BES) with more than 40 prin-



cial investigators, alongside postdoctoral researchers and 60 PhD students.

Equality and diversity are central to our activities at the University of Stirling. We believe everyone should be treated with respect and we deal with people as equals. We promote equality and celebrate diversity through a variety of initiatives. The University has been awarded the Athena SWAN Bronze award, the national charter for women in science, which recognises and promotes good practice in advancing women's careers in STEMM academia (Science, Technology, Engineering, Mathematics and Medicine). In addition, Biological & Environmental Sciences holds a departmental Athena Swan bronze award. Further details can be found here:

<http://www.stir.ac.uk/equalityanddiversity/-athenaswan/> <https://www.stir.ac.uk/news/2015/-10/athena-swan-awards/>

We welcome applications from everyone irrespective of gender and ethnic group, but we especially encourage applications from women and members of ethnic minority groups. Appointment will be based on merit alone.

#### Description of Duties

- Maintenance of insect colonies (as well as related equipment and facilities) for experimental purposes.
- Growing of plant material for insect food, and the monitoring and maintenance of plant growth facilities.
- Assisting with experiments using herbivorous insects and plants.
- Assisting with fungal biopesticide cultivation for experiments.
- Conducting bioassays using fungal biopesticides in the laboratory.
- Assisting with the preparation of laboratory trials and data collection.
- Sourcing and ordering of necessary materials.
- Routine molecular analysis of insect samples.
- Maintaining records and reporting updates to supervisors.

#### Essential Criteria

- BSc (or similar) in a relevant discipline, such as biology, zoology, entomology, environmental biology, evolutionary biology, or agriculture.
- Experience in working with insects.
- Excellent ability to plan, organise and schedule work to effectively facilitate the research programme.
- Strong IT skills (especially in using MS Excel), good data handling and management skills, and resource management skills
- Ability to accommodate flexible working hours (e.g., availability for some weekend work) required during laboratory experiments to ensure scientific objectives are met.

#### Desirable Criteria

- Excellent experimental design skills.
- Basic molecular biology skills (DNA extraction, PCR, sample

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>

## StMarysC Maryland 1yr EvolutionaryCoastalBiologist

Evolutionary Biologists working on coastal systems are encouraged to apply.

The Department of Biology at St. Marys College of Maryland invites applications for the position of \*Visiting Assistant Professor in Coastal Biology \*beginning August 2019. Teaching responsibilities include Coastal Ecology, an environmentally focused non-majors biology course, and an upper division elective in their specialty. This is a one year position with the departments option to extend to two years. Ph.D. required; postdoctoral training and/or teaching experience preferred. The SMCM Biology Department maintains estuarine/marine aquatic facilities that would be available for faculty and student research.

Non-sectarian since its founding in 1840, St. Mary's College of Maryland is a public Carnegie Baccalaureate Arts and Sciences institution which has been designated as Maryland's public honors college. With selective admissions policies, academically talented students, and a rigorous curriculum, we offer a small college experience similar to that found at exceptional private colleges. The quality of life is enhanced by the recreational opportunities of the Chesapeake region and by our proximity to Washington, D.C. and Baltimore.

St. Marys College ([www.smcm.edu](http://www.smcm.edu)) embodies diversity and inclusion in its mission. We encourage inquiries from applicants who will contribute to our cultural and ethnic diversity. Application materials should include a cover letter, curriculum vitae, statement of teaching philosophy, statement of research interests, and three letters of recommendation which can be submitted confidentially by letter writers through our Interfolio account. Applicants should indicate in their cover letter how their teaching at the College will contribute to a culture of inclusion and campus diversity. Applications are being accepted online at: \* [apply.interfolio.com/62622](http://apply.interfolio.com/62622) \* Questions may be directed to Jordan Price at 240-895-2216.

Review of applications will begin immediately and continue until the position is filled. Employment will be contingent upon successful completion of a criminal

background check, and candidates must produce the necessary documentation to legally work in U.S. upon hire. St. Marys College of Maryland is an affirmative action/equal opportunity employer.

Kevin J Emerson, PhD Associate Professor of Biology  
Biology Department St. Mary's College of Maryland  
18952 E. Fisher Rd St. Mary's City, MD 20686-3001  
kjemerson@smcm.edu <http://faculty.smcm.edu/kjemerson>  
Office: 240 - 895 - 2123, Schaefer Hall 231

"Emerson, Kevin" <kjemerson@smcm.edu>

---

## U Aberdeen 14 Evolutionary Biology

U.Aberdeen.14tenure-trackPosts.BiologicalSciences

The School of Biological Sciences at the University of Aberdeen is a vibrant and dynamic centre, internationally renowned for excellence both in teaching and research. Hosting over one hundred academic and research staff, 120 research students, 80 postgraduate taught students and 400 undergraduates; it is a close knit and friendly community. Based on the main campus at Kings College, the School also has facilities at the Cromarty Lighthouse, a field station at Bettyhill and a presence at the National Decommissioning Centre at Newburgh. We are committed to equality, diversity and inclusion, and opportunities for flexible working and childcare are available.

The school is currently recruiting up to 14 tenure-track positions at the Lecturer/Senior lecturer level (equivalent to Assistant/Associate Professor). Eight of these posts are Research Fellow positions, which will be expected to develop internationally excellent research programs in their area of expertise, and will transition to Teaching and Research posts after 5 years. The other six posts are Teaching and Research positions aimed to complement our existing departmental strengths in Ecological and Functional Genomics, Biogeochemistry, Marine Biology, and Fish Health. Salary range: £40-58K.

Please consult the following web pages for further details:

[https://www.abdn.ac.uk/research/jobs/-?search\\_sectionV7146&search\\_division=-&search\\_category=&additional\\_free\\_text=#SBS056A](https://www.abdn.ac.uk/research/jobs/-?search_sectionV7146&search_division=-&search_category=&additional_free_text=#SBS056A)

Closing date: 12 May 2019.

"Lancaster, Lesley" <lesleylancaster@abdn.ac.uk>

---

## UBristol Phylogenetics Cultural Evolution

Postdoc position in Cultural Phylogenetics

We have extended our search for a Postdoctoral Research Assistant with expertise in comparative phylogenetic methods. The post is a PDRA position in a European Research Council Starting Grant project entitled 'VariKin: Cultural Evolution of Kinship Diversity' led by Professor Fiona Jordan in the Department of Archaeology & Anthropology at the University of Bristol. We require an individual with expertise in phylogenetic comparative methods and techniques for understanding macroevolutionary processes, particularly in language and culture. The project team has amassed a large global database of kinship terms, and the objective for this role is to explore the cultural evolutionary dynamics and patterns of kinship terms.

The successful candidate will primarily be responsible for the design, implementation and analysis, and writing-up of two investigations. The post is offered on an open-ended basis with fixed funding for 12 months (full-time). The project and funding is due to come to an end November 30th 2020. Start timing is flexible, but we hope for the successful candidate to be in post as soon as possible.

Supplementary Info

You will have a PhD in evolutionary approaches to biology, anthropology, or language, or a similar field. It is essential that you have skills in a range of phylogenetic comparative methods, particularly BayesTraits and relevant R packages. Phylogenetic inference skills to examine reticulation (e.g. NeighbourNet etc) may also be useful. Broad experience with quantitative and computational data analysis (preferably using R), and with parallel/cluster computing, is highly desirable. There will be an opportunity for further skills training. Preference will be given to candidates who have worked with cultural/linguistic datasets although this is not essential.

You will require excellent organisational, communication and presentation skills. Experience with comparative data collection from written sources, database maintenance, and careful data curation are essential. You should demonstrate that you can engage in interdisciplinary collaborative work with the other VariKin

team members. Your particular role will work closely alongside the PI and PhD student investigating kinship system evolution across cultures, but there is scope to contribute to other strands in the project (developmental field studies of children's kinship knowledge, and cross-linguistic corpus analyses).

For informal enquiries you are encouraged to contact the PI Fiona Jordan (Fiona.jordan@bristol.ac.uk) and see our lab website at <http://excd.org/varikin>

See the further particulars and apply through the UoB portal here. <http://www.bristol.ac.uk/jobs/find/-details.html?nPostingID@914&nPostingTargetID3394&optionH&sortASC&respu=1&ID=Q50FK026203F3VBQBV7V77V83&Resultsperpage&lg=UK&mask=uobext> Please provide a cover letter that describes your skills and experience, your research interests, and details how you meet the criteria; and your current CV.

For more information on the Department of Anthropology and Archaeology see: <http://www.bristol.ac.uk/-archanth/> Closing date for applications May 22nd.

Fiona Jordan < <http://www.bristol.ac.uk/school-of-arts/people/fiona-m-jordan> > Professor of Anthropology Evolution of Cross-Cultural Diversity Lab < <https://excd.org> > Department of Anthropology and Archaeology

School Research Director sart-srd@bristol.ac.uk School of Arts

University of Bristol 43 Woodland Road Bristol BS8 1UU Tel: +44 (0)117 954 6078

twitter: @fiona\_jordan

Secretary, Cultural Evolution Society <https://culturalevolutionsociety.org/> Fiona Jordan  
<Fiona.Jordan@bristol.ac.uk>

---

## UCollege London CancerEvolution

About the role: We are seeking a talented computational postdoc to join the Secrier lab (<https://secrierlab.github.io/>) at the UCL Genetics Institute, where they will take the lead on an exciting project that aims to understand how genomic instability and complex structural rearrangements in cancer evolution. The successful applicant will employ bioinformatics, statistics, data integration and machine learning methods to investigate mutational processes that impact the transition

from early cancer to progressive disease.

The post is initially funded until 30/04/2021.

About the lab: The Secrier lab is a multidisciplinary group working at the interface of cancer genomics and immunology. We employ bioinformatics, statistics, machine learning and data integration methodology to investigate aspects of genomic instability and tumour-microenvironment interactions for the purpose of early cancer detection and understanding of neoplastic progression. We have an established track record in oesophageal adenocarcinoma and various collaborations with partners of the UK-wide Oesophageal Cancer Clinical and Molecular Stratification (OCCAMS) Consortium, including with the Universities of Cambridge, Southampton and Belfast. We also have ongoing collaborations in various other cancers, such as prostate, breast, glioma and sarcoma with clinicians and biologists at the UCL Cancer Institute, Queen Mary University and the German Centre for Neurodegenerative Diseases, among others, as well as industry partners. We are ideally based at the UCL Genetics Institute, where we benefit from a supportive and collaborative environment with a focus on method development for big genomics data.

Qualifications and skills: The successful candidate must have a PhD (or be studying towards it) in bioinformatics, computational biology, statistics, mathematics, computer science or similar area, be fluent in R, Python, Perl, C++ or other programming language, have a good knowledge of statistics and a strong interest in cancer biology. Broad knowledge of machine learning and bioinformatics methodologies, previous experience with NGS data and experience with cancer genomics and/or transcriptomics data are among the desirable criteria.

How to apply?

For a full job description and to apply online for this vacancy please click here: <http://tinyurl.com/y4dgy525> Informal enquiries should be directed to Maria Secrier on [m.secrier@ucl.ac.uk](mailto:m.secrier@ucl.ac.uk)

Closing date for applications: 21st April 2019

"Secrier, Maria" <[m.secrier@ucl.ac.uk](mailto:m.secrier@ucl.ac.uk)>

---

## UCollege London Evolutionary Biol

Professor or Associate Professor of Evolutionary Biology  
Research Department of Genetics, Evolution and Environment in the Division of Biosciences, University College London

Grade 9: £56,266- £61,181 per annum

Grade 10: from £64,710 per annum (negotiable according to relevant skills, knowledge, experience and achievement)

**Duties and Responsibilities** As a central component of the UCL scientific strategy, we seek to appoint a scientist as Professor or Associate Professor based in the UCL Centre for Life's Origins and Evolution (CLOE), a subdivision of the Department of Genetics, Evolution and Environment in the Division of Biosciences, Faculty of Life Sciences.

The successful candidate will have an international reputation in Evolutionary and Comparative Biology. Their research will fit into one or more of CLOE's research themes: the origins of life and its major innovations; the pattern of evolution at all time scales and across the tree of life; and the processes that underpin the emergence of biological complexity and diversity. Research interests may include, but are not restricted to: comparative genomics/genetics; the diversification of major groups; the evolution of within and cross species interactions; the genetic basis of key transitions in evolution; organelle origins and evolution; the evolution of multicellularity; the evolution of developmental form and function. We welcome applicants working on any taxa using a range of experimental and/or computational/theoretical approaches. The department has a priority for appointments in plant and fungal research.

The Research Department of Genetics, Evolution and Environment (GEE) is one of four Research Departments in the Division of Biosciences at UCL, one of the world's leading centres for basic biological sciences and part of the UCL Faculty of Life Sciences. GEE is home to world-class geneticists, evolutionary biologists, computational biologists and ecologists. The appointee will be expected to develop links with other CLOE researchers, with members of other GEE institutes, including the Centre for Biodiversity and Environmental Research (CBER), UCL Genetics Institute (UGI) and the Institute for Healthy Ageing (IHA) and with re-

searchers in other Departments and Faculties. GEE has strong links to the wider community of London-based researchers, especially the Zoological Society of London and the Natural History Museum.

**Key Requirements** The successful applicant will demonstrate capability for teaching and will contribute to the development of teaching at undergraduate and masters levels. The successful candidate will have an internationally recognised record of research in Evolutionary and Comparative Biology; a record of running a productive, independent research group; publishing original research in highly regarded journals; attracting external funding throughout their career; and experience teaching graduate and undergraduate students. The appointee will possess a PhD or equivalent qualification.

Further Details and to Apply <https://go.nature.com/-2OQ1fkf> Closing Date: 28 May 2019

Interview Date: Early July 2019

"Williamson, Fiona" <[f.williamson@ucl.ac.uk](mailto:f.williamson@ucl.ac.uk)>

---

## ULiverpool ResFellow 35mths Evolutionary Biol

Research Fellow Grade 8

Evolution, Ecology And Behaviour

011366

40,792 pa

29-Apr-2019 23:30

We are seeking to appoint an independent research fellow with research interests that align with those of the Department of Evolution, Ecology and Behaviour. Notable strengths of the department include: mammalian behavioural biology; evolutionary and population genomics; evolutionary ecology, particularly including the responses of ecosystems to environmental perturbation; the evolution and ecology of host-symbiont and host-parasite interactions in health and disease. During this fixed-term position you will develop an independent research programme, as well as seek further independent funding. You will be supported in building your research programme and developing your career by the Institute, which provides an environment that fosters and supports the development of future research leaders. You will have full access to communal facilities in the Institute and some start-up funds. Although this is a

research post, you will have the option to contribute to some undergraduate teaching. You should have a PhD in a relevant discipline, have a strong research portfolio that shows evidence of research independence, and high quality publications, appropriate to your career stage. The post is available for 35 months.

Contact: Carole Thomas [carolet@liverpool.ac.uk](mailto:carolet@liverpool.ac.uk)

Closing date: 29 April 2019

Best wishes,

Bernie

Bernie Shacklady Management Services Administrator  
Institute of Integrative Biology University of Liverpool  
Biosciences Building Liverpool L69 7ZB Tel: 0151 795 4410  
[bking@liv.ac.uk](mailto:bking@liv.ac.uk) <http://www.liverpool.ac.uk>  
"Shacklady, Bernadette" <[B.King@liverpool.ac.uk](mailto:B.King@liverpool.ac.uk)>

---

## UMichigan SummerFieldTech PlantEvol

The Baucom Lab at University of Michigan is looking for an undergrad field tech for the summer, based in both MI and TN. ~35 hrs/week, \$15/hr, housing paid for (July/August) while in TN. If interested, pls send an email to [asoble\[at\]umich\[dot\]edu](mailto:asoble[at]umich[dot]edu) with brief statement of interest, prev experience & 3 refs. Undergrad tech will help maintain plants in field, score flowering time/number, and take various types of data! All day outdoors in pretty hot conditions. Projects will be focused on agricultural weeds and herbicide.

For more information about the lab you can go through the following website: <https://baucomlab.wordpress.com/> or direct questions to [asoble\[at\]umich\[dot\]edu](mailto:asoble[at]umich[dot]edu).

Anah Soble <[asoble@oberlin.edu](mailto:asoble@oberlin.edu)>

---

## UNewMexico Albuquerque FishCollectionsManager

Senior Science Museum Collection Manager Division of Fishes Museum of Southwestern Biology University of New Mexico

The Museum of Southwestern Biology (MSB) is seeking a Senior Collection Manager for the Division of Fishes (<http://msb.unm.edu/divisions/fishes/-index.html>). The Fish Collection is located in a state-of-the-art facility in the center of the University of New Mexico (UNM) Main Campus in Albuquerque, a vibrant research and education facility associated with the Department of Biology in the College of Arts and Sciences. The MSB develops and maintains natural history collections explicitly for use in research and education, benefiting the university, science, and society. The scientific role of the MSB is to facilitate and engage in specimen-based studies of ecology, evolution, systematics, and biodiversity informatics, and to train students in these disciplines. The MSB Division of Fishes also serves conservation science and management of aquatic resources in the southwestern United States and beyond. The MSB Fish Collection is the largest of its type in the southwestern US and comprises more than 100,000 lots of more than 4.5 million specimens. Research in the collection focuses on long-term population studies, community ecology, reproductive biology, and genomics. The collection provides an exceptionally well-documented record of the profound changes to biodiversity that have occurred in the desert southwest over the last century.

We seek candidates with a strong commitment to a vision of the Fish Collection as a key resource for research and education within the University, and to the scientific and conservation community nationally and internationally. Within the context of the curatorial priorities of the Fish Collection, this position offers opportunities for mentoring, career development, research, public outreach, fieldwork, and involvement in undergraduate and graduate education.

**Education and Experience:** A Masters Degree with at least 5 years of collection experience is required, and a Ph.D. can substitute for some of the experience. The successful candidate should demonstrate strong skills in collection management, organization, and supervision, and should have a record of accomplishment with respect to the development, promotion and use of collections. Demonstrated database skills are also essential. Imaging skills and genetic resource management skills are desirable.

**Knowledge, Skills, and Abilities:** The successful applicant must have demonstrated expertise in ichthyology, preferably with knowledge of taxonomy of global and regional (southwestern US and northern Mexico) fishes, and have experience in natural history collection use and management. Candidates should have experience with relational databases (such as Microsoft Access or Arctos), as well as familiarity with online data aggrega-

gators and current digitization efforts in biodiversity collections. Curation and digital management of genetic resources (tissues) is an important component of this position. The Collections Manager of Fishes will serve as an advocate for natural history collections, and must be able to communicate their importance to members of the public and to the university and scientific communities alike. Exceptional organizational skills are required.

**Essential Functions:** Curation (care, maintenance, improvement, and growth of collection, as well as database management, and processing of loans). Service (including grant writing), outreach, & professional development. Research as appropriate in the context of curatorial priorities.

**Duties and Responsibilities:** 1. Curate physical specimens, including specimen preparation, and organization, care, and housing of specimens and associated tissues or other ancillary materials (such as field notes). Conduct and coordinate processing of new and existing collections, including accessioning, physical preparation, labeling, cataloguing, and loans. 2. Establish priorities for collection care and management in coordination with curatorial and research staff. 3. Develop and implement collections management policies aligned with best museum practices and University policy. 4. Provide collection access to the research community, including assisting visitors to the collection and processing specimen loans. 5. Digitize and document collections and their use, including capturing and managing in a database digital images of specimens and their associated information and field notes. 6. Maintain electronic and digital records, and update taxonomic and auxiliary information. 7. Collaborate and liaise with external biological data repositories and partners, including but not limited to VertNet, iDigBio, and GBIF. 8. Provide periodic support to the museum, university, and professional communities, such as serving on MSB and institutional committees 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>

## UOslo Systematic Mycology

Associate Professor in Systematic Mycology Natural History Museum University of Oslo, Norway

The Natural History Museum, University of Oslo, is recruiting an Associate Professor in Systematic Mycology. This is an attractive position with 50% research time, 50% curation of the mycology collections, as well as possibilities for teaching. Application deadline 19 May 2019.

The Natural History Museum (NHM) seeks a dynamic researcher for an associate professorship in systematic mycology. The successful candidate should have a research profile in integrative systematics of fungi, which preferably addresses questions of both deep phylogeny and species delimitation and intraspecific diversity. He/she should also master up-to-date molecular and bioinformatic methods in systematic biology. It is expected that the applicant will develop an independent research program that will have synergistic effects within the research group 'Integrative Systematics of Plants and Fungi (ISOP) as well as with other research groups at NHM. The successful candidate will be expected to attract extramural research funding and should document ability and potential to be successful in this respect.

NHM has an array of research facilities, including advanced microscopes and a specialised library prep lab with in-house high throughput sequencing equipment. The museum also collaborates with the Department of Biological Sciences on several research facilities, and has access to state-of-the-art HTS sequencing and HPC computing.

Candidates who combine fundamental research questions with powerful molecular and computational approaches within a collection-based context, will therefore be preferred.

NHM has a collaborative agreement with the Department of Biological Sciences about teaching and supervision of students at the bachelor and master level, and with the Faculty of Mathematics and Natural Sciences in the education of doctoral candidates. NHM also hosts an international Research School in Biosystematics (ForBio). The successful candidate will be expected to teach students at all academic levels, including supervision of PhD students and postdocs. Working time will be devoted to research, curating collections, teaching

and supervision of students, outreach and administrative tasks at NHM. Lectures and tuition are given in Norwegian and English. Foreign language speakers are expected to be able to teach in a Scandinavian language within two years after being hired.

<https://www.jobbnorge.no/en/available-jobs/job/-166957/associate-professor-in-systematic-mycology>  
Hugo de Boer

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

Plant.ID MSCA-ITN project leader Leader of ForBio - Research School in Biosystematics Plant Evolution and DNA Metabarcoding group

Hugo de Boer <h.de.boer@nhm.uio.no>

---

### UVirginia ResAssist SocialNetworkEvolution

The Brodie Lab at University of Virginia is looking for a full-time, permanent research assistant/lab manager. This person will assist with fieldwork in the summers at Mountain Lake Biological Station, and will provide research and lab support in Charlottesville the rest of the year. Current projects include natural and experimental studies of social network evolution and behavioral ecology in forked fungus beetles, and continuing work on coevolutionary interactions of amphibians and reptiles.

Official job description and application at the link below. Email Butch Brodie at [bbrodie@virginia.edu](mailto:bbrodie@virginia.edu) with questions. Looking to fill the position in time for field season mid May.

[https://uva.wd1.myworkdayjobs.com/en-US/-UVAJobs/job/Charlottesville-VA/Laboratory-Technician-2\\_R0003458](https://uva.wd1.myworkdayjobs.com/en-US/-UVAJobs/job/Charlottesville-VA/Laboratory-Technician-2_R0003458) [butchbrodie@gmail.com](mailto:butchbrodie@gmail.com)

---

### UZurich SystematicBotany

The Faculty of Science at the University of Zurich invites applications for an

Assistant Professor Tenure Track in Systematic and Comparative Botany

We seek innovative applicants with a strong record in research; experience in teaching is desirable. Applicants with expertise in plant macroevolution, phylogenomics, comparative morphology, biodiversity-informatics, macroecology, or herbarium genomics are particularly encouraged to apply.

The successful applicant is expected to develop a complementary and independent research program in systematic botany and to acquire external funding. Contributions to the existing undergraduate and graduate teaching efforts in systematics, evolution, and organismic botany will also constitute an integral part of the position. The successful applicant will be located at the campus Botanical Garden of the University of Zurich.

The University of Zurich provides generous research support, including dedicated funds for personnel, running expenses and competitive start-up packages. Zurich's scientific environment includes a rich spectrum of research activities across the sciences and provides extensive opportunities for collaboration with research groups at the University of Zurich and other leading Swiss research institutions. The Department of Systematic and Evolutionary Botany holds an extensive herbarium being a nationally and internationally significant collection.

The employment conditions for this position follow the legal regulations of the University of Zurich (see [www.prof.uzh.ch/de.html](http://www.prof.uzh.ch/de.html)), which include part-time options. The University of Zurich is an equal opportunity employer and in particular strives to increase the percentage of women in leading positions (see <https://www.mnf.uzh.ch/en/mnf-gleichstellung.html>). Therefore, qualified female researchers are particularly encouraged to apply. The city of Zurich combines a stimulating cultural scene in a modern European city with easy access to a beautiful natural landscape.

Academics with the appropriate qualifications are kindly invited to submit their applications including:

- a curriculum vitae - lists of publications and research funding - outlines of research and teaching programs - plans to develop the discipline further (major problems and possible solutions) - names and contact details of three referees

Please address your application to Prof. Roland Sigel, Dean of the Faculty of Science. Upload your application as a single pdf file to <http://www.mnf.uzh.ch/SCB> by 31 May 2019.

For further information, please contact Prof. Florian Schiestl at [florian.schiestl@systbot.uzh.ch](mailto:florian.schiestl@systbot.uzh.ch)

[dekanat@mnf.uzh.ch](mailto:dekanat@mnf.uzh.ch)

---

## Vienna Bioinformatics

Applications are invited as a programmer to work with larger project entitled “Genome-wide molecular dating” (<https://www.wwf.at/programmes/mathematics/-MA16-061>) at the Institute of Population Genetics, Vetmeduni Vienna. Starting date will be August/September or shortly thereafter. The position is for at least 12 months, and it is quiet flexible (e.g., it could also be part-time or a short-term postdoc position).

Standard phylogenetic methods reduce entire populations to single points in genotypic space by modelling evolution as a process in which a single gene mutates along the branches of a phylogeny. In this project, we are developing new theory and software to tackle the problem of species tree estimation and molecular dating genome-wide. Visits to St Andrews, Budapest and Aarhus for collaborations with Carolin Kosiol, Gergely Szöllösi and Asger Hobolth are possible.

The successful candidate should have programming experience in language such as C, C++, Java and a scripting language such as Python or Perl. They will have a degree in Bioinformatics, Computer Science, Statistics, Mathematics, Physics or a related field. Prior experience with either phylogeny or population genetics, or comparative genomics is a benefit.

To receive full consideration, applicants should submit a single PDF file by e-mail to Carolin Kosiol ([carolin.kosiol@vetmeduni.ac.at](mailto:carolin.kosiol@vetmeduni.ac.at) or [ck202@st-andrews.ac.uk](mailto:ck202@st-andrews.ac.uk)) including (i) Cover letter with a brief summary of previous experience and motivation for the position and (ii) CV including a list of publications (iii) The names and contact details of 2-3 references. Informal enquires are welcome. Screening will start on the 26th April till the position is filled.

Carolin Kosiol <[carolin.kosiol@vetmeduni.ac.at](mailto:carolin.kosiol@vetmeduni.ac.at)>

---

## Wageningen EvolutionaryEcol

The Netherlands Institute of Ecology (NIOO-KNAW) is a top research institute of the Royal Netherlands Academy of Arts and Sciences (KNAW). NIOO-KNAW

conducts fundamental and strategic research on individual organisms, populations, communities and ecosystems. Its mission is to carry out excellent research in ecology. In 2018, NIOO received an 'excellent' rating in a peer review by an international review committee. There are four departments, along with seven dynamic research themes that cut across these departments.

NIOO's department of Animal Ecology is offering a Tenure-track position for an Evolutionary or Population Ecologist Vacancy number TT-AnE-019009

Research in the department of Animal Ecology is centred around the evolutionary and population ecology of animals, and combines long-term population studies of birds with experimental work in aviary and water bird facilities and with the use of avian genomic tools. The department has an outstanding reputation within the international scientific community.

Personal profile and requirements - We are looking for an enthusiastic scientist with several years of post-doctoral experience, of which at least two years abroad, and an excellent track record in evolutionary or population ecology in terms of both publications and the acquisition of research grants. (S)he is expected to build a strong research line within the department, to bring in expertise complementary to the other scientists (see <https://nioo.knaw.nl/en/department-animal-ecology>) and to play an active role within the department, the themes and the institute. - Furthermore, her/his research preferably makes use of the department's unique triangle of facilities: long-term populations in the wild, amenities for studying birds under controlled conditions, and avian genomics tools. The candidate must have a track record of acquiring and supervising externally funded PhD students. With this appointment, we aim to increase the gender diversity of senior researchers in the Department, and therefore we explicitly invite female scientists to apply. - Scientists at NIOO have no obligation to teach at university level. However, supervision of external master's and PhD students is expected as part of normal research activity. Scientific communication is carried out in English, so knowledge of the Dutch language is not a prerequisite for this position, but a commitment to learning the language is expected in longer-term staff.

Appointment - In principle, the appointment is for a tenure-track position: the appointed scientist will be appointed on a temporary basis for a maximum of 6 years. After 3 and 5 years of employment, there will be an assessment of performance based on criteria that will be specified at the time of appointment (for procedures and general criteria see our Tenure-track Guidelines and Annex. - Based on these assessments, the researcher may be promoted to the rank of senior researcher with



tenure. In exceptional cases, outstanding candidates can be offered tenure directly. - We offer an extensive package of fringe benefits. Salary depends on training and work experience. The regular tenure track appointment gross salary starts at 3,111.- (scale 10.4) per month to the maximum gross monthly salary of a full-time appointment at 4,978.- (scale 11.11) per month, Collective Agreement for Dutch Universities (CAO Nederlandse Universiteiten), excluding 8% holiday pay and a year-end bonus.

Location Wageningen.

Information More information can be obtained from Prof. Marcel E. Visser (m.visser@nioo.knaw.nl or +31-317-473439), head of the department of Animal Ecology.

Applications Please send your application letter including a brief research statement, a complete curriculum vitae and names of three referees to vacature@nioo.knaw.nl. The closing date for applications is 15 May 2019, the interviews will take place on 11 and 12 June.

“Pol, Martijn van de” <M.vandePol@nioo.knaw.nl>

---

## Other

BlueGreatTit ColourationCollaborativeProject .... 73	Software NewRelease BALi-Phy 3 4 1 ..... 77
Estimating Haplotype Frequencies ..... 74	SouthAfrica VolResAssist MoleRat HormonesBehaviour .. 77
Evolution2020 CallForSymposia ..... 74	SSE GraduateStudentAdvisoryCouncil ApplicationsApr15 ..... 78
EvolutionInUrbanEnvironments CallForSubmissions 75	Teaching Evolution Schools ..... 78
Meaning Of OD Taxonomy ..... 75	UCRiverside NSF REU Livebearing Fish Placenta Evolution ..... 79
Meaning Of OD Taxonomy answer ..... 75	
NewWebsiteFor Seqphase ..... 76	
PeerCommunity ..... 76	
SocietyMolluscEvolution NominationsForCouncil .. 77	

---

## BlueGreatTit ColourationCollaborativeProject

Dear Blue/Great Tit researchers,

Together with my team, I'm running now a project aimed at studying the physiological and genetic aspects of feather colouration, using the Blue Tit as a model species.

One component of this project is a survey of tit coloura-

tion spanning the whole European continent, to discover geographical patterns in tit colouration and pigment composition. Blue Tit colouration, although serving as a model for plumage colour evolution, is still poorly understood, both from the point of view of proximate mechanisms governing its expression and from the point of view of genetic mechanisms controlling it. By studying the extent of blue tit feather colouration across the whole continent we hope to fill one of the gaps in our knowledge about this trait: namely, how consistent (or environment-specific) it is.

Our analysis will comprise: 1) colorimetric measurements of sampled feathers (both yellow breast feathers

and blue crown feathers in both sexes); 2) biochemical analysis of pigments generating the yellow colour using extraction and HPLC analysis of their content; 3) electron-microscopy analysis of the nano-structure of blue feathers.

All described methods have already been used in my team and very validated in terms of their efficiency and consistency.

The project is focused on Blue Tits. However, since quite often Blue Tits are studied in parallel with Great Tits, and there are also many excellent Great Tit-focused studies across Europe, we do not exclude the possibility of also including Great Tit yellow feathers in our study, which would give it an interesting cross-species context.

If you study Blue and/or Great Tits and would like to contribute to the project - please let me know by filling in this form: <https://forms.gle/sF1HDmcefDy7aihWA>. Once I hear from you, I will contact you with the details of what is needed in order to take part in the project, and a detailed protocol of how to proceed with sampling and what to consider when selecting sampled birds etc. Briefly, I will ask you to provide us with a fresh (i.e. year 2019 or 2020 if 2019 is off-limits) sample of male and female feathers (2-3 individuals per study population per sex), sampled and secured in a way ensuring their safe travel and subsequent measurements (we use a method developed in our projects that makes the whole process very easy and repeatable). The feathers can be sent in a regular letter within Europe, which makes the whole process even easier. Once the feathers get to us, we will measure their colour using an Ocean Optics Maya spectrophotometer and extract feather pigments (yellow feathers only) for subsequent HPLC assay.

Of course, all contributions will be treated equally and all contributors will be offered co-authorship of all resulting publications.

Please do not hesitate to contact me if you have any questions or comments.

Looking forward to hearing from you, Szymon Drobniak Institute of Environmental Sciences, Jagiellonian University (PL) & School of Biological, Environmental & Earth Science, University of New South Wales (AU)

Szymek Drobniak JU <[szymek.drobniak@uj.edu.pl](mailto:szymek.drobniak@uj.edu.pl)>

---

## Estimating Haplotype Frequencies

As part of a recent project, my collaborators and I derived an expression for the expected pairwise linkage disequilibrium under neutral evolution in the absence of recombination. I would like to compare these predicted values to actual linkage disequilibria in the genomes of clonally reproducing organisms or in non-recombinant regions of the genome in sexually reproducing organisms.

To do so, I need phased haplotype data from a large number of individuals taken from the same population - where the genomes of each individual are either sequenced/phased separately, or if pooled, the reads are sufficiently long to include multiple segregating sites.

The haplotype data would have to come from (minimally) hundreds of individuals, ideally thousands for allele frequency and LD estimation. The model organism doesn't matter so much - mt DNA from humans or other animals, single cell sequence data from tumors, long-read data from unsegmented viruses, etc.

If anybody can recommend a suitable publically available source with this type of data, I would appreciate any suggestions.

Thank you, Max Shpak

Max Shpak, Ph.D. St. David's Medical Center 1015 East 32nd Street, Suite 414 Austin, TX 78705 (512) 544-8077

[shpak.max@gmail.com](mailto:shpak.max@gmail.com)

---

## Evolution2020 CallForSymposia

Call for Symposia for the 2020 Annual Evolution Meeting The SSE Council invites proposals for two SSE-sponsored symposia to be held at the 2020 Evolution meeting in Cleveland, OH, USA on June 19-23, 2020. SSE Council considers the novelty of the topic and likely interest among its members when selecting symposia to sponsor. Sub-fields or taxonomic groups that have been underrepresented in past symposia will be considered preferentially. SSE Council seriously considers the diversity of participants as a criterion for symposium funding.

Symposium organizers are expected to take into account gender, seniority, nationality, and other axes of diversity traditionally underrepresented in Society symposia, and to describe their efforts in the proposal. To be assured of full consideration, proposals must be received by midnight Eastern Standard Time on June 1, 2019. Learn more here < <http://www.evolutionsociety.org/content/society-awards-and-prizes/sponsored-symposia.html> >

\*Kati Moore\* \*Communications Specialist\*  
 \*Society for the Study of Evolution\*  
 communications@evolutionsociety.org  
[www.evolutionsociety.org](http://www.evolutionsociety.org) SSE Communications  
 <communications@evolutionsociety.org>

---

## EvolutionInUrbanEnvironments CallForSubmissions

\*\*\*We invite contributions to a special feature on evolution in urban environments to be published in *Evolutionary Applications* in 2020. Instructions on how to be considered for this special feature are provided below. This information is also available at: [https://urbanevolution-litc.com/evoapp\\_submission/](https://urbanevolution-litc.com/evoapp_submission/) \*\*\*

Urban areas are among the fastest growing ecosystems on earth and the driver of local and global climate change. Despite this importance, little is known about the consequences of urbanization for evolutionary biology, and its application to human society and environmental sustainability. Consequently, the study of evolution in urban environments is among the fastest growing research areas in evolutionary biology, with important implications for fundamental questions in evolutionary biology and applied problems that relate to human health, conservation biology, environmental sustainability, and urban planning. To advance this research area, *Evolutionary Applications* will be hosting a Special Issue examining how urbanization affects the evolution of organisms living in or near cities, edited by Marc Johnson, Elizabeth Carlen, Lindsay Miles, and Kristin Winchell.

To be considered for the special issue, we invite Abstract submissions that propose original theoretical or empirical research, quantitative reviews/meta-analyses or perspective articles that offer a novel view on urban evolution. Contributions from diverse and cross-disciplinary fields are especially encouraged. We also encourage submissions from any country and research discipline. Papers should examine the effects of ur-

banization on evolution, or the applied consequences of urban evolution on urban planning and sustainability, conservation, genetics, human evolution, and the integration of ecological and applied research with an evolutionary perspective. Abstract submissions should be 250-400 words and can be submitted using this form: <https://forms.gle/9BdwShrQz29MNh1j9>. The deadline for abstract submissions is June 1st, 2019, and all decisions on invited papers will be communicated by July 1. Invited contributors should plan to submit manuscripts for peer review by February 1, 2020.

Please note that *Evolutionary Applications* is an Open Access journal, and the fee schedule for publications can be found on their site: [https://onlinelibrary.wiley.com/page/journal/17524571/-homepage/article\\_publication\\_charges.htm](https://onlinelibrary.wiley.com/page/journal/17524571/-homepage/article_publication_charges.htm). For questions, please contact one of the co-editors: Marc Johnson V [marc.johnson@utoronto.ca](mailto:marc.johnson@utoronto.ca) Elizabeth Carlen V [ecarlen@fordham.edu](mailto:ecarlen@fordham.edu) Lindsay Miles V [lindsay.miles@utoronto.ca](mailto:lindsay.miles@utoronto.ca) Kristin Winchell V [kmwinchell@wustl.edu](mailto:kmwinchell@wustl.edu)

“Winchell, Kristin” <[kmwinchell@wustl.edu](mailto:kmwinchell@wustl.edu)>

---

## Meaning Of OD Taxonomy

Dear Colleagues,

I am looking for the meaning of OD Taxonomy and Phylogeny. Could you help me with the meaning of “OD”?

Thanks in advance

Prof. José Serrano Catedrático de Zoología Facultad de Veterinaria, Campus de Espinardo 30100 Murcia

Jose Serrano <[jserrano@um.es](mailto:jserrano@um.es)>

---

## Meaning Of OD Taxonomy answer

Thanks to all colleagues that have replied my question. The O. D. abbreviations are used in Belgium to designate the Operational Directory (i.e., Research Unit) of Taxonomy and Phylogeny, at the Royal MUseum in Brussels.

Cheers.

– Prof. José Serrano Catedrático de Zoología Facultad de Veterinaria, Campus de Espinardo 30100 Murcia

Jose Serrano <jserrano@um.es>

---

## NewWebsiteFor Seqphase

Dear EvolDir members,

The server hosting my online program SeqPHASE was turned off by my former institution and I am presently looking into moving it to a new place. As a temporary fix, SeqPHASE is available to users at <http://techfnord.de/ap/seqphase/>. Best regards, Jean-François

– Jean-François Flot Associate Professor Evolutionary Biology & Ecology - C.P. 160/12 Université Libre de Bruxelles Avenue F.D. Roosevelt 50 B-1050 Brussels - Belgium <http://ebe.ulb.ac.be/ebe/Flot.html> Jean-François Flot <jflot@ulb.ac.be>

---

## PeerCommunity

Dear colleagues We invite you to submit your preprints to Peer Community in Evolutionary Biology (PCI Evol Biol, <https://evolbiol.peercommunityin.org>) in order to obtain a recommendation from this community after peer-reviewing.

**\*\*Some numbers:\*\*** -We're now more than 400 editors at PCI Evol Biol -We've received 107 submissions of preprints. We've recommended 46 and are still evaluating 24 of them. -Mean time to 1st decision: 49 days

PCI Evol Biol is a group of scientists who review and recommend preprints in evolutionary biology, free of charge and transparently. It is a research community working for researchers to create a new publication system that is completely free of charge and independent of private publishers. This community already includes 400 researchers (the full list can be found at <https://evolbiol.peercommunityin.org/public/-recommenders>) motivated to review and recommend preprints.

**\*\*Some important points:\*\*** -PCI Evol Biol is free

for all users (readers AND authors); -PCI Evol Biol is supported by scientific societies including the Society for the Study of Evolution, the Society of Systematic Biologist, the Nordic Society Oikos, the French Ecology and Evolution Society (the SFE2), etc. (<https://peercommunityin.org/who-supports-peer-community-in/>); -PCI Evol Biol does not publish the preprints (they stay on the preprint server) but the associated reviews and recommendations; -PCI Evol Biol does not evaluate preprints already submitted for publication in a journal, in order to avoid parallel reviewings; -Authors can submit their preprints to traditional journals once they have been recommended by PCI Evol Biol. Reviews obtained before the recommendation can help improve the quality of the preprint; -Journals such as JEB, Evolution, Ecology Letters, Plos Biol, TREE, Evolutionary Applications, etc. (<https://peercommunityin.org/pci-friendly-journals/>) indicated that they will consider the preprints recommended by PCI Evol Biol and that they will take into account the reviews and recommendations of PCI Evol Biol in their own editorial process if adequate. -PCI Evol Biol's recommendations are transparent (reviews and recommendations are published, recommendations are signed, reviewers can remain anonymous if they wish); -Only reviews leading to a recommendation are published; -A preprint recommended by PCI Evol Biol is scientifically validated and can therefore be cited; -PCI Evol Biol's recommendations have a DOI, are referenced and can therefore also be cited; -Four other communities (PCI Ecology, PCI Paleontology, PCI Animal Science, PCI Entomology) also exist. -Anonymous submissions are possible

To submit your preprints, simply go to <https://evolbiol.peercommunityin.org> click the 'Submit a preprint' button and follow the instructions.

We hope to have aroused your interest,

The Managing Board of PCI Evol Biol  
<https://evolbiol.peercommunityin.org> contact@evolbiol.peercommunityin.org  
<https://youtu.be/4PZhpnc8wwo> Thomas Guillemaud  
 <thomas.guillemaud@inra.fr>

---

## SocietyMolluscEvolution NominationsForCouncil

Dear all

Unitas Malacologica, the world society for mollusc biology, is seeking new faces to serve as our elected council members. Unitas is a global organisation with international representation on council; the principle activity of the organisation is the tri-annual World Congress of Malacology. You may nominate any suitable person, including yourself, for this position (subject to election by the membership). We need enthusiastic and energetic people to fill these roles and take UM forward.

There are currently openings for members of council \*and\* officers for three-year terms, terms start after the 2019 General Assembly at the WCM in California.

We need Secretary - responsible for council business, including annual research awards Treasurer - responsible for society funds and budget; as the accounts are in euros, it would be preferable to have a treasurer based in a eurozone country General members of council (two openings)

We also welcome expressions of interest for the position as Communications Officer - responsible for the website (and the currently defunct newsletter)

Nominations require a proposer and a seconder. As self-nomination is acceptable this is generally the nominee and another supporter (the proposer or seconder can also be a current member of council). Members of council must be members of UM but the nominee can join at the time of nomination.

UM constitution and membership information are here (cf. Article IV, Section 1; Article V, Section 4): <http://www.unitasmalacologica.org/membership.html> The deadline for nominations for these positions is 4 June 2019. A ballot must be held before the Annual General Meeting in August, and will be circulated in advance in June to current members.

Please send your nominations, suggestions and questions to me ([j.sigwart@qub.ac.uk](mailto:j.sigwart@qub.ac.uk))

Cheers,

Julia

Dr Julia D Sigwart Queen's University Belfast, Marine Laboratory Portaferry, Northern Ireland e.

[j.sigwart@qub.ac.uk](mailto:j.sigwart@qub.ac.uk) m. +44 (0)780 5665 863  
<http://www.qub.ac.uk/qml/People/Sigwart> new book!  
"What Species Mean: Understanding the Units of Biodiversity" <https://www.crcpress.com/What-Species-Mean/Sigwart/p/book/9781498799379> Julia Sigwart  
<[j.sigwart@qub.ac.uk](mailto:j.sigwart@qub.ac.uk)>

---

## Software NewRelease BALi-Phy 3 4 1

Hi,

BALi-Phy version 3.4.1 is now available (<http://www.bali-phy.org>) for Windows, Mac, and Linux. The main new features are: (<http://www.bali-phy.org/releases/3/>) - Faster and uses less memory (since 2.3). - RNA stem models for fixed alignment regions: RNA.16a. etc. - Improved codon models: gy94, mg94, fMutSel, m3, m8, branch\_site, etc. - Package manager bali-phy-pkg (for packages like <https://github.com/bredelings/BayesianEstimatorSelfing>) - CIPRES interface. - Linux packages (Debian/Ubuntu) and Mac packages (homebrew).

BALi-Phy is a Bayesian MCMC program for estimating alignments and phylogenies simultaneously from unaligned sequence data. BALi-Phy alignments can be 3.5 times more accurate than alignments using MAFFT.

BALi-Phy can also be used to safely infer phylogenies from ambiguous regions like ITS - <http://bali-phy.org/Examples/ITS/ITS12-tn93-free3/> You can download binaries for Linux, Mac, and Windows here: - <http://www.bali-phy.org/download.php> If you have any trouble using bali-phy, please post your questions to [bali-phy-users@googlegroups.com](mailto:bali-phy-users@googlegroups.com). I should be able to respond fairly quickly.

-BenRI

Ben Redelings <http://www.ben-redelings.org> Benjamin Redelings <[benjamin.redelings@gmail.com](mailto:benjamin.redelings@gmail.com)>

---

## SouthAfrica VolResAssist MoleRat HormonesBehaviour

We are looking for two volunteer research assistants to carry out exciting experiments with captive Damara-land mole-rats, a cooperatively breeding subterranean

rodent, at the Kuruman River Reserve in the South African Kalahari Desert.

The research the successful applicants will be taking part aims to experimentally investigate the hormonal and transcriptomic mechanisms underlying dominance and the transition from cooperation to conflict in social social vertebrates.

This position is particularly suited, but not exclusively, for people aiming to carry on their academic education. Successful applicants can expect to gain invaluable experience in animal handling procedures and in conducting and managing experiments. They will also gain database skills (MySQL) and will be provided with the opportunity to work on a personal analysis project. Costs of food and accommodation while at the project will be covered. A contribution towards travel costs will be made (300 Euros/Year) Applicants should be available for 6 to 12 months. They should be hardworking, enthusiastic, physically fit, and prepared for long hours in the laboratory. Successful applicants will be responsible to run experiments and will be involved in data collection, data editing and animal handling. Previous experience in the dissection and tissue collection of rodents (including brain) will be considered an asset.

If you are interested in this position send your CV and cover letter stating your availability to Philippe Vulliod (philippe.vulliod@gmail.com).

Shortlisted applicants will be invited for a Skype interview.

Deadline: 10th May 2019: (spontaneous applications beyond this date are welcome)

Philippe Vulliod <philippe.vulliod@gmail.com>

---

## SSE Graduate Student Advisory Council Applications Apr 15

\*Society for the Study of Evolution (SSE) Graduate Student Advisory Council (GSAC) Applications Due April 15\*

The SSE Graduate Student Advisory Council <<http://www.evolutionsociety.org/index.php?module=content&type=user&func=view&pidD>> (GSAC) is in search of three additional PhD student members to serve in the 2020 cohort! GSAC values diversity, and encourages applications from the full diversity of the

student and postdoc evolutionary biology community, including (but not limited to) all aspects of identity and background, types of institution, or scientific approach. Applicants should be organized, possess leadership skills, and be interested in working with SSE members to contribute to the society. The GSAC represents student and postdoc interests to the SSE Council and facilitates interaction among students and postdocs and between students, postdocs, and mentors. Our goal is to become a source of information for students to use both during their graduate school career and as they make career transitions. \*\*Apply HERE <<http://www.evolutionsociety.org/index.php?module=content&type=user&func=view&pidD#JoinGSAC>> by April 15!\*

\*Kati Moore\* \*Communications Specialist\* \*Society for the Study of Evolution\* [communications@evolutionsociety.org](mailto:communications@evolutionsociety.org) [www.evolutionsociety.org](http://www.evolutionsociety.org) [communications@evolutionsociety.org](mailto:communications@evolutionsociety.org)

---

## Teaching Evolution Schools

Dear friends,

I am teaching evolution for Biology undergraduate students in a Brazilian University and some schools are requesting activities about how biological evolution works. I am visiting some schools and discussing evolution with high school students but.... I would like to receive suggestions about games, videos, figures I could use in these activities.

A new and small Science Museum is starting activities in our region and I would like to help them to create a display about biological evolution. My first idea was to show the importance of variation and how natural selection works.

Any ideas, suggestions? Thanks for any help!

Prof. Dr. J. C. VOLTOLINI

Grupo de Pesquisa e Ensino em Biologia da Conservação - ECOTROP

Universidade de Taubate, Departamento de Biologia Taubate, SP.

E-Mail: [jcvoltol@uol.com.br](mailto:jcvoltol@uol.com.br)

\* Grupo de pesquisa ECOTROP CNPq:

<http://dgp.cnpq.br/buscaoperacional/detalhepesq.jsp?pesq=37155809735635>

\*

Currículo Lattes: <http://lattes.cnpq.br/8137155809735635> \* Assessoria Estatística: <http://assessoria-estatistica.blogspot.com.br/>  
 \* Fotos de Cursos e Projetos: [https://www.facebook.com/ecotrop/photos\\_albums](https://www.facebook.com/ecotrop/photos_albums)  
 VOLTOLINI <jcvoltol@uol.com.br>

---

## 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

---

## PostDocs

AarhusU 3 EvolutionOfCancerAndCancerGenomics 80	UCalifornia Berkeley FishPopGenomics ..... 100
AarhusU PlantMacroecologyAndEvolution ..... 81	UCalifornia Berkely 2 EvolutionaryGenomics ..... 101
ArizonaStateU BiodiversityInformatics ..... 82	UCampinas SpiderAdaptation ..... 101
ArizonaStateU PopGen ..... 82	UDenver EvolutionAnimalCommunication ..... 101
Caltech MicrobesSocialParasiteBeetles ..... 83	UEdinburgh 2 GenomicConflict ..... 102
CarnegieMNH Pittsburgh AmphReptiles ..... 84	UEdinburgh EvolutionaryGenetics ..... 103
ChapmanU UCSantaCruz PlantSpeciation ..... 85	UFlorida MechanismsOfSeasonalAdaptation ..... 104
CharlesU SpeciationGenomics ..... 86	UFlorida SharkEvoDevo ..... 105
ClemsonU DrosophilaGenetics ..... 87	UIDaho ModelingLassaVirusEvolution ..... 106
ClemsonU OrganismalDiversity ..... 87	ULausanne BarnOwlEvolution ..... 106
CornellU Metabarcoding ..... 88	ULausanne EvolutionaryComputationalBiol ..... 107
DalhousieU BioinformaticsAntimicrobialResistance 88	ULausanne EvolutionColourPolymorphism ..... 107
FrederickNatLLab EvolutionaryBioinformatics ..... 89	ULiverpool EvolutionaryGenetics ..... 108
JagiellonianU Poland InsectMicrobiomes ..... 90	UMichigan AdaptiveLimits ..... 108
JustusLiebigU ComparativeVenomics ..... 91	UMinnesota 3yrNIH TrainingProgram ..... 109
KansasCity CaveAdaptations ..... 91	UMinnesota SpeciationTheoryGenomics ..... 110
LingnanU HongKong HerpCollectionPopGenomics .92	UNottingham 2 PopGenomicsAdaptationDuplication 110
LMU-UQ-AIMS Munich SeastarsDynamics ..... 93	UppsalaU AncientDNA ..... 111
NewYorkBotanicalGarden Bioinformatics ..... 94	UppsalaU HumanPopgenHistoryAfrica ..... 112
NewYorkU AbuDhabi PlantEvolutionaryGenomics 94	UQueensland EvolutionaryGenomics ..... 113
NHM UOslo EvolutionaryBiolOrnithology ..... 95	UToronto BacterialEvolutionaryGenomics ..... 114
Norwich BacteriaAMRMolecularEvolution ..... 96	UWisconsinMadison PopulationGenomics ..... 115
NRM Stockholm InsectBiodiversityBioinformatics .96	Vairao Portugal GoatMicrobiome ..... 115
QueensU TickMicrobiome ..... 97	VLIZ Belgium BioinformaticsMarineSystemsBiol . 116
Scandinavian ResSchool Biosystematics ..... 98	
TexasAMU ProgramCoordinator EvolutionaryBiolBio- diversity ..... 99	

---

### AarhusU 3 EvolutionOfCancerAnd- CancerGenomics

I have three open bioinformatic post doc positions in cancer genomics and big data analysis at Department of Molecular Medicine, Aarhus University. I'm looking for candidates with interests some combination of cancer evolution, gene regulation, analysis of large genomics data sets, and quantitative modelling.

Job call: <https://www.au.dk/om/stillinger/job/-postdocs-in-cancer-genomics-and-medical-big-data-analysis/> . The application deadline is May 7, 2019.

' Further details:

The Department of Molecular Medicine (MOMA), Department of Clinical Medicine at Faculty of Health at Aarhus University invites applications for three positions as Postdoc in the field of bioinformatics, as per 1 July 2019 or as soon as possible thereafter. The positions are full-time positions for up to 24-36 months.

The Department of MOMA MOMA (<https://moma.dk/>) offers a vibrant and unique interdisciplinary research environment with more than 20 years' experience in genomics, transcriptomics, and translational cancer research. The department houses state-of-the-art laboratory facilities, comprehensive cancer biobanks, an extensive next-generation sequencing facility, access to a large HPC facility, and extensive genomics data infrastructure. The department also plays a central role in the recently established Danish National Genome Center and will house genome sequencing.



About the research group Jakob Skou Pedersen's research group (<https://moma.dk/bioinf-2/pedersen-group>) studies cancer evolution and gene regulation. The research is primarily based on computational analysis of local and third-party large cancer genomics data sets, typically with thousands of samples. Projects may include statistical modelling and methods development. They may be supplemented by collaborative experimental hypothesis evaluation. There are close collaborations with local groups in statistics, bioinformatics, molecular biology, and clinical oncology as well as numerous international collaborations, including participation in the International Cancer Genome Consortium (ICGC) and the Pan-Cancer Analysis of Whole Genomes Project (PCAWG). Jakob has a dual affiliation at the Bioinformatics Research Center (BiRC), Faculty of Science and Technology, where part of the research projects may be carried out.

Your job responsibilities As a Postdoc in bioinformatics, your position is primarily research-based. You will contribute to the development of the department through research of high international quality. In your daily work, you will work closely with colleagues on your project, where you will receive supervision and guidance.

You will be joining one of the following research projects:

A) Cancer evolution (1-2 positions): Explore the mutational processes underlying cancer development and progression. A key question will be how repair deficiencies shape mutational patterns. The analysis will involve thousands of whole cancer genomes and rely on integration of somatic mutations at both the single nucleotide and structural level, germline variants, expression data, epigenetic data, layers of genomics annotation, etc. Depending on your background, the analysis may rely on existing tools and methods or involve statistical modelling and method development. Concrete hypotheses may be sought validated in local patient cohorts or in wet-lab experiments through ongoing local collaborations.

B) Gene regulation and non-coding RNAs (1-2 positions): Explore tens of thousands of gene expression data sets to learn about non-coding RNAs and post-transcriptional regulation in cancer. One of your possible aims is to characterise intronic RNAs in cancer from large local and third-party total RNAseq data sets. Another possible aim is to use statistical modelling to identify and characterise non-coding RNAs and RNA binding proteins that affect post-transcriptional regulation in cancer, by correlating gene expression patterns with presence of binding sites across large sample cohorts. Functional hypotheses may be sought experi-

mentally evaluated through local collaborations.

You must indicate which positions you would like to be considered for.

Your competences You have academic qualifications at PhD level, preferably within bioinformatics, statistics, computer science or a related discipline. You have a strong relevant publication track-record, with first-author publications in peer-reviewed articles in international recognized journals. Proficiency in statistical data analysis and scientific computing is required. Experience with genomics data analysis, software development and experience with R or Python programming languages is advantageous. Knowledge of cancer biology, mutational processes, the DNA damage response system, or non-coding RNAs is also advantageous. We

— / —

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>

---

## AarhusU PlantMacroecologyAndEvolution

The department of Bioscience, Aarhus University, Denmark invites applications for a 2-year postdoc position in plant macroecology and evolution.

The position is available from 01/06/2019 or as soon as possible hereafter. Please read more and apply here: <http://international.au.dk/about/profile/vacant-positions/job/postdoc-in-plant-macroecology-and-evolution/> Job description: This postdoc is part of TropiToL, a five-year project funded by VILLUM FONDEN aiming to use the Tree of Life to understand the biological hyperdiversity of tropical rainforests. Rainforests are estimated to harbour 50% of the worlds species on less than 10% of its terrestrial surface, a biological phenomenon that remains insufficiently explained. You will gather distributional data and apply species distribution modelling techniques to build improved models of tropical rainforest plant diversity in a global context. You will then use a global phylogenetic tree of plants, provided by other project members, and use a combination of macroecological and macroevolutionary methods to model the impact of speciation, extinction and dispersal on rainforest diversity in a spatially explicit way. You will be

expected to lead at least 2 papers per year in this research area, as well as collaborate with other team members, including students, sharing skills, helping solving problems in your area of expertise and more generally contributing ideas and concepts to the project.

Your profile: You have a PhD degree (or submitted your PhD thesis for assessment before the application deadline) in biology or another relevant discipline (e.g. geography). You have a strong background in statistics and computation, and do not mind working on a project that does not involve any (physical) data collection. You have experience with geospatial modelling techniques and/or macroevolutionary modelling, ideally both, but training can be provided in both areas. You have demonstrated your ability to efficiently handle large datasets and publish the results at high international level. You enjoy working in a highly collaborative environment including a good mix of ecologists and evolutionary biologists who are used to working across discipline boundaries.

If you have any questions please contact Associate Professor Dr Wolf Eiserhardt (wolf.eiserhardt@bios.au.dk, +45 8715 6136).

Wolf Eiserhardt <wolf.eiserhardt@bios.au.dk>

---

## ArizonaStateU BiodiversityInformatics

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](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 open and rolling until the search is closed. Start date is flexible, but with a preference for an immediate start.

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.

Beckett Sterner <beckett.sterner@asu.edu>

---

## ArizonaStateU PopGen

The Jensen Lab and Pfeifer Lab at Arizona State University are searching for a joint postdoctoral hire to join an NIH-funded project in the area of population genetic method development and inference. Applicants with a strong computational background and an interest in the study of virus evolution are desirable. Start date is flexible.

Further information about the labs may be found at [jjensenlab.org](http://jjensenlab.org) and [spfeiferlab.org](http://spfeiferlab.org). The labs are integrated in an excellent and highly interactive evolutionary genomics community at ASU ([ASUpopgen.org](http://ASUpopgen.org)).

Interested applicants should please send a CV and a brief cover letter stating research interests to [jefrey.d.jensen@asu.edu](mailto:jefrey.d.jensen@asu.edu) by May 10, 2019.

Susanne Pfeifer <spfeife1@asu.edu>

---

**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 sym-

biosis:

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](mailto: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](mailto:joep@caltech.edu)>

---

## CarnegieMNH Pittsburgh AmphReptiles

Post-Doctoral Researcher Carnegie Museum of Natural History Pittsburgh, PA

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](http://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 work 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.

Appointment is available for one year and renewable for a second year after successful performance evaluation. Salary is commensurate with experience and includes benefits and employee health insurance. Start date is negotiable, but will ideally be between May and September 2019. Pittsburgh is a vibrant city with numerous unique and affordable neighborhoods, an excellent fine arts scene, and a burgeoning international food scene.

To Apply: Visit <http://www.carnegiemuseums.org/-opportunities> .Click on Search Jobs and Click on Apply within this job posting (Req #224). Please provide a CV with contact information for three academic references, a 1 page cover letter describing your research experience and how a museum-based post-doc addresses your future goals, and a 2 page proposal outlining your proposed research and how it addresses topics that complement those of the Curator, using amphibians and reptiles. These documents must be combined into a single file

for uploading to the museum job portal. Word or pdf is acceptable.

Review of applications will begin 20 April and continue until the position is filled.

**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](mailto:BrooksG@CarnegieMuseums.Org)>  
"Brooks, Glenn" <[BrooksG@CarnegieMuseums.Org](mailto:BrooksG@CarnegieMuseums.Org)>

---

## ChapmanU UCSantaCruz PlantSpeciation

Biological Sciences at Chapman University and Ecology and Evolutionary Biology at the University of California, Santa Cruz

Postdoctoral Scholar in tropical plant demography and ecophysiology

### DESCRIPTION

The Biological Sciences Program at Chapman University and the Department of Ecology and Evolutionary Biology at the University of California, Santa Cruz (UCSC) invite applications for the position of Postdoctoral Scholar under the direction of Professor Jennifer Funk and Associate Professor Kathleen Kay, funded by an NSF Dimensions of Biodiversity grant (“Biotic and abiotic drivers of Neotropical plant speciation”). The scholar will investigate divergent adaptation underlying speciation in the spiral gingers (monocot genus *Costus*). The project is a collaboration among PIs Kathleen Kay (UCSC), Jennifer Funk (Chapman University), Carlos Garcia-Robledo (University of Connecticut), Dena Grossenbacher (Cal Poly SLO), and Santiago Ramirez (UC Davis) to uncover patterns and mechanisms of speciation in a recent, rapid plant radiation throughout Central and South America. We seek a broadly-trained, collaborative plant ecologist with expertise in demography and ecophysiology to spearhead multiple reciprocal transplants of sister species at four field sites in Costa Rica. Primary responsibilities include experimental design, coordinating and conducting data collection, managing and analyzing large datasets, mentoring field assistants and students, coordinating research collaborators, and contributing to the dissemination of results through manuscripts, presentations, public outreach, and government/agency reports. The ideal candidate will have experience relating plant physiology to abiotic and biotic environmental conditions and fitness, experience conducting field reciprocal transplants, experience with demographic population modeling, a strong interest in plant adaptation and speciation, and a track record of publishing in leading journals. The candidate must have a valid passport through 2022 and excellent logistical planning and time management skills. Ability to speak some Spanish is desirable. The scholar will spend the majority of their time in Costa Rica, with ample opportunities for lab visits and exchanges in the US. More

information on the Funk Lab can be found at <http://www1.chapman.edu/~jlfunk/>, and more information on the Kay Lab can be found at <https://kay.eeb.ucsc.edu/>. ACADEMIC TITLE

Postdoctoral Scholar

### SALARY

Minimum annual salary of \$50,000, commensurate with qualifications and experience.

### BASIC QUALIFICATIONS

Â Ph.D. or foreign equivalent in Biology or related field

Â A minimum of two years experience in plant ecology research.

### POSITION AVAILABLE

August 1, 2019. Start date could be as late as December 1, 2019. Ph.D. must be in hand at time of the initial appointment.

### MAXIMUM DURATION OF SERVICE IN A POST-DOCTORAL TITLE

Postdoctoral Scholar appointments are full-time; the initial appointment is for two years through Chapman University, with the possibility of reappointment for an additional year through UCSC. Reappointment will be contingent upon positive performance review and availability of funding. The total duration of an individual’s postdoctoral service may not exceed five years, including postdoctoral service at any institution. Under limited circumstances, an exception to this limit may be considered, not to exceed a sixth year.

### APPLICATION REQUIREMENTS

Applications should be emailed to Jennifer Funk (jlfunk@chapman.edu). All documents and materials must be submitted as PDFs. Informal inquiries may be sent to Jennifer Funk (jlfunk@chapman.edu) or Kathleen Kay (kmkay@ucsc.edu).

#### Documents/Materials

§Cover letter describing past research experience and qualifications for this position (required)

§Current curriculum vitae (required)

§A list of three references that includes their contact information (required)

§Up to three copies of published manuscripts-submitted as separate pdfs (required)

### RECRUITMENT PERIOD

Full consideration will be given to applications completed by June 30, 2019. Applications received after this date will be considered only if the position has not

been filled. The position will remain open until filled, but not later than 12/31/19.

Chapman University is an equal opportunity employer committed to fostering a diverse and inclusive academic global community. The University is dedicated to enhancing diversity and inclusion in all aspects of recruitment and employment. All qualified applicants will receive consideration for employment without regard to race, color, religion, age, sex, sexual orientation, gender identity, gender expression, national origin, ancestry, citizenship status, physical disability, mental

— / —

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>

## CharlesU SpeciationGenomics

\*Postdoc position on speciation history in nightingales\*

\*Available from June 2019 to December 2021 (the starting date is flexible) Evaluation of applications starts on 1st of May 2019 and will continue until the position is filled.\*

\*Project description:\* Patterns of genetic variation within and between species enable to make inferences about demographic history of species, levels of post-divergence gene flow as well as evolutionary forces acting on specific genes. Such information can provide a valuable insight into the history and mechanisms of speciation. This project aims at understanding the complex history of speciation in two closely related passerines, the Common Nightingale and the Thrush Nightingale, that hybridize in a zone of secondary contact. The successful candidate will use the whole-genome sequences from multiple individuals of both nightingale species from sympatric as well as allopatric populations. These data will be used to (1) model the demographic history of species divergence, (2) explore the genomic landscape of interspecific differentiation and divergence and identify specific genomic regions with reduced introgression between species that underlie reproductive isolation, (4) identify specific genes with signs of adaptive introgression, and (3) seek for signatures of selection on sympatric populations, which might unravel mechanisms of reinforcement and/or ecological character displacement at

the genetic level. The results will provide a unique insight into the mechanisms or species origin as well as the role of genetic introgression in adaptive evolution.

\*Candidate experience:\* The successful candidate will be mainly responsible for the bioinformatic part of the project. The position requires experience in analysis of large-scale next-generation sequence data and the ideal candidate should have background in population genetics. Programming skills are desirable. Experience in the wet lab is a plus, but is not necessary. The candidate may be involved in the fieldwork if he/she wishes.

\*Research group:\* The selected candidate will work in a young independent research group of population and speciation genetics. The group is based at the Department of Zoology, Faculty of Science, Charles University, which belongs to the leading research institutions in the Czech Republic. The Faculty of Science is situated in the center of Prague, one of the world's most beautiful and monumental cities. Please see the web pages of the group for more details (<http://web.natur.cuni.cz/~radkas/>).

\*How to apply:\* If interested, please, send (1) CV including a list of publications, (2) copy of PhD diploma, (3) motivation letter, and (3) contact details for 2'3 references to Radka Reifova ( [radka.reifova@natur.cuni.cz](mailto:radka.reifova@natur.cuni.cz)). The evaluation of applications starts on 1st of May 2019 and will continue until the position is filled.

– RNDr. Radka Reifová, Ph.D. Phone: +420 221 95 1852 E-mail: [radka.reifova@natur.cuni.cz](mailto:radka.reifova@natur.cuni.cz), [radkas@natur.cuni.cz](mailto:radkas@natur.cuni.cz) Web page: [www.natur.cuni.cz/~radkas/](http://www.natur.cuni.cz/~radkas/)

Department of Zoology Charles University Faculty of Science ViniĀn 7, 128 44 Praha 2

Katedra zoologie Univerzita Karlova Pırodovdeck fakulta ViniĀn 7, 128 44 Praha 2

“RNDr. Radka Reifov, Ph.D.”  
<[radka.reifova@natur.cuni.cz](mailto:radka.reifova@natur.cuni.cz)>

and should be submitted via Interfolio at: <https://apply.interfolio.com/45561> Trudy Frances Mackay <tmackay@clemson.edu>

---

## ClemsonU DrosophilaGenetics

The laboratories of Trudy Mackay and Robert Anholt at the Clemson University Center for Human Genetics invite applications for a postdoctoral fellow to support an NIH grant, Genetics of Cocaine and Methamphetamine Sensitivity in *Drosophila*. The Center is housed in Self Regional Hall on the campus of the Greenwood Genetic Center and provides state-of-the-art facilities for genomic and systems genetic research.

Illegal use of psychostimulants, such as cocaine and methamphetamine, presents a worldwide health problem. Illicit drug use alone accounts for \$181 billion in health care, productivity loss, crime, incarceration, and drug enforcement. However, little information is available regarding genetic susceptibility to the effects of these drugs in human populations. *Drosophila melanogaster* presents a powerful model system to study the genetic underpinnings of drug susceptibility, since both the genetic background and environment, including exposure to drugs, can be controlled precisely. Many effects of psychostimulants on people are replicated in flies, including suppression of sleep, arousal, suppression of food intake, and locomotor effects; and 70% of fly genes have human orthologs. The successful candidate will assess the role of variation in brain morphology on naïve and experience-dependent drug consumption, and perform bulk and single cell RNA and ATAC sequencing of *Drosophila* Genetic Reference Panel lines that are genetically divergent for drug consumption behaviors.

Applicants with expertise in any aspect of genetics/genomics, including molecular, developmental, behavioral, quantitative or statistical genetics, and aptitude for analyses of large data sets are encouraged to apply. Salaries are commensurate with NIH postdoctoral pay scale and postdoctoral fellows will receive an annual \$15,000 discretionary research supplement along with ample opportunities to travel to conferences both nationally and internationally.

Enquiries should be addressed to Dr. Trudy F. C. Mackay, Self Family Endowed Professor and Director of the Center for Human Genetics, Clemson University, Self Regional Hall, 114 Gregor Mendel Circle, Greenwood, SC 29646 (tmackay@clemson.edu).

This position is available immediately. Applications should include a curriculum vitae with list of publications and the names of three references,

---

## ClemsonU OrganismalDiversity

Postdoctoral position in organismal diversity and macroevolution

I am recruiting a postdoctoral researcher to work broadly within the fields of biodiversity, ecomorphology and macroevolution. The precise project is flexible, with opportunities to develop independent research working on a variety of questions and systems. Research in the Price lab ([www.evovirt.com](http://www.evovirt.com)) utilizes phylogenetic comparative approaches to address macroevolutionary questions, with the aim of identifying repeating themes and general principles governing the evolution of vertebrate diversity. We study living and sometimes fossil animals and use data and techniques from across evolutionary and organismal biology and data science. Additional consideration will be given to researchers interested in working with a large database (+16,000 specimens) of teleost fish body morphology generated as part of a collaborative project with Peter Wainwright's lab at UC Davis.

The postdoc will be expected to assist in data collection and analysis and to consistently write and publish scientific papers, as well as help mentor undergraduate and graduate researchers. Clemson University has a diverse group of researchers across life sciences and collaboration with other labs is encouraged, we also have access to the Palmetto High Performance Computing cluster on campus. It is a one-year appointment renewable for one or more additional years conditional upon performance. Applicants should have completed a Ph.D. or expect to do so prior to starting in the position.

Starting date summer 2019, precise date negotiable.

Review of applications will begin on May 25th 2019 and the position will remain open until filled.

A successful applicant will have: - A doctoral degree in a relevant subject - A solid track record of scientific publications and international conference presentations commensurate with career stage and experience.

- One or more of the following macroevolutionary skill sets: phylogenetic comparative analyses, functional morphology or ecomorphology, phylogenetics, palaeobiology, vertebrate diversity and natural history.

Interested candidates should apply via interfolio: <http://apply.interfolio.com/62664> and provide (1) an application letter summarizing research interests, goals and qualifications (2) a CV and (3) contact information for at least two references. Please don't hesitate to contact me if you wish to discuss the position prior to applying: Dr. Samantha Price [sprice6@clermson.edu](mailto:sprice6@clermson.edu)

Samantha Price, Ph.D.

Assistant Professor Department of Biological Sciences  
Clemson University SC 29634 Tel: +1 864-656-3961  
Website: [www.evovert.com](http://www.evovert.com) Samantha Ann Price  
<[sprice6@clermson.edu](mailto:sprice6@clermson.edu)>

---

## CornellU Metabarcoding

Postdoc position: Genetic tracing of marine fish sources for aquaculture feeds

The Therkildsen and McIntyre Labs at Cornell University, in partnership with the Environmental Defense Fund's Oceans Program, are hiring a postdoc for a new project evaluating the sources of fish used to feed the global expansion of aquaculture. The project will apply metabarcoding methods to examine the taxonomic composition of aquaculture feeds collected worldwide. The resulting species lists will be used to assess the global geography of connections between the harvest of wild fish and the production of farmed fish.

The ideal candidate will have completed a PhD by May 2019, have strong skills in molecular ecology (metabarcoding and bioinformatics experience is especially relevant), an interest in fisheries, and a strong publication record commensurate with career stage. We expect the postdoc to help design and then execute genetic analyses in the lab, and to lead bioinformatic data processing and biogeographic inferences based on metabarcoding results, fish distribution patterns, and fisheries landing data. Equally important, the postdoc will be encouraged to serve as an intellectual co-leader of the project, and assist with seeking further funding. This project is a collaborative effort, and will require a team-oriented approach as the postdoc works with both Cornell PIs, EDF staff, and another postdoc studying mercury contamination in aquaculture feeds.

The desired start-date is during June 2019. A competitive salary and benefits package will be provided, and residence in Ithaca, NY is expected. The postdoc will join a vigorous multidisciplinary community of scholars

in the Department of Natural Resources and Atkinson Center for a Sustainable Future at Cornell University.

To apply, please submit a 2-page letter of interest, a CV, pdfs of up to three publications, and contact information for three references. Application materials should be sent to both Nina ([nt246@cornell.edu](mailto:nt246@cornell.edu)) and Pete ([pbm3@cornell.edu](mailto:pbm3@cornell.edu)), using the subject line "Application for aquaculture barcoding postdoc position". We welcome pre-application inquiries and questions. Review of applications will begin on 25 April, and will continue until the position is filled.

[nt246@cornell.edu](mailto:nt246@cornell.edu)

---

## DalhousieU BioinformaticsAntimicrobialResistance

The Beiko lab at Dalhousie University (Halifax, Nova Scotia, Canada) is seeking two postdoctoral fellows to work on the recently funded 'Antimicrobial Resistance: Emergence, Transmission, and Ecology (ARETE)' project (project page: <http://arete-amr.ca>). The overarching goal of the project is to perform analysis of thousands of microbial genomes to identify risk factors for lateral gene transfer (LGT) of antimicrobial-resistance determinants, and map transmission between habitats using phylogenetic and related methods. The Comprehensive Antibiotic Resistance Database (CARD; <https://card.mcmaster.ca/>) will serve as the reference database for the projects. ARETE is a partnership between several academic institutions, as well as the Public Health Agency of Canada and Agriculture and Agri-Food Canada, and is part of the larger IRIDA initiative (<https://www.irida.ca/>).

Postdoctoral Fellow #1 (position ID 2019-06) will build on existing tools (see for example <http://kiwi.cs.dal.ca/-Software/RSPR>) to infer phylogenetic trees and perform large-scale inference of LGT. Key challenges include robust, large-scale phylogenomic inference, and synthesizing different lines of evidence to build a comprehensive picture of gene transfer in large genomic datasets. This position requires someone with a background in either bioinformatics or computer science. Key technical skills include: Phylogenetics Microbial genomics and evolution Some programming (Python sufficient; C++ an asset)

Postdoctoral Fellow #2 (position ID 2019-07) will develop methods to map inferred LGT events into an ecological context. This will include the association of



events with specific habitat parameters (e.g., geographic location, habitat type, specific patterns of antibiotic usage), as well as 'gene-ecology' methods that examine the distributional dynamics of microbial genes and map these into traditional ecological frameworks (see for example <https://academic.oup.com/femsre/article/38/1/90/510792>). This position requires an individual with a background in bioinformatics and/or ecology. Key technical skills include: Microbial ecology Community ecology / metacommunity theory Analysis in R/Python

Additionally, we are seeking a postdoctoral fellow to extend existing work in the inference of antimicrobial-resistance genes from metagenomic data. This work extends the current AMRtime project ( <https://github.com/beiko-lab/AMRtime>), which uses rapid homology filtering and search alongside machine-learning methods to assign metagenomic sequences to specific classes of AMR genes. Postdoctoral Fellow #3 (position ID 2019-08) will augment AMRtime with new models to better detect novel AMR variants that fall outside currently defined strict criteria for detection. Extending these models will require a combination of methods that encompass taxonomic assignment, sensitive homology search, mobile-element detection, and phylogenetics to differentiate legitimate AMR matches from homologs that do not confer a resistance phenotype. All postdoctoral fellows will collaborate with other members of the project team, and be expected to give conference presentations and prepare journal articles based on their work. There will be opportunities to gain project-management experience through the ARETE project.

Please send a CV and statement of research interests to Elvira Mitraka, project manager ([elvira.mitraka@gmail.com](mailto:elvira.mitraka@gmail.com)). Applicants should indicate the position ID in the email subject header. Review of applications will begin on April 20, 2019. To receive full consideration, please submit your application by this deadline. Applications received after April 20 may also be considered.

Elvira Mitraka, PhD Postdoctoral Fellow Faculty of Computer Science Dalhousie University

Elvira Mitraka <[elvira.mitraka@gmail.com](mailto:elvira.mitraka@gmail.com)>

---

## FrederickNatLab EvolutionaryBioinformatics

This is a general posting, for a postdoctoral candidate that will be placed in the lab of their choice and that fits their experience, abilities, and interests. There is considerable evolutionary genomics and population genetic research conducted under this job req, and at the Frederick National Laboratory in general.

—  
Job ID: req390 Facility: Frederick: Ft Detrick Location: PO Box B, Frederick, MD 21702 USA

The Frederick National Laboratory is dedicated to improving human health through discovery and innovation in the biomedical sciences, focusing on cancer, AIDS, and emerging infectious diseases.

Position Overview:

### PROGRAM DESCRIPTION

The Advanced Biomedical Computing Sciences (ABCS), part of the Biomedical Informatics and Data Science (BIDS), provides scientific computing, modeling, imaging, and bioinformatics support, engages in scientific consultation and collaboration, and offers training to NCI and NIH scientists and staff. The Data Solutions and Systems Biology (DSSB) group in ABCS strives to streamline and provide innovative solutions for the NCI/NIH community to access and use biological information collected across different sources and formats. Integrating diverse data sources to streamline project requests and analysis workflows, enable disease agnostic access and analysis, variant impact annotation, identifier conversions across species, and merging clinical and research data enabling translation from basic to the goal of precision medicine.

### KEY ROLES/RESPONSIBILITIES

- Work with scientific experts to determine key focus areas for rare disease informatics
- Review literature, research websites and data sources to identify data sets of interest
- Work with the development team to build use cases and prioritize informatics tasks
- Identify and/or develop algorithms to answer specific research questions such as determining genotype/phenotype correlations
- Document approaches and processes clearly and comprehensively

## BASIC QUALIFICATIONS

- Possession of a doctoral degree in computer science, Math or Biomedical Science or a related field from an accredited college or university according to the Council for Higher Education Accreditation. (Additional qualifying experience may be substituted for the required education). Foreign degrees must be evaluated for U.S. equivalency - No Experience is required beyond the educational requirements - Demonstrated ability to research and critically review data required for understanding of disease mechanisms - Experience in determining genotype/phenotype correlations and clinical impact of genomic variants - Ability to self-direct with little or abstract day-to-day instruction - Excellent written and verbal communication skills / ability to document and communicate complex scientific concepts for a variety of audiences - Must be able to obtain and maintain a security clearance

## PREFERRED QUALIFICATIONS

Experience with analyzing NGS datasets Experience with determining disease prevalence and incidence rates Experience with web and database technologies Equal Opportunity Employer (EOE) | Minority/Female/Disabled/Veteran (M/F/D/V) | Drug Free Workplace (DFW)

Justin Lack [Contractor] Bioinformatics Manager/Lead, NIAID Collaborative Bioinformatics Resource (NCBR) Frederick National Laboratory for Cancer Research Leidos Biomedical Research, Inc. Post Office Box B Frederick, MD 21702 Phone: 405-314-4356 justin.lack@nih.gov  
 “Lack, Justin (NIH/NIAID) [C]” <justin.lack@nih.gov>

---

## JagiellonianU Poland InsectMicrobiomes

The newly forming Symbiosis Evolution research group ([www.symbioses.pl](http://www.symbioses.pl)) at the Institute of Environmental Sciences of Jagiellonian University in Kraków, Poland ([www.eko.uj.edu.pl](http://www.eko.uj.edu.pl)), is looking to hire a Postdoctoral Researcher. This is a full-time, 48-month position funded by the Polish National Agency for Academic Exchange (NAWA) project Insect Microbiomics, available from 1st July 2019.

The Postdoc will join a dynamic collaborative team aiming to describe the broad patterns of the microbial diversity across insects, and the dynamics of the insect microbiomes in time and space. The work will be conducted

in close collaboration with a massive insect biodiversity project, Insect Biome Atlas ([www.insectbiomeatlas.com](http://www.insectbiomeatlas.com)) that does extensive insect community sampling and characterization in Sweden and Madagascar. The Postdoc will initially focus on the development of protocols for high-throughput, automated next-generation sequencing (NGS) library preparation in the context of insect microbiome studies, as well as bioinformatic pipelines for the analysis of the resulting data. Later, they will lead the microbiome characterization in extensive collections of insects from Sweden, Madagascar, and/or Greenland.

The Postdoc will be based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe, in a medieval city known as the cultural capital of Poland, with good access to outdoor recreation opportunities and well-connected to the rest of Europe. They will be encouraged to spend time in the laboratories of collaborators from Insect Biome Atlas project in Sweden and engage in other international collaborations. We offer a competitive salary relative to the cost of living, flexible schedules, and extensive opportunities to acquire cutting-edge research skills and to network.

The candidates must have a Ph.D. in Biological Sciences or a related field, or anticipate completion of doctoral studies by 30th June 2019. They should be able to demonstrate experience with molecular biology techniques and bioinformatic analyses of NGS data and be fluent in English. An ideal candidate will be able to demonstrate interest and scientific achievements related to the planned project, in particular regarding the diversity and biology of host-microbe interactions and the analysis of microbial communities using NGS. Laboratory experience in the preparation of NGS libraries, familiarity with the Linux / Unix shell and scripting languages such as Python / Perl / R, and interest in participating in international collaborations and research travel preferred.

The candidates are asked to submit a cover letter, a CV, and contact details of two references, to Dr. Piotr Łukasik ([p.lukasik@gmail.com](mailto:p.lukasik@gmail.com)). The review of applications starts in early May 2019.

For further information and informal inquiries, please contact Dr. Piotr Łukasik.

Piotr Łukasik <[p.lukasik@gmail.com](mailto:p.lukasik@gmail.com)>

---

## JustusLiebigU ComparativeVenomics

### Postdoc position in Comparative Venomics

In the interdisciplinary Animal Venomics group based at the Institute for Insect Biotechnology, Justus-Liebig-University Gießen, a fulltime postdoctoral researcher position is available as soon as possible for two years (Experience depending the salary band will be TV-H 13, 100%) within the German Science Foundation funded project:

Venom evolution in solitary and eusocial aculeate hymenopterans

Tasks - Working in the project that focuses on comparative venomics and toxin evolution of social and solitary bees and wasps. One aim is to understand better processes that drive toxin evolution in hymenopterans. Genomes will be analyzed to complementary proteomics and transcriptomics data to tackle this major aspect of mechanisms in venom evolution. - Proteomics is in parallel conducted via collaborations, depending on the results activity tests and assays are planned for some interesting toxin candidates. - If interested and suitable the possibility exists to help to establish proteomic methods.

Demanded skills and profile: - Diploma/Master degree in Biology or related natural sciences - PhD in Biology or related natural sciences

- Candidates should have a background in evolutionary biology, trait evolution and/or venomics - Proven background in transcriptomics and genomic work and analyses is necessary - Bioinformatics skills are important, experience in Perl or Python of advantage - Candidates should be highly motivated, self-organized but as well team players - Good communication and English skills are important. - Fieldwork experience and taxonomic knowledge of hymenopterans is a further asset - Laboratory experience in RNA extraction, library reconstruction and/or HMW DNA extraction and general knowledge in proteomic work (HPLC, and MassSpec) is an advantage.

We offer a unique opportunity to grow and participate in an integrative environment within the new Animal Venomics group creating workflows comprising genomics, transcriptomics, proteomics, and protein characterization with evolutionary and applied perspectives. The

main PI in this project is Dr. Björn M. von Reumont.

Gießen is a vibrant student town at the river Lahn in the green heart of the State Hessen, very central in Germany. Other, old university cities like Marburg or Wetzlar are located within 20 km. The metropolis Frankfurt with its large international airport is roughly 50 km away and its center can be reached from Gießen within 40 minutes by regional trains.

Please send applications without photograph and without date of birth as single PDF file including a CV (with two references), certificates, motivation letter (â1 page) with additionally a short summary of previous work and applied methods (â 1 page), and one reference letter to: Bjoern.Von-Reumont@agrar.uni-giessen.de.

The JLU Gießen promotes equal opportunities and diversity in its employment relations. Women are expressly encouraged to apply and given priority in accordance with the Equal Opportunities Act. We expressly welcome applications from individuals with severe disabilities or people of equivalent status. Severely disabled applicants of equal merit and qualifications will be given priority.

Application deadline is the 07.06.2019

Dr. Björn M. von Reumont Research Associate LOEWE Center Translational Biodiversity Genomics University of Gießen & Fraunhofer IME Animal Venomics Winchesterstr 2 35394 Gießen Germany Tel +49 (0)641-99-39503

mob +49 (0) 151-61997924 www <http://www.reumont.net> Björn Marcus von Reumont <bmv@arcor.de>

---

## KansasCity CaveAdaptations

Postdoctoral Research Associate (Evolutionary Genetics)

The Rohner Lab at the Stowers Institute for Medical Research has an opening for a Postdoctoral Researcher to develop an independent project investigating the molecular, genetic, and developmental mechanisms of how cavefish maintain health under diabetes-like phenotypes. The lab has previously found that the cavefish *Astyanax mexicanus* develop high-blood sugar and insulin resistance as part of their natural strategy to survive in the caves but without the usually associated health problems (Riddle et al. Nature. 2018 Mar 29;555(7698):647-651).

Visit <http://research.stowers.org/rohnerlab/> for more information.

The selected candidate will investigate the molecular mechanism underlying these impressive adaptations. The candidate will closely work with the core facilities at the institute to perform single-cell RNA sequencing, proteomics, and functional validation in vitro and in vivo. The candidate will receive strong support from the core facilities that provide advice, training and service to enhance the Institute's interdisciplinary and collaborative research programs. Current core facilities are staffed by over 100 scientists with expertise in bioinformatics, cytometry, histology, imaging, microarray, next generation sequencing, transgenic and ES cell technologies, proteomics and molecular biology. The Stowers Institute offers a highly competitive compensation and benefits package.

The position is funded for two years through a grant by the Juvenile Diabetes Research Foundation and can be renewed for up to five years in order to allow enough time to develop a research program/publication record that makes the postdoc a strong candidate for an independent position. The Rohner Lab has a strong commitment for mutual success and is dedicated to providing support for all lab members.

Minimum requirements include a doctoral degree in the life sciences, chemistry, or biomedical engineering. Experience in one or more of the following areas is desirable: molecular biology, developmental biology, genetics, genomics, evodevo, physiology.

In addition to excellent verbal and written communication skills, successful candidates must be dynamic and highly motivated, work independently and creatively, able to work in a team-oriented environment, and proficient at problem solving. Application Instructions: To apply, please submit (1) a brief cover letter, (2) a current CV, and (3) contact information for two professional references to Dr. Nicolas Rohner at [nro@stowers.org](mailto:nro@stowers.org) cc: [careers@stowers.org](mailto:careers@stowers.org).

About the Stowers Institute for Medical Research

The Stowers Institute for Medical Research is a world-class basic biomedical research organization focused on improving our understanding of fundamental mechanisms of biology and using this knowledge to guide the development of innovative treatments to improve human health.

Our dedicated scientists collaborate across a variety of disciplines, studying many different aspects of health and disease. A primary goal of our research is to understand the principles that guide the function and behavior of living organisms and individual cells. Dis-

coveries resulting from this kind of research often prove to be major milestones along the path toward novel therapies and cures (visit [www.stowers.org](http://www.stowers.org)). Jim Stowers, founder of American Century Investments, and his wife, Virginia, opened the Institute in 2000. Since then, the Institute has spent over 900 million dollars in pursuit of its mission.

Currently, the Institute is home to almost 550 researchers and support personnel; over 20 independent research programs; and more than a dozen technology-development and core facilities. The Institute has been ranked 3rd place by the Scientist for best places to work in the world: <https://www.the-scientist.com/features/-best-places-to-work-academia-2012-40676> Kansas City is an emerging metropolitan city in the Midwest with a high quality of living and affordability. Visit <https://www.visitkc.com> for information about living and working in Kansas City.

"Herbers, Jennifer" <[JHerbers@stowers.org](mailto:JHerbers@stowers.org)>

---

## LingnanU HongKong HerpCollectionPopGenomics

Postdoctoral Fellow / Research Assistant Science Unit, Core Curriculum and General Education Office (Post Ref.: 19/132/W)

The appointee will conduct an empirical study in the research area of ecology and evolutionary biology. He/she will be primarily responsible for a project focusing on amphibians of Hong Kong. There are two major goals for this project: (1) build a specimen collection for the amphibians of Hong Kong, (2) perform a population genomics study on Romers tree frog (*Liuixalus romeri*) using the ddRADseq method. An ideal candidate will have experience with laboratory work (particular NGS), data analysis of molecular data, fieldwork with amphibians and reptiles, and preparation/curation of specimens.

Requirements Applicants should have (i) a Ph.D. (post-doctoral fellow) or Bachelors degree or above (research assistant) in Biology, Environmental Science, or relevant disciplines; (ii) proficient communication skills in both written and spoken English; (iii) strong statistical skills; and (iv) self-motivation and an independent work attitude.

Enquires can be directed to Prof. Jonathan Fong ([jonfong@ln.edu.hk](mailto:jonfong@ln.edu.hk)) or Ms. Mei Chan ([meichan@ln.edu.hk](mailto:meichan@ln.edu.hk)).

Salary and Benefits Remuneration will be commensurate with qualifications and experience. Appointment will be made on a fixed-term contract for one year and renewable subject to performance.

**Application Procedure** Applicants are invited to send a cover letter, a CV and a completed application form (Form R1 which is obtainable at <http://www.LN.edu.hk/hr/employment-opportunities/-application-forms>) to the Human Resources Office, Lingnan University, Tuen Mun, Hong Kong by post or by email: [recruit@LN.edu.hk](mailto:recruit@LN.edu.hk) (as attachment in MS Word format) by 6 May 2019. Please quote the reference number of the post in all correspondence. Personal data collected will be used for recruitment purposes only.

The University reserves the right not to make an appointment for the post advertised, or to fill the post by invitation or by search. We regret that only shortlisted candidates will be notified.

[jonfong@ln.edu.hk](mailto:jonfong@ln.edu.hk)

---

## LMU-UQ-AIMS Munich SeastarsDynamics

\*We are seeking expressions of interest for a post-doctoral position, funding to be acquired through an EU Horizon 2020 Marie Skłodowska-Curie Global Fellowship (deadline 11 Sept. 2019).\*

\*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 a highly motivated PostDoc with experience in theory and/or modelling related to spatial population genetics or spread dynamics of invasive species or pathogens. 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 München, Germany).

To be considered for the PostDoc you will have demonstrated experience and track record in theory and/or modelling related to spatial population genetics or spread dynamics of invasive species or pathogens. You are also willing to work with the project investigators to develop an application for an EU Horizon 2020 Marie Skłodowska-Curie Global Fellowship for a maximum of 36 months, to spend the first two years based at UQ (Brisbane) and the last year at LMU (Munich). The fellowship would legally be based at LMU Munich.

The prestigious Global fellowships are open to early career researchers from European member states and associated countries (see the following websites for eligibility and other information: < [https://ec.europa.eu/research/mariecurieactions/node\\_en](https://ec.europa.eu/research/mariecurieactions/node_en) > < <https://ec.europa.eu/info/funding-tenders/-opportunities/portal/screen/opportunities/topic-details/msca-if-2019> > The 2019 call deadline is 11 September 2019 at 17:00h Brussels Time.

Expressions of interest should include a CV including 3 potential referees and pdfs of two publications or manuscripts demonstrating relevant research.

Please contact Cynthia Riginos ([c.riginos@uq.edu.au](mailto:c.riginos@uq.edu.au)) and Gert Worheide ([woerheide@lmu.de](mailto:woerheide@lmu.de)) for further details. Review of expressions of interest will start immediately and continue until a suitable candidate is identified, who then will be invited to apply.

Prof. Dr. Gert Worheide Department of Earth and Environmental Sciences, Paleontology & Geobiology & GeoBio-Center LMU Ludwig-Maximilians-Universität München, and Director, Bavarian State Collections of Palaeontology and Geology Richard-Wagner-Straße 10 80333 München Germany

Phone: +49 (89) 2180-6718 Fax: +49 (89) 2180-6601 E-Mail: [woerheide@lmu.de](mailto:woerheide@lmu.de) [www.palmuc.de](http://www.palmuc.de) | [www.geobiology.eu](http://www.geobiology.eu) [www.facebook.com/molpalaeo](https://www.facebook.com/molpalaeo) [twitter.com/gwoerhe](https://twitter.com/gwoerhe)

[www.itn-ignite.eu](http://www.itn-ignite.eu) Publications: <http://bit.ly/-2HEBv6Q> [orcid.org/0000-0002-6380-7421](https://orcid.org/0000-0002-6380-7421)

Gert Woerheide <[woerheide@lmu.de](mailto:woerheide@lmu.de)>

---

## New York Botanical Garden Bioinformatics

The Bioinformatics Postdoctoral Research Associate will process large genomic sequence in a LINUX command-line environment.

**Specific Duties and Responsibilities:** This position is part of an NSF funded project (IOS 1758800) to sequence and characterize gymnosperm genomes. Specifically, the postdoctoral researcher will

- \* Apply machine learning to gymnosperm genomes to identify genes
- \* Elucidate gene function, compare genomes, and highlight associations between genome structure/content and organismal characteristics
- \* Some curation, annotation, and assembly of genome sequences will be required
- \* The postdoctoral researcher will be expected to apply existing algorithms and develop new algorithms (application of existing algorithms will most likely require new, more efficient, implementations be produced by the researcher)

**Requirements:**

- \* PhD in bioinformatics, machine learning, computer science, or botany; computer programming experience (C++ preferred)
- \* Fluency in LINUX command-line environments including BASH and high-performance computing frameworks (e.g. HTCondor)
- \* Practical knowledge of efficient data processing

If you are interested in applying for a position at the New York Botanical Garden, please go to <http://www.nybg.org/employment> to submit your application.

EOE/M/F/Disabled/Veteran

Thank you, Jenna Vasquez

Jenna Vasquez Talent Acquisition and Training Manager  
The New York Botanical Garden 2900 Southern Boulevard Bronx, NY 10458 O: 718.817.8872  
jvasquez@nybg.org nybg.org

“Vasquez, Jenna” <jvasquez@nybg.org>

---

## New York University Abu Dhabi Plant Evolutionary Genomics

### POSTDOCTORAL OPENING

Evolutionary/Comparative Genomics of Date Palms

Center for Genomics and Systems Biology

New York University Abu Dhabi

The Purugganan Laboratory has an opening for a postdoctoral fellow to work on comparative genomics, genome evolution and evolutionary genomics of date palms at its New York University Abu Dhabi lab. Candidates should have a Ph.D. with good bioinformatic and/or population genomic/comparative genomic analyses skills, a strong record of research productivity, and able to work semi-independently will be a good fit..

The position is based in the NYU Abu Dhabi Center for Genomics and Systems Biology, and will be part of a small but highly productive group. NYU Abu Dhabi has a thriving research group that also includes colleagues working on falcon genomics, human population genomics, amphibian evolution, as well as neuroscience, chemical genomics and systems biology.

The pay is very competitive, and includes a very generous housing, commuter and travel allowance. The position will be available starting 1 September 2019, and is an annual contract renewable for up to 3 years.

Interested candidates should send a letter of interest and CV to Michael Purugganan, mp132@nyu.edu

### About NYUAD

NYU Abu Dhabi is a degree-granting research university with a fully integrated liberal arts and science undergraduate program in the Arts, Sciences, Social Sciences, Humanities, and Engineering. NYU Abu Dhabi, NYU New York, and NYU Shanghai, form the backbone of NYU's global network university, an interconnected network of portal campuses and academic centers across six continents that enable seamless international mobility of students and faculty in their pursuit of academic and scholarly activity. This global university represents a transformative shift in higher education, one in which the intellectual and creative endeavors of academia are shaped and examined through an international and multicultural perspective. NYUAD serves as a center for scholarly thought, advanced research, knowledge cre-

ation, and sharing, through its academic, research, and creative activities.

EOE/AA/Minorities/Females/Vet/Disabled/Sexual Orientation/Gender Identity Employer

UAE Nationals are encouraged to apply.

Qualifications

A Ph.D. in plant biology, evolutionary biology and/or genomics. This position is not located in the United States. You must be willing to relocate to Abu Dhabi, United Arab Emirates.

Michael Purugganan

Dean for Science, Faculty of Arts and Science 6 Washington Square North New York University New York, NY 10003 Tel. (212) 998 3800

Silver Professor of Biology Department of Biology Center for Genomics and Systems Biology 12 Waverly Place New York University New York, NY 10003 Tel. (212) 992 9628

Web: \*<http://as.nyu.edu/biology/directory.michael-purugganan.html> Michael Purugganan <mp132@nyu.edu>

---

## NHM UOslo EvolutionaryBiolOrnithology

For the following Postdoctoral fellowship (Jobbnorge ID: 169624), please apply at <https://www.jobbnorge.no/en/available-jobs/job/169624/postdoctoral-fellowship-in-evolutionary-biology-ornithology> The deadline for applications is 19.05.2019.

**Job description** A position as Postdoctoral Research Fellow in Evolutionary Biology/Ornithology is available at the Natural History Museum, University of Oslo. The position is placed in the 'Sex and Evolution Research Group' (SERG). The appointment is a fulltime position and is made for a period of four years with 25 % duty work devoted to teaching, supervision, collection management (curatorial work in the ornithological collection of NHM), outreach activities and administration. The postdoctoral fellow is expected to acquire basic pedagogical competency in the course of the fellowship period within the duty component of 25 %. The main purpose of the fellowship is to qualify researchers for work in higher academic positions within their disciplines. Starting date no later than 01.10.2019.

**More about the position** The position is placed in the Sex and Evolution Research Group (SERG). The research group currently consists of two professors, two researchers and two PhD-students, as well as master students. The research themes are concentrated on the importance of sex, sex roles and sexual conflict in shaping evolutionary processes such as speciation, hybridization, diversification and adaptation. These processes are studied at different levels of organization, like genes, genomes, gametes, individuals, populations and species. Most projects use birds as their study systems. The research group has access to large museum collections in ornithology, including a unique collection of formalin-preserved sperm cells from more than 500 species, and a DNA bank with more than 50 000 bird tissue samples. Field work for comparative studies is often carried out abroad and in collaboration with other institutions and research groups.

We invite a highly motivated researcher to work on and develop a project entitled 'Macroevolution of avian spermatozoa' in close collaboration with the scientific staff in the SERG group. The project will consist of three main parts, (1) a descriptive analysis of the major patterns of sperm phenotype differentiation across the passerine phylogeny, (2) analyses of evolutionary rates of sperm variation among and within lineages, and (3) investigation of the genomic mechanisms underlying sperm trait evolution. The approach will be largely phylogenetically controlled comparative analyses combined with in-depth phylogenomics of selected taxa. There will also be a need for additional field work to sample important taxa currently lacking in our sperm database.

**Qualification requirements** The candidate must have a PhD in ecology, evolution or avian systematics. We seek a highly competent and motivated early career evolutionary biologist, with skills in comparative analyses and evolutionary modelling and experience with bioinformatic tools for handling large genomic data sets. Experience with ornithological field work and good knowledge in bird systematics is required, while experience with work on spermatozoa, including microscopy and morphometry, and other natural history collection work, will be considered advantageous. A good command of written and spoken English is required.

We offer - Salary NOK 515 200 - 597 400 per annum depending on qualifications in position as Postdoctoral Research Fellow (position code 1352) - Challenging research questions and a friendly working environment - Full funding of the project research-related activities, including field work, lab work and presentation of results at international conferences - Membership in the Norwegian Public Service Pension Fund - Attractive welfare benefits

How to apply The application must include: - Application letter (statement of motivation, background and research interests) - CV (summarizing education, positions, pedagogical experience, museum experience, administrative experience, popular science experience and other qualifying activity) - Copies of educational certificates and transcript of records - A complete list of publications and up to 5 academic works (in pdf format) that the applicant wishes to be considered by the evaluation committee - Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number). The references will be contacted if necessary. Letters of recommendation are therefore not required for the initial application.

The application with attachments must be delivered in our electronic recruiting system. Please remember that all documents should be in English or a Scandinavian language.

Evaluation of the applicants

— / —

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>

---

## Norwich BacteriaAMRMolecularEvolution

We have a 2-year postdoc position in microbial genomic epidemiology available at the new Quadram Institute in Norwich UK, investigating the drivers and dynamics of antimicrobial resistance (AMR) in Salmonella in pig and poultry production. The project provides an incredible opportunity to address key questions in this field, such as the relative importance of horizontal gene transfer and the impact of antimicrobial use on AMR, and the position includes working with fantastic collaborators at the University of São Paulo. More information can be found at the following link or by emailing me at [alison.mather@quadram.ac.uk](mailto:alison.mather@quadram.ac.uk):

<http://jobs.quadram.ac.uk/Details.asp?vacancyID425>  
The closing date for applications is 23rd April 2019.

Lucy W <[lucy.weinert@googlemail.com](mailto:lucy.weinert@googlemail.com)>

---

## NRM Stockholm InsectBiodiversityBioinformatics

The Swedish Museum of Natural History (Naturhistoriska Riksmuseet - NRM, <http://www.nrm.se>) is one of the leading institutions of its kind in Europe. It combines a venerable tradition and unique collections with cutting-edge research in geology, paleontology, and biology. The research at the Department of Bioinformatics and Genetics focuses on computational phylogenetics, population genetics, and genomics. We run a DNA sequencing facility and host several national and international infrastructures. More information is available at <http://www.nrm.se/en/forskningochsamlingar/bioinformatikochgenetik.9000580.html> NRM Department of Bioinformatics and Genetics is looking to fill a position of:

POSTDOCTORAL RESEARCHER IN BIOINFORMATICS

The postdoc will be employed in Insect Biome Atlas (IBA; [www.insectbiomeatlas.com](http://www.insectbiomeatlas.com)), a five-year international project aimed at characterizing the diversity of insects in Sweden and Madagascar. The project uses metabarcoding of thousands of Malaise trap and soil samples to study the size, origins, structure and function of the insect biomes. The IBA is a collaboration between the Swedish Museum of Natural History (Fredrik Ronquist), the Swedish University of Agricultural Sciences (Tomas Roslin), Stockholm University (Ayco Tack), SciLifeLab/KTH Royal Institute of Technology (Anders Andersson), the Madagascar Biodiversity Centre (Brian Fisher, California Academy of Sciences) and Jagiellonian University in Kraków, Poland (Piotr Lukasik).

The postdoc will lead the development of bioinformatic pipelines for the comprehensive analysis of insect community metabarcoding data and apply them to an unprecedented collection of bulk insect community samples from across Sweden and Madagascar. The postdoc will also be expected to contribute to the development of molecular methods for the phylogenomic characterization of a large number of insects. The position will be based at the Swedish Museum of Natural History in close collaboration with Anders Andersson at KTH/SciLifeLab and Piotr Lukasik at Jagiellonian University. The candidate is expected to spend some time at collaborating institutions.



The candidate must hold a Ph.D. degree in molecular biology, bioinformatics, evolutionary biology or a related field. Previous experience with the analysis of Next Generation Sequencing (NGS) data is essential. It will be an advantage if the candidate has: - proven interest in biodiversity and community ecology - experience in analyzing metabarcoding data, particularly in the context of eukaryotic diversity - experience working in the Unix/Linux environment and programming skills in R and/or Python - experience with molecular methods relevant to biodiversity and NGS library prep - excellent communication skills in English

The starting date is 1st of June 2019, or soon thereafter, and the position is for two years. Additional funding may be available. The appointment will be either at a Postdoc or at a Researcher level, depending on the number of years since the successful applicant's Ph.D. award.

For more information about the position, contact Fredrik Ronquist (fredrik.ronquist@nrm.se). Trade union representatives are Ingimar Erlingsson, Saco-S and Anna Sandberg, ST. All can be reached at telephone number +46 8 519 540 00.

The application should consist of a personal letter and a CV with contact details of 2-3 references. Mark your application with dnr 2.3.1-279-2019 and send it to rekrytering@nrm.se no later than 12th May 2019.

Piotr Ā ukasik

Researcher, Insect Biome Atlas Department of Bioinformatics and Genetics Swedish Museum of Natural History / Naturhistoriska Riksmuseet Svante Arrhenius vÅĀg 3 114 18 Stockholm, Sweden Phone: + 46 (0) 8 5195 4007 Email: piotr.lukasik@nrm.se

Piotr Lukasik <Piotr.Lukasik@nrm.se>

---

## QueensU TickMicrobiome

**\*\*Postdoctoral Researcher in Bioinformatics & Metagenomics\*\***

Queen's University, Kingston, ON Canada April 25, 2019

A Post-Doctoral position is available in the computational analysis of high-throughput sequencing data (Illumina + Oxford Nanopore) for the study of microbial communities, with an emphasis on ticks and tick-borne pathogens in an ecological and evolutionary context.

The successful applicant will join a team of early-career and established researchers who are dedicated to mitigating health risks associated with tick-borne pathogens. Our expertise spans a broad range of disciplines including human medicine, veterinary science, biochemistry, and ecology/evolution.

**Applicant Profile:** A PhD in any relevant discipline  
 Good programming and data management skills  
 Proficiency in R and/or Python for open and reproducible science  
 Proficiency in bash/Unix/Linux for analysis of high-throughput sequence data  
 Preference for individuals who have experience with common analysis pipelines for population genomics and/or metagenomics (whole shotgun and/or metabarcoding), and/or familiarity with community ordination analysis.

**About us:** Based at Queen's University in historic Kingston, Ontario, Canada, the successful candidate will enjoy a relatively low cost of living and high quality of life. As a diverse and inclusive group of researchers dedicated to improving representation in STEM research, we especially encourage applications from any candidates whose academic record has been challenged by socioeconomic background, discrimination, parental leave, personal life events, and/or other considerations. Applicants are encouraged to include these important considerations as part of their application package.

**Salary:** \$40,000 per year, plus benefits and other costs (e.g. child care for conference attendance)

**Co-supervisors:** Dr. Robert Colautti (Queen's U) Dr. Qingling Duan (Queen's U)

**Collaborators:** Dr. Katie Clow (U Guelph) Dr. Rylan Egan (Queen's U) Dr. Claire Jardine (U Guelph) Dr. Manisha Kulkarni (U Ottawa) Dr. Stephen Lougheed (Queen's U) Dr. Samir Patel (Ontario Public Health) Dr. Prameet Seth (Queen's U & Kingston General Hospital) The Canadian Lyme Disease Research Network (CLyDRN)

Interested applicants should contact Rob Colautti (Robert[dot]Colautti <at>queensu{dot}ca).

Dr. Robert I. Colautti Biology Department Queen's University Web: bit.ly/colautti Twitter: @colauttilab

Robert Colautti <robert.colautti@queensu.ca>

---

## Scandinavian ResSchool Biosystematics

Considering a postdoc in systematics, speciation or organismal evolution in Scandinavia?

ForBio - the Scandinavian Research School in Biosystematics is organising a training program for outgoing and incoming postdoctoral fellows to apply for European Commission H2020 MSCA Individual Fellowships.

The training program is open to potential incoming fellows to, and outgoing fellows from, research groups in systematic biology in Scandinavia, including systematics, taxonomy, phylogenetics, biogeography, macroevolution, metagenomics, etc. The target group are academically-engaged senior PhD students, postdocs and junior researchers. This covers the IF programs ER-ST (Standard European), ER-CAR (Career Restart Grant), ER-SE (Society and Enterprise), ER-RI (Reintegration), and GF (Global). We aim to have a mixed group of incoming and outgoing fellows. These programs are open to citizens of all countries.

The program runs from June 1st to the submission deadline of the H2020 MSCA-IF call on September 11th 2019. The training includes match-making between fellows and hosts, coaching, an intensive 3-day workshop in Oslo, writing support, peer review, and liaison with EU coordination offices.

For more information about teachers, target group, course plan, costs and registration, see: <https://www.forbio.uio.no/events/courses/2019/MSCAIF.html> For potential hosts for incoming fellows see below and here (<https://www.forbio.uio.no/events/courses/2019/msca-if-hosts.html>), but also consider any relevant host at the University of Oslo, NTNU Trondheim, University of Bergen, University of Tromsø, Gothenburg University, Uppsala University, Stockholm University, The Natural History Museum of Denmark, University of Copenhagen, Swedish Museum of Natural History, University of Aarhus, etc etc. SE (Society and Enterprise) fellowships can include mobility to research agencies, SMEs and NGOs.

Registration: Interested fellows should register online and provide contact information of their host before May 10th. Registered fellows will be evaluated and notified by May 21st regarding acceptance and participation in the training program. Make sure the reserve the dates

12-14 June for the workshop.

If you have any questions, contact Hugo de Boer ([hugo.deboer@nhm.uio.no](mailto:hugo.deboer@nhm.uio.no)) for more information.

Best,

Hugo

Hugo de Boer

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

Plant.ID MSCA-ITN project leader Leader of ForBio - Research School in Biosystematics Plant Evolution and DNA Metabarcoding group

Selected hosts that might be of interest:

Inger Greve Alsos, Tromsø Museum, The Arctic University Museum of Norway, Tromsø PI of ERC CoG IceAGenT: IceAge Genomic Tracking of Refugia and Postglacial Dispersal PI of NFR Toppforsk ECOGEN: Ecosystem change and species persistence over time: a genome-based approach <https://www.ecogen.no/> [https://en.uit.no/forskning/-forskingsgrupper/gruppe?p\\_document\\_id=5399](https://en.uit.no/forskning/-forskingsgrupper/gruppe?p_document_id=5399)

[https://en.uit.no/om/enhet/ansatte/-person?p\\_document\\_id4266&p\\_dimension\\_id&8852](https://en.uit.no/om/enhet/ansatte/-person?p_document_id4266&p_dimension_id&8852)

<https://scholar.google.no/citations?user=-phK0JuEAAAAJ&hl=no> Torkild Bakken, NTNU University Museum, Norwegian University of Science and Technology. Biodiversity of marine macrobenthic organisms, coast-deep sea, Annelida, DNA barcoding, biogeography <https://www.ntnu.edu/employees/-torkild.bakken> [https://www.researchgate.net/profile/-Torkild\\_Bakken](https://www.researchgate.net/profile/-Torkild_Bakken)

Mika Bendiksby, NTNU University museum, Norwegian University of Science and Technology, Trondheim (also guest researcher at NHM, UiO) Biodiversity; biogeography (ecological- and historical-); biosystematics; speciation (allopolyploid-, cryptic- etc.); evolution (accelerated-, stagnant-, convergent- etc.); integrative taxonomy; lichenized fungi; phylogenetics (molecular- and spatial-) <https://www.ntnu.edu/employees/mika.bendiksby> <https://www.nhm.uio.no/english/about/organization/-research-collections/people/annamb/>

[TQ9AcAAAAJ https://scholar.google.no/citations?hl=en&user=TQ9AcAAAAJ](https://scholar.google.no/citations?hl=en&user=TQ9AcAAAAJ) Hugo de Boer, Plant Evolution and DNA metabarcoding, Natural History Museum, University of Oslo Plant systematics; Molecular

— / —

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

## TexasAMU ProgramCoordinator EvolutionaryBiolBiodiversity

Position Announcement Joint Program Coordinator Ecology and Evolutionary Biology Ph.D. Program (EEB) and Applied Biodiversity Science Program (ABS)

The Ecology and Evolutionary Biology Ph.D. program (EEB) and the Applied Biodiversity Science program (ABS) at Texas A&M University are seeking a full-time joint Program Coordinator. This PhD-level coordinator position is a hub for the EEB and ABS programs. The program coordinator will become a central communicator and facilitator for faculty, students, and the international network, and be engaged in the research and teaching missions of these programs. The position supports opportunities for research and professional development and is appropriate for postdocs. The position is based on the College Station campus.

EEB is an interdisciplinary program that offers a Ph.D. in the field of Ecology and Evolutionary Biology. We offer a world-class training program that incorporates many fields relevant to EEB, spanning from evolutionary genomics to animal behavior to landscape ecology. Our faculty and students are spread over 11 departments and seven colleges across Texas A&M University, bringing together a diverse array of perspectives in the study of EEB.

The ABS Program is a multidisciplinary graduate training program. ABS promotes integrative research in biological and social sciences applied to biodiversity conservation around the world, including the US, Latin America, and Africa. Faculty and students spread over nine departments and five colleges.

More about these two program at: <http://eeb.tamu.edu> and <http://biodiversity.tamu.edu>. Qualifications ' the Program Coordinator will have a foundation in the natural or social sciences and demonstrated experience with administrative and organizational tasks.

Minimum requirements: Â B.Sc. degree (PhD strongly preferred) in the social or natural sciences by the start date of the position.

Â At least 2 years of administrative, management, or leadership experience.

The ideal EEB/ABS Joint Program Coordinator will have: Â Excellent interpersonal skills.

Â Excellent organizational skills.

Â Outstanding leadership skills.

Â Demonstrated ability to work as part of multidisciplinary teams and in diverse cultural settings.

Â Ability to communicate in Spanish is not required but is desirable.

Responsibilities ' The Program Coordinator is a hub for the EEB and ABS programs. S/he will become a central communicator and facilitator for faculty, students, and postdoctoral researchers. The Program Coordinator will have a direct leadership role in both EEB and ABS Programs.

Specific duties include: Â managing day-to-day activities and information requests; Â grant writing; Â facilitating contacts with local and international partners; Â facilitating interactions among members; Â coordinating logistics for field courses and on-campus events; Â organizing and teaching orientation course for incoming EEB students; Â assisting the EEB Executive Committee with various tasks; Â supervising webmaster for design and updates to the websites; Â coordinating course schedules and enrollment; Â organizing outreach and recruitment activities; Â arranging interviews for applicants to both programs; Â tracking student progress; Â managing graduate applications; Â processing and reporting expenses; Â coordinating program assessment activities and compiling assessment data; Application Process ' Applications should include a letter of interest emphasizing a track record in multidisciplinary activities, administrative/management experience, relevant research, and how the candidate can contribute to the interdisciplinary mission of ABS and EEB.

Include a complete Curriculum Vitae and list of two professional references. Applicants can apply here: [https://tamus.wd1.myworkdayjobs.com/en-US/-AgriLife\\_Research\\_External](https://tamus.wd1.myworkdayjobs.com/en-US/-AgriLife_Research_External). Search for position "R-018558"

Inquiries about this position should be directed to: Gil Rosenthal, Department of Biology: [grosenthal@bio.tamu.edu](mailto:grosenthal@bio.tamu.edu) Jason Martina, EEB and ABS: [jpmartina@tamu.edu](mailto:jpmartina@tamu.edu) Lee Fitzgerald, Wildlife and Fisheries Department: [lfitzgerald@tamu.edu](mailto:lfitzgerald@tamu.edu) Amanda Stronza, Recreation, Park and Tourism Sciences: [astronza@tamu.edu](mailto:astronza@tamu.edu) Application review will begin 22 April 2019 and will continue until position is filled.

What we offer Salary commensurate with education and experience Attractive benefits package.

Great community and work environment.

Opportunities for graduate level teaching and research engagement.

About the Community ' Texas A&M University main campus is located in College Station, which is part of a metropolitan community of 200,000 people, including the city of Bryan. In addition to excellent health, education, and recreation services, the community affords a rich variety

— / —

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>

---

## UCalifornia Berkeley FishPopGenomics

Postdoctoral position on the genomics and development of specialized craniofacial morphology in Caribbean pupfishes

The Martin Fish Speciation Lab at the University of California, Berkeley in the Department of Integrative Biology and Museum of Vertebrate Zoology (starting July 2019) seeks a postdoc for genomic or developmental studies of adaptive phenotypes in a radiation of trophic specialist pupfishes. Pupfishes present a rare opportunity to investigate the recent origins of adaptive radiation and the evolution of novel niches (e.g. scale-eating) localized to a single Bahamian island despite thousands of similar Caribbean environments. Our lab also investigates Cameroon crater lake cichlids, one of the most celebrated examples of sympatric speciation in nature, and the endangered Devils Hole pupfish.

At this time we are seeking postdoctoral applicants with specific expertise in either \*population genomics, transcriptomics, or craniofacial development\*.

A multi-year position is available (initial 12 month appointment with the possibility of renewal for three more years). Start date is flexible, but must be after July 1st, 2019. Salary is scaled to the standard NIH postdoctoral rates.

Potential projects in the lab include:

1) Characterization of candidate adaptive alleles within Caribbean pupfishes using a combination of QTL mapping, genome scans, GWAS, gene annotation, transcriptomics, and analyses of selective sweeps and introgression.

2) Validation of candidate adaptive alleles using in situ hybridization experiments, reporter assays, CRISPR, and other functional approaches in the pupfish system.

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

Required qualifications:

Ph.D. or equivalent degree in biology, evolution, genetics, development, bioinformatics, or related field. Publication of work based on dissertation. Programming experience in R, bash, and python.

Preferred qualifications:

Strong background in either population genomics or evolutionary developmental biology.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sexual orientation, gender identity, national origin, disability, age, or protected veteran status. Applicants from under-represented backgrounds are strongly encouraged to apply.

UC Berkeley has a world-class community of integrative biologists studying adaptive radiation spanning the Department of Integrative Biology, the Museum of Vertebrate Zoology, the Department of Environmental Science, Policy, and Management, the Department of Molecular and Cell Biology, the Center for Theoretical Evolutionary Genomics, and more. UC Berkeley offers competitive salaries, excellent benefits, and is an equal opportunity employer. The City of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

Interested candidates should submit a cover letter detailing their interest in the position and relevant experience along with their CV and contact information for three references to Chris Martin at [chmartin@berkeley.edu](mailto:chmartin@berkeley.edu)

This position is open until filled, but applications will be reviewed starting two weeks after this posting. Please feel free to contact me at the below email address with any questions.

Christopher Martin

Assistant Curator of Ichthyology, Museum of Vertebrate Zoology

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

[chmartin@berkeley.edu](mailto:chmartin@berkeley.edu)

<http://labs.bio.unc.edu/martin/> @fishspeciation  
christopher.h.martin@gmail.com

---

## UCalifornia Berkely 2 Evolutionary Genomics

Postdoc in Evolutionary Genomics, UC Berkeley

Two NIH-funded postdoctoral positions are available in Doris Bachtrog's group at UC Berkeley.

The details of the projects are flexible, but should fall within the general interests of the lab. Current research focuses on using cutting-edge genomic and molecular techniques to study sex chromosomes, heterochromatin, centromeres, transposable elements, meiotic drive, and speciation in insects. For more information on current research, see: <https://-bachtroglabberkeley.wordpress.com/> Candidates must have a background in either Drosophila molecular genetics (including transgenics) and genomics, or must have solid programming and bioinformatics skills.

Our group shares newly renovated office space with the groups of Rasmus Nielsen, Monty Slatkin and John Huelsenbeck, and strong intellectual ties, including weekly meetings, with other research groups of the Center for Theoretical Evolutionary Genomics at UC Berkeley ([cteg.berkeley.edu/](http://cteg.berkeley.edu/)).

Informal inquiries as well as applications (including a CV, and two letters of recommendation) should be emailed to Doris Bachtrog <[dbachtrog@berkeley.edu](mailto:dbachtrog@berkeley.edu)>. The target start dates are July 2019, but are flexible.

Doris Bachtrog UC Berkeley <https://-bachtroglabberkeley.wordpress.com/> Doris Bachtrog <[dbachtrog@gmail.com](mailto:dbachtrog@gmail.com)>

---

## UCampinas Spider Adaptation

The Laboratory of Genetic Diversity, Department of Genetics, Evolution, Microbiology and Immunology of the University of Campinas invites applications for a two year postdoc fellowship. The postdoc will join the team of a recently funded collaboration between researchers from São Paulo, Brazil, and USA.

The research project aims to study genomic signatures of adaptation in Brazilian Dry Diagonal spiders using genetics and genomics. The activities will comprise fieldwork, sequencing and assembly of genomes, transcriptome analyses, modelling and statistical analyses. An evolutionary background during PhD and published papers in evolution are required. Fieldwork experience is recommended. The fellowship is R\$7373.10 monthly, for full time dedication.

Any questions can be sent to Vera N Solferini - [veras@unicamp.br](mailto:veras@unicamp.br)

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 two references to [veras@unicamp.br](mailto:veras@unicamp.br), up to April 15th, 24:00GMT.

Vera Nisaka Solferini

Full Professor

Inst. of Biology - Univ. of Campinas

Campinas, SP, Brazil

– Vera Nisaka Solferini IB - Unicamp R. Monteiro Lobato  
255 13083-862 Campinas SP

tel: 55 19 3521 6240 skype: verasolferini

Vera Solferini <[vera.solferini@gmail.com](mailto:vera.solferini@gmail.com)>

---

## UDenver Evolution Animal Communication

Postdoctoral opportunity: Evolution of animal communication Posting snapshot: Looking for a highly motivated, creative scientist to join the Tinghitella research group at the University of Denver to study the evolution of sexual signaling systems and the evolutionary genetics of diversification. Salary and benefits are competitive.

Position summary: Primary duties will include conducting research on rapid evolutionary change in the sexual signals of Hawaiian field crickets, their genetic/genomic underpinnings, and implications for reproductive isolation. The project capitalizes on an unprecedented opportunity to observe the emergence of what may be a new sexual signal, track its coevolution (or not) with the preferences and sensory systems of intended and unintended receivers (females and natural enemies), and examine the signals evolutionary origin and genomic architecture. 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. There will be ample opportunities to also participate in a new science communication program explicitly aimed at broadening participation in the sciences.

Diversification and even speciation are believed to be tied to the evolution of novel communication systems. There is a growing appreciation for the role of sexual selection in speciation processes, but comparisons are necessarily made between closely related species or populations that have differed in sexual signals for many, many generations. Less than two years ago we discovered a population of crickets that produce songs (purring) with properties that differ dramatically from the ancestral type (typical). Purring crickets are now found in several long-studied locations where they were not previously, affording us an opportunity to observe the origin and subsequent evolution of a novel song and its potential consequences for sexual isolation in real time.

Minimum qualifications: Experience generating and analyzing phenotypic (morphology, behavior) and fitness data; knowledge of quantitative and/or evolutionary genetics; experience and willingness to do longer-term field work; excellent analytical skills; demonstrated ability to publish good quality papers; strong communication and writing skills. Ph.D. required in a related field of biology.

Desired qualifications: Experience in population genomics and/or analysis of auditory signals desired. The position provides additional opportunities for independent research in related areas for motivated postdoctoral scientists.

The academic environment: The University of Denver has a growing group of faculty, students, and postdocs studying Ecology and Evolution (see <https://dueeb.weebly.com>). The EEB program is a dynamic and highly interactive group. The postdoc will work closely with collaborators Erica Larson (University of Denver) and Dale Broder (St. Ambrose University) who have expertise in genomics and evolutionary ecology.

Denver and the Front Range: Denver is an awesome western city of ~700,000 people with a vibrant art community, music and nightlife, and access to amazing recreation in the Rocky Mountains. We also have 300 days of sunshine a year!

Apply: Contact Robin Tinghitella ([robin.tinghitella@du.edu](mailto:robin.tinghitella@du.edu)) with questions and apply directly at <http://jobs.du.edu/cw/en-us/job/492328/-postdoctoral-research-associate>. To apply, you will

need a CV, cover letter indicating your interest and qualifications for the position, and names and contact information for 3 references. Review of the applications will begin immediately. The initial hire is for 1 year with renewal for an additional year pending satisfactory progress.

Robin M Tinghitella Assistant Professor Department of Biological Sciences University of Denver

Office: Boettcher West 243 Phone: 303-871-3658 Web: <http://tinghitellalab.weebly.com>

[Robin.Tinghitella@du.edu](mailto:Robin.Tinghitella@du.edu)

---

## UEdinburgh 2 GenomicConflict

I am recruiting two postdocs to join my lab at the University of Edinburgh as part of a recently funded ERC starting grant. Details below.

thanks and best wishes,

Laura Ross

Post Doctoral Research Associate in Insect Reproduction and Epigenetics

A 3-year postdoctoral research position is available to work on a newly-funded ERC project in the lab of Laura Ross (Institute of Evolutionary Biology, University of Edinburgh, UK) entitled 'How to break Mendel's laws? The role of sexual conflict in the evolution of unusual transmission genetics'. We are looking for an enthusiastic and motivated postdoc interested in evolutionary/molecular genetics, epigenetics and reproductive biology.

The project focuses on the evolution and mechanism of Paternal Genome Elimination, a type of reproduction found across thousands of insects where males lose their father's genome during spermatogenesis and only transmit maternally-derived chromosomes to their offspring. We will use genomic, cytogenetic and experimental approaches in mealybugs to understand how chromosomes from the mother and father are recognized within sons, how this affects the expression of maternal and paternal alleles ("genomic imprinting"), how the paternal genome is eliminated and how this elimination affects offspring sex. The project will be carried out in close collaboration with several Project Partners in the UK and abroad.

Within the project, the postdoc will be able to develop independent lines of research with a view to establishing

themselves as an independent investigator. The project includes substantial funds for sequencing, consumables, computing, training, and to attend international conferences. The position is initially funded for 3 years with an approximate start date of June 1st 2019.

Applicants should have a strong background in evolutionary genetics/molecular biology and a PhD (or soon to be obtained) in a relevant subject area (genetics, evolutionary biology, molecular biology, cell biology). Experience working with genomic data, molecular biology wet lab and bioinformatics skills are essential, as is a strong track record of independent and creative thinking. Applicants should be willing to take on the challenges of working with a non-model organism. Experience with insect model systems, bisulfite and ChIP-seq sequencing data, RNAi experiments, FISH/in situ hybridization would be very advantageous.

Informal enquiries to [laura.ross@ed.ac.uk](mailto:laura.ross@ed.ac.uk). more information [https://www.vacancies.ed.ac.uk/pls/corehrrecruit/-erq-jobspec-version.4.jobspec?p\\_id7352](https://www.vacancies.ed.ac.uk/pls/corehrrecruit/-erq-jobspec-version.4.jobspec?p_id7352) This post is offered on a full time, fixed term basis for 36 months.

Salary: pounds 33,199 to pounds 39,609

Closing date for applications is Tuesday 23 April at 5pm (GMT).

Postdoctoral Research Associate in Sexual Conflict and Genome Evolution

A 3-year postdoctoral research position is available to work on a newly-funded ERC project in the lab of Laura Ross (Institute of Evolutionary Biology, University of Edinburgh, UK) entitled 'How to break Mendel's laws? The role of sexual conflict in the evolution of unusual transmission genetics'. We are looking for an enthusiastic and motivated postdoc interested in sexual conflict, evolutionary genomics, population genetics and sex chromosome evolution.

The aim of the project is to investigate how intragenomic sexual conflict affects genome and sex chromosome evolution in species where inheritance does not comply to the classic rules of Mendelian inheritance. The primary focus is on species that reproduce through Paternal Genome Elimination, a type of reproduction where males lose the complete haploid genome derived from their father during spermatogenesis and only transmit maternally-derived chromosomes to their offspring. The variability between species 'with males of some haploid, others diploid, some still retaining ancestral sex chromosomes' provides a unique opportunity to test how patterns of gene expression and inheritance affect the evolution of genes under sexual conflict. The project will involve comparative genomics, experimental approaches and developing new population genetic the-

ory, and will be carried out in close collaboration with several Project Partners in the UK and abroad.

Within the project, the postdoc will be able to develop independent lines of research with a view to establishing themselves as an independent investigator. The project includes substantial funds for sequencing, consumables, computing, training and to attend international conferences. The position is funded for 3 years with an approximate start date of June 1st 2019.

Applicants should have a strong background in evolutionary genetics/population genetics and a PhD (or soon to be obtained PhD) in a relevant subject area (genetics, evolutionary biology, bioinformatics). Experience working with genomic data and good

— / —

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>

---

## UEdinburgh EvolutionaryGenetics

Postdoctoral Position in Evolutionary Genetics

A postdoctoral position is available to join the group of Peter Keightley to work on the evolutionary impact of spontaneous mutations. As the ultimate source of genetic variation, new mutations play a central role in evolutionary biology. The rate of spontaneous mutation and the genetic basis of variation from mutations are key to many unresolved questions, including the fate of small populations, the evolution of ageing and the genetic basis of quantitative trait variation.

We aim to study two unique resources developed in our lab, in which mutations are expected to accumulate at radically different rates. The first is a highly replicated set of spontaneous mutation accumulation (MA) lines in mice, the first such set of lines in any mammalian species. Each MA line is bred for many generations in the near-absence of natural selection, leading to molecular and phenotypic divergence among lines. The second is a set of replicated MA lines (maintained for ~1,000 generations) in different strains and species of the single-celled green alga *Chlamydomonas*. We will address questions concerning the nature of the new mutational variation affecting the genome, gene expression and quantitative traits.

Applicants should have or shortly obtain a PhD in a relevant subject, e.g., evolutionary genetics or genomics. Experience in bioinformatics will be an advantage. Candidates should have an outstanding academic track record commensurate with their career stage and experience. She/he is expected to be active in developing the project and to contribute to an enthusiastic working atmosphere. Candidates will benefit from training in a vibrant intellectual and collaborative environment in the UK's largest evolutionary biology institute. The project is funded by an ERC Advanced Grant to Peter Keightley and Diethard Tautz (MPI Ploen, Germany) and has substantial funds for computing, sequencing and travel. The position is available immediately until 31st December 2021.

To apply, go to <http://www.ed.ac.uk/human-resources/jobs> and search for vacancy 047680. Closing date for applications 17th May 2019.

Prospective applicants should contact peter.keightley@ed.ac.uk to discuss the project.

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

Peter Keightley <peter.keightley@ed.ac.uk>

---

## UFlorida MechanismsOfSeasonalAdaptation

Postdoc: Mechanisms of seasonal adaptation. Dan Hahns Lab, University of Florida

A postdoctoral position is available to work on the mechanistic, genetic and physiological architecture of insect dormancy and overwintering responses. The position is available as of summer 2019 with funding for 2 years, and possible extension for a 3rd year. The postdoctoral associate will be responsible for addressing the physiological basis of rapid evolution of diapause timing using a combination of approaches (see below for more description and related publications). In addition to contributing to our main grant aim, the person will have substantial opportunities to creatively work in other areas of evolutionary physiology including local adaptation and genetic variation in thermal hardiness, predicting winners and losers in the face of climate change, rapid evolution upon laboratory colonization, beneficial plasticity treatments that improve organismal performance, and more.

Applicants must have a PhD by the time of hire, a

strong publication record in peer-reviewed journals, and an interest in evolutionary physiology. A background that includes biochemistry, physiology, molecular biology, development, or neuroscience is desirable, as are strong quantitative skills. Evolutionary ecologists with good big-picture and quantitative skills that wish to learn more sub-organismal perspectives are also encouraged to apply. This problem can be tackled from a number of perspectives and we will work together to play to the candidates strengths and to facilitate learning new perspectives and approaches. The successful candidate will be a broad thinker and have the capacity to develop exciting new research directions and lead a team of students. Our group has a solid history of career development and additional opportunities for professional and career development will be based on individual development planning with the candidate. These opportunities could include additional training in teaching and scholarship of teaching and learning, public outreach and extension, skills pertinent to industry jobs, and more.

For more information or to apply contact Dan Hahn directly (dahahn@ufl.edu). For applications, please e-mail me a single PDF document including your CV, a brief statement of previous research, and contact information for three references. Review of applications will begin May 15th, 2019 and continue until the position is filled.

Daniel A. Hahn, Professor

Department of Entomology and Nematology, University of Florida

dahahn@ufl.edu

<http://entnemdept.ifas.ufl.edu/people-directory/daniel-hahn/> Background for the project:

Animals and plants must synchronize their life-history timing to exploit good times and avoid bad times of the year. Synchronization among interacting species makes seasonal responses a critical organizational component of ecological communities. Adaptation in seasonal timing can create and maintain biodiversity. Reproduction is often seasonal. Therefore, shifts in seasonal timing can disrupt reproductive timing among populations, catalyzing speciation. Moreover, formation of new taxa creates opportunities for other, interacting organisms to diversify in kind. Shifts in seasonal timing can have reverberating effects generating new biodiversity through ecosystems. Contemporary climate change is driving changes in seasonality. The capacity of ecological communities to evolve in concert with changing conditions will impact whether interactions among community members will be maintained or disrupted under new climatic regimes.



Our broader collaborative research team, including Jeff Feder at Notre Dame, Greg Ragland at University of Colorado-Denver, Tom Powell at Binghamton University New York, and Dan Hahn at University of Florida is investigating the role of seasonal adaptation in the origin and maintenance of insect biodiversity. *Rhagoletis pomonella*, the apple maggot fly, is a fruit-feeding agricultural pest that has recently evolved (since the mid 1880s). Seasonality drives diversification; apple flies evolved an earlier life cycle than their hawthorn-feeding ancestors to feed on earlier ripening apple fruits. Superimposed on seasonal partitioning of plant-feeding flies are additional radiations involving parasitic wasps. Three wasps have similarly diverged in life cycle timing to match the seasonal shift of their *R. pomonella* hosts to earlier fruiting apples.

This multidisciplinary project will test whether the same physiological, molecular, and genomic mechanisms underlying the shift in life history timing allowing *Rhagoletis* to attack apples are also involved in sequential shifts and seasonal adaptation of the parasitic wasps attacking apple flies.

This group of laboratories has a strong history of inter-institution

— / —

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>

---

## UFlorida SharkEvoDevo

Postdoctoral Position in Shark Evolutionary Developmental Biology, Stem Cell Biology and Tooth Regeneration

A postdoctoral position is available in the Laboratory of Gareth Fraser ([www.fraser-lab.net](http://www.fraser-lab.net)) at the Department of Biology, University of Florida. Our lab is focused on a range of research projects based around the central theme of vertebrate evolutionary developmental biology - they include tooth development and regeneration, craniofacial diversity, EvoDevOmics, and skin appendage evolution and development.

We are looking for a motivated and creative scientist to continue to develop the shark and ray as comparative evodevo models for a range of research projects. The primary focus of this position will be stem cell mediated

tooth regeneration in sharks and rays, however we do encourage development of the candidates own creative research ideas and interests, so there is potential here to develop a project that suits the candidate in line with the focal themes of the lab. The salary is competitive and commensurate with qualifications and experience, and includes a full benefits package. The applicant selected for this position would begin the beginning of the Fall 2019 term. The anticipated date would be August 16, 2019.

### Qualifications

Candidates should have an interest in evolutionary developmental biology, and vertebrate diversity. Knowledge of developmental biology techniques, RNAseq analyses or stem/regenerative biology is desirable.

### Application Instructions

For full consideration, applications must be submitted online at <http://apply.interfolio.com/62577> and must include: (1) a letter of application summarizing the applicant's qualifications and interests, (2) a complete curriculum vitae, (3) a statement on research goals, and (4) ) a list of at least three references. After initial review, applicants who are chosen to receive further consideration will be asked to request confidential letters of recommendation from the references. If you would like further information about the position please contact Gareth Fraser. Email: [g.fraser@ufl.edu](mailto:g.fraser@ufl.edu). Application deadline is May 29, 2019.

All candidates for employment are subject to a pre-employment screening which includes a review of criminal records, reference checks, and verification of education.?

The selected candidate will be required to provide an official transcript to the hiring department upon hire. A transcript will not be considered "official" if a designation of "Issued to Student" is visible. Degrees earned from an educational institution outside of the United States require evaluation by a professional credentialing service provider approved by the National Association of Credential Evaluation Services (NACES), which can be found at <http://www.naces.org/>. The University of Florida is an equal opportunity institution dedicated to building a broadly diverse and inclusive faculty and staff. Searches are conducted in accordance with Florida's Sunshine Law. If an accommodation due to disability is needed in order to apply for this position, please call (352) 392-2477 or the Florida Relay System at (800) 955-8771 (TDD).

The Department particularly welcomes applicants who can contribute to a diverse and inclusive environment through their scholarship, teaching, mentoring, and pro-

fessional service. The university and greater Gainesville communities enjoy a diversity of cultural events, restaurants, year-round outdoor recreational activities, and social opportunities.

Gareth J. Fraser, Ph.D Department of Biology University of Florida 512 Carr Hall Gainesville, FL, 32611 (352) 273-4758 [www.fraser-lab.net](http://www.fraser-lab.net) “Fraser,Gareth John” <g.fraser@ufl.edu>

---

## UIIdaho ModelingLassaVirusEvolution

A postdoctoral position developing mathematical and computational models of Lassa virus evolutionary dynamics is anticipated to become available in my group ([www.leef.org](http://www.leef.org)) in October 2019. The specific goal of this project is to predict genetic variation and sequence diversity of Lassa virus in its natural reservoir, *M. natalensis*, within Sierra Leone. Unique opportunities exist to evaluate and refine model performance using viral sequence data being collected from natural reservoir populations within Sierra Leone and experimental infection studies conducted at Rocky Mountain Laboratories. This project is part of an international collaborative effort (<https://preempt.ucdavis.edu/>) to forecast the spillover of Lassa virus into the human population and develop a transmissible vaccine to eliminate it from its animal reservoir. The post-doc will work directly with the broader University of Idaho team, including Chris Remien and Jim Bull, and will have opportunities to work with our international collaborators. Flexibility exists to develop side-projects that work toward overall project goals.

Scott Nuismer Professor Department of Biological Sciences and Mathematics Program in Bioinformatics and Computational Biology University of Idaho Moscow, ID 83844 <https://www.leef.org/> “Nuismer, Scott (snuismer@uidaho.edu)” <snuismer@uidaho.edu>

---

## ULausanne BarnOwlEvolution

Postdoctoral position in Movement Ecology

The Roulin Group is proposing a postdoctoral position in movement ecology in the Department of Ecology and Evolution at the University of Lausanne, Switzerland. The postdoc will join a dynamic team working mainly on the evolution, maintenance and genetics of melanin-based polymorphism. For more information, see <https://www.unil.ch/dee/roulin-group>. Research project: Barn owl (*Tyto alba*) breeding pairs have been equipped since 2016 with GPS and/or Accelerometer tags. In parallel, individual and reproductive parameters were monitored, as well as landscape and weather data. In this framework, the postdoc research projects will be defined based on her/his personal interests and competences. We are seeking to recruit someone with a strong interest in evolutionary biology and movement ecology, with skills in at least one of the following: GPS-based habitat selection methods; GPS- and/or Accelerometer-based behavior classification; Movement data statistical analyses. Experience with fieldwork, bird handling and GPS tagging could be an advantage. The applicants should also have a strong ability to work in team as PhD students are also involved in this project.

Contract information: We propose a postdoctoral position at 100% for one year, with two possible renewals of two years each (maximum 5 years). While most of the time will be dedicated to research, teaching will also be expected (including master supervision). Expected start date: 01.08.2019 or to be agreed.

Host University The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. Although French is the common language in Lausanne region, the department research activities and seminars are conducted in English. The campus is located on the shore of the Geneva Lake, with the view on the Alps.

Applications

Informal enquiries should be sent to Alexandre Roulin ([alexandre.roulin@unil.ch](mailto:alexandre.roulin@unil.ch)), and formal applications should include a coverletter 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 plat-

form (<https://bit.ly/2Ftaz9B>). All applications received by 1 June will receive full consideration, but review of applications will begin immediately.

The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

Alexandre Roulin <[alexandre.roulin@unil.ch](mailto:alexandre.roulin@unil.ch)>

---

## ULausanne EvolutionaryComputationalBiol

Postdoctoral associate in evolutionary computational biology

Expected start date: 01.09.2019 or to be agreed  
Contract length: 1 year, renewable 2 x 2 years, up to 5 years  
Activity rate: 100% Workplace: University of Lausanne, Génopode, 1015 Lausanne

The Dessimoz Lab at the University of Lausanne (<http://lab.dessimoz.org>) is recruiting a postdoctoral associate in evolutionary bioinformatics.

The ideal candidate will demonstrate enthusiasm for interdisciplinary research, keen to productively interact with evolutionary biologists, genome biologists and computer scientists, and read the corresponding range of scientific literature.

There will also be opportunities to gain teaching experience (e.g. via student project supervision and contribution to undergraduate or graduate teaching).

Working conditions in Lausanne are extremely competitive, and include access to state-of-the-art computing and sequencing facilities. The environment is highly international, and all activities are conducted in English.

Profile Sought

Essential:

- Doctorate degree - Solid programming experience (min. 3 years) with languages such as Python, C/C++, Java, or R - High level of motivation - Ability to collaborate in an interdisciplinary environment - Excellent spoken and written English proficiency - Up to 4 years after PhD by the starting date (unfortunately, this is a requirement by the funder)

Desirable:

- Publications in peer-reviewed journals - Past contribution to open access software packages - Experience in

phylogenetic methods - Experience in high-performance computing

Furthermore, please note that the laboratory is committed to promoting gender equality and strongly encourages applications from female candidates.

How to apply

The application should fill in the form linked below and provide the following elements:

- Cover letter describing the research and career aspirations, and motivation to join our laboratory - Curriculum vitae including a list of publications - Reference to best paper accompanied by a brief supporting statement (approx. 200 words) - The names and contact details of 2-3 references - Copy of official PhD certificate

Applications should be submitted via the UNIL HR system using this following link: <http://bit.ly/swisspostdoc>

Committed to promoting equal employment opportunities among its staff members, the University of Lausanne particularly encourages applications by women.

To ensure full consideration, applications should be received by 30 April 2019.

Christophe Dessimoz <[Christophe.Dessimoz@unil.ch](mailto:Christophe.Dessimoz@unil.ch)>

---

## ULausanne EvolutionColourPolymorphism

Postdoctoral position in the evolutionary ecology of colour polymorphism

The Roulin Group is working on the evolution, maintenance and adaptive function of melanin-based colour polymorphism. To this end, we work with the barn owl because in the same population conspecifics vary in the degree of ventral plumage coloration from white to dark reddish. We could already show that this polymorphism is associated with diet and is locally adapted. Our goal in this project is to investigate whether differently colored owls forage in different habitats, whether they use different foraging methods and whether they achieve a different foraging success. To this end, we will monitor foraging behavior using GPS fixed on the back of adult barn owls. We thus propose a postdoctoral position in movement ecology in the Department of Ecology and Evolution at the University of Lausanne, Switzerland. The postdoc will join a dynamic team working mainly on the evolution, maintenance and genetics of melanin-based polymorphism. For more information,

see <https://www.unil.ch/dee/roulin-group> . Research project: Barn owl (*Tyto alba*) breeding pairs have been equipped since 2016 with GPS and/or Accelerometer tags. In parallel, individual and clutch parameters were monitored, as well as landscape and weather data. In this framework, the postdoc research projects will be defined based on her/his personal interests and competences. We are seeking to recruit someone with a strong interest in evolutionary biology and movement ecology, with skills in at least one of the following: GPS-based habitat selection methods; GPS- and/or Accelerometer-based behavior classification; Movement data statistical analyses; Energetics. Experience with fieldwork, bird handling and GPS tagging could be an advantage. The applicants should also have a strong ability to work in team as PhD students are also involved in this project.

Contract information: We propose a postdoctoral position at 100% for one year, with two possible renewals of two years each (maximum 5 years). While most of the time will be dedicated to research, teaching will also be expected (including master supervision). Expected start date: 01.08.2019 or to be agreed.

Host University The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. Although French is the common language in Lausanne region, the department research activities and seminars are conducted in English. The campus is located on the shore of the Geneva Lake, with the view on the Alps. Applications

Informal enquiries should be sent to Alexandre Roulin ([alexandre.roulin@unil.ch](mailto:alexandre.roulin@unil.ch)), and 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. The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

Alexandre Roulin <[alexandre.roulin@unil.ch](mailto:alexandre.roulin@unil.ch)>

---

## ULiverpool EvolutionaryGenetics

The Betancourt lab in at the University Liverpool, UK, is seeking a postdoctoral researchers for a 3-year appointment, with possibility of extension to the end of the 5-year grant. This position is funded by an ERC grant to investigate transposable element invasions using *Drosophila* as a model. Informal enquires to

[A.Betancourt@liverpool.ac.uk](mailto:A.Betancourt@liverpool.ac.uk) very welcome.

You should have a PhD in a relevant field, and experience in bioinformatics or population genetics. You will work as part of a team that includes the PI, another postdoc, and a full-time research technician, and will be encouraged to develop their own research interests.

Dr. Betancourt's group has tackled a wide variety of questions in evolutionary genetics, addressing the role of recombination and sex-linkage in evolution, and the spread of selfish elements in *Drosophila* (more information here: <http://www.flyevolution.net/>).

The Institute of Integrative Biology (IIB) at the University of Liverpool houses a large and active research faculty (see: <https://www.liverpool.ac.uk/integrative-biology/about/>), and includes several active groups in evolutionary biology (see <https://www.liverpool.ac.uk/-integrative-biology/staff/evolution-ecology-and-behaviour/>). IIB also houses several excellent core facilities, including a genomics and proteomics centres (more here: <https://www.liverpool.ac.uk/integrative-biology/facilities-and-services/>).

Apply at the link below (or search for the appropriate job reference at <https://recruit.liverpool.ac.uk>). You'll need to include a cover letter, CV, and details for three references.

Bioinformatics/Population genetics Postdoctoral Research Associate Grade 7 Department: : Evolution, Ecology And Behaviour Job Reference: : 011484 Salary : £33,518 - £38,833 pa Closing Date : 06-May-2019 23:30 <https://bit.ly/2UKELH0> Cheers, Andrea

Andrea Betancourt | Senior Lecturer Department of Evolution, Ecology, and Behaviour (DEEB) | Institute for Integrative Biology (IIB) University of Liverpool Biosciences Building Rm 238 / Crown St. / L69 7ZB Liverpool / United Kingdom <http://www.flyevolution.net> | +44 (0) 151 795 4516 | [aabt@liverpool.ac.uk](mailto:aabt@liverpool.ac.uk)

Andrea Betancourt <[andrea.jbetancourt@gmail.com](mailto:andrea.jbetancourt@gmail.com)>

---

## UMichigan AdaptiveLimits

A working group (Brian Weeks, Benjamin Winger, and Kathleen Bergen) at the newly-formed Institute for Global Change Biology at the University of Michigan is hiring a Postdoctoral Research Fellow. The Fellow will work on predicting the limits to adaptive shifts in range and migration phenology in migratory birds, with a focus

on the interaction of these phenomena with concomitant changes in morphology and allometry. While past efforts to predict shifts in species ranges and phenologies have focused largely on projecting changes in climatic niche envelopes, the extreme physiological demands of migration may impose constraints on these adaptive strategies in migratory species. In particular, the observation that many migratory birds are getting smaller as temperatures increase (see: <https://www.biorxiv.org/content/10.1101/610329v1>), suggests that morphological adaptation may be a key dimension of climate change adaptation. Understanding how morphological change may facilitate or inhibit adaptive shifts in range and phenology through changes in optimal migratory dynamics as well as relationships to landscape/habitat change is the goal of this position.

The position will begin Fall 2019, is based at the School for Environment and Sustainability at the University of Michigan in Ann Arbor, is for 2 years, and comes with a competitive salary and benefits. The postdoc will be supervised by Weeks, Winger, and Bergen.

Qualifications: The position requires a PhD in ecology and evolutionary biology or a related field. The ideal applicant would have research experience related to bird migration, strong quantitative and modeling skills, and demonstrated success in publication of original research. Familiarity with GIS/remote sensing is a benefit.

Application Instructions and Deadline: Applicants should send a CV, contact information for two references, and a cover letter outlining their interest in the position and their relevant skills and experience to Brian Weeks ([bcweeks@umich.edu](mailto:bcweeks@umich.edu)). Review of applications will begin on May 15, 2019, with an expected start date of September 1, 2019.

Background: The School for Environment and Sustainability's overarching mission is to contribute to the protection of the Earth's resources and the achievement of a sustainable society. Through research, education, and outreach, the faculty, staff, and students are devoted to generating knowledge and developing policies, techniques, and skills to help practitioners manage and conserve environmental resources to meet the full range of human needs on a sustainable basis. The University of Michigan is an equal opportunity/affirmative action employer.

Brian Weeks <[bcweeks@umich.edu](mailto:bcweeks@umich.edu)>

---

## UMinnesota 3yrNIH Training Program

The \*Training Research Educators in Minnesota\* \*(TREM)\* program is a National Institutes of Health funded Institutional Research and Academic Career Development Award (IRACDA). The IRACDA mechanism recognizes that current training of future faculty is inadequate, and understands the considerable benefits and need for diversity throughout academia and the biomedical workforce. The goals of IRACDA are two-fold: (1) Train the next-generation of higher education faculty (particularly those interested in becoming faculty with strong graduate or undergraduate research programs) through a strongly mentored research program (75% effort), coupled to substantive training and experience in teaching (25% effort). (2) Increase the number of underrepresented minority students who ultimately become leaders in the biomedical research enterprises of Minnesota and beyond. TREM will enable our brightest postdocs in the biomedical sciences to have a balanced training in research and teaching. \*TREM is a three year future faculty postdoctoral training program providing 100% salary-benefits and tuition throughout.\*

TREM start date of August 31st 2019. The deadline is \*May 6th 2019\*. Decisions will be made before the end of May. Please find application materials and information at:

<https://cbs.umn.edu/info/postdocs/about/TREM>  
<https://cbs.umn.edu/info/postdocs/about/TREM/-application-process> A quick summary:

- 3 year NIH training program for postdocs interested in pursuing a faculty position. - 75% research : 25% teaching - Candidates must be within two years of their terminal doctoral degree, and a US citizen / permanent resident - Chose from a list of current mentors here: <https://cbs.umn.edu/info/postdocs/about/TREM/currentmentors> Thank you!

Assistant Professor Ecology, Evolution, and Behavior  
University of Minnesota 234 Cargill Building for Microbial and Plant Genomics Campus Delivery Code 6127  
1500 Gortner Avenue Saint Paul, MN 55108-1023 phone: 612-624-6143

Suzanne McGaugh <[smcgaugh@umn.edu](mailto:smcgaugh@umn.edu)>

---

## UMinnesota SpeciationTheoryGenomics

Postdoctoral Positions at the University of Minnesota, Twin Cities

We are seeking postdocs to work on an NSF-funded project on the contribution of mating system evolution to speciation. The initial hire will focus on both theoretical questions in the evolution of character displacement, speciation genetics, and mating system, and the generation and analysis of complementary population genomic data.

The project is a collaboration among three labs at the U. of Minnesota: Yaniv Brandvain (brandvainlab.wordpress.com), Emma Goldberg (umn.edu/~eeg), and David Moeller (moellerlab.wordpress.com). The project integrates field experiments, population genomics, and mathematical modeling to investigate the evolution of character displacement and reinforcement between incipient species of *Clarkia xantiana*, an annual plant with a long history of research in evolutionary biology.

Some of the major goals of the project are to (1) examine the role of natural selection in the evolution of reproductive character displacement using a combination of mathematical models and field experiments, (2) quantify the ecological and genetic costs of hybrid formation using field experiments and genomic analysis, and (3) assess the consequences of pre- and post-zygotic isolating mechanisms for genome-wide patterns of introgression. As a part of the broader project, we are sequencing and assembling the genome of *C. xantiana*.

For the initial postdoc hire, we are particularly interested in a candidate with interests in mathematical modeling and genomic analysis. The ideal candidate has expertise in one of these areas along with serious interest in developing skills in another aspect of the project. The postdoc would be expected to contribute primarily to this funded project, but would also have the freedom to develop work outside of it.

A second postdoc hire will be made in the near future. For that position, we are particularly interested in candidates with expertise in ecological genetics and field experimentation, along with interests in developing skills in genomic analysis. We would be happy to discuss this position and timing if interested.

Initial appointment will be for one year with competitive salary (\$48,426) and full benefits. Renewal for 1-2 more years is possible, pending excellent performance and mutual agreement. The start date is flexible.

Informal inquiries are encouraged, directed to any of the PIs (ybrandva, eeg, or moeller, all at umn dot edu). To apply, please assemble (i) a 1-3 page cover letter that highlights how your research interests and skills fit with this project, (ii) a CV, and (iii) names and contact information for three professional references. Materials should be submitted online at <https://humanresources.umn.edu/jobs> (Click on the tab in the center of the page that corresponds to their situation; Search Job ID# 327218). Review of completed applications will begin June 10, 2018, but candidates will be considered until the position is filled.

The Twin Cities campus of the U. of Minnesota is home to an exciting and diverse set of scientists, expertise, and resources, particularly within the Departments of Ecology, Evolution & Behavior (cbs.umn.edu/eeb) and Plant and Microbial Biology (cbs.umn.edu/plantbio), the U. of Minnesota Genomics Center (genomics.umn.edu), the Minnesota Supercomputing Institute (msi.umn.edu), and the Bell Museum of Natural History (bellmuseum.umn.edu). The campus is located in the heart of the Minneapolis-Saint Paul metropolitan area, which is rich in cultural attractions, has an extensive park system, lies close to a diverse array of natural areas, and is consistently ranked as one of the best places to live in the U.S.

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, veteran status, or sexual orientation.

Yaniv Brandvain <ybrandva@umn.edu>

---

## UNottingham 2 PopGenomicsAdaptationDuplication

2 postdoc positions are available in Population Genomics in the lab of Levi Yant

Closing Date: Friday, 10th May 2019 <https://www.nottingham.ac.uk/jobs/currentvacancies/-ref/MED115719> Our projects employ large scale population genomics, but at the same time have

explicitly phenotype-first orientations. In each case we aim to determine the genetic basis and evolutionary repeatability of adaptation to intense, quantifiable selection pressures, both environmental and intracellular. We do this by applying population genomics to wild plant populations that have evolved to overcome demonstrable hazards.

We currently focus on adaptation to genome duplication as well as adaptation to highly challenging, quantifiable environmental stressors in species ranging from *Arabidopsis arenosa*, to *Chamerion angustifolium*, to *Mimulus guttatus* and back throughout the Brassicaceae to *A. lyrata* and *A. thaliana*. We also work on polyploidy in frogs and fish. There's lots of awesome field work in the mountains and chances in interact with international collaborators too. See <http://yant.jic.ac.uk/> for more.

The role: Primary activities will include conducting large-scale population genomic projects. This includes exhaustive demographic and selection analyses of population genomic data. We require candidates who are not only motivated to run with these objectives, but who can also propose new creative project contributions. By the end of your postdoctoral term with us, we expect you to be able to, for example, begin your own group, bringing along your project from our work together. We also expect to engender the development of new directions as a result of discoveries in our group that can spur independent trajectories for your future research.

The ideal candidate: Applicants passionate about evolutionary genetics or population genomics are encouraged to apply. The successful candidate will possess a PhD and a strong relevant publication history. They will also have good knowledge of population genetics and demonstrable use of computational methods in an evolutionary context. The ideal candidate will have initiative, analytical skills, and a drive to push forward on new problems in evolutionary genomics as part of a highly collaborative team.

Candidates must hold A PhD or be near to completion of, a PhD or studying towards a PhD or equivalent in Genetics, Ecology, Evolution, Bioinformatics, or closely related area.

These full-time, fixed-term posts are available from 1st July 2019 until 30th June 2021. Job share arrangements may be considered.

Salary: pounds 27025 to pounds 39609 per annum, (pro rata if applicable) depending on skills and experience (minimum pounds 30395 with relevant PhD). Salary progression beyond this scale is subject to performance  
Additional information: To apply for this role please

include a covering letter with your application explaining your specific motivations to join the Yant Lab, as well as some specific description of your use of computational genomic or population genetic methods. This is a required element of the application process.

Informal enquiries may be addressed [levi.yant@nottingham.ac.uk](mailto:levi.yant@nottingham.ac.uk). Please note that applications sent directly to this Email address will not be accepted.

The School of Life Sciences holds an Athena Silver SWAN Award, in recognition of our commitment to supporting and advancing women's careers in the life sciences (STEMM). You can read more about this initiative at <http://www.nottingham.ac.uk/life-sciences/-documents/athena-swan-silver-award.pdf> Our University has always been a supportive, inclusive, caring and positive community. We warmly welcome those of different cultures, ethnicities and beliefs ' indeed this very diversity is vital to our success, it is fundamental to our values and enriches life on campus. We welcome applications from UK, Europe and from across the globe. For more information on the support we offer our international colleagues, visit; <https://www.nottingham.ac.uk/-jobs/applyingfromoverseas/index2.aspx> Reference: MED115719

Levi Yant <[Levi.Yant@nottingham.ac.uk](mailto:Levi.Yant@nottingham.ac.uk)>

---

## UppsalaU AncientDNA

\*Postdoctoral fellowship in ancient DNA and population genomics\*

\*Project description\*: The process of domestication has fascinated biologists since the early days of the evolutionary theory. Domestication represents observable evolutionary change in a relatively short time span making it an ideal subject to study these processes. Recent technological advances in archaeogenomics allow to study such evolutionary changes through time by obtaining genomic data from populations across time and space. The project will conduct temporal sampling of sheep populations in Central Asia in order to understand how neutral and selective processes changed these populations over time.

\*Qualifications\*: A doctoral degree in a relevant field is required at the starting date. The ideal candidate is highly motivated with a thorough education and strong interest in archaeo-/palaeogenomics, evolutionary and

population genetics. Experience in working in a molecular biology research lab is required, previous experience in working in an ancient DNA lab is a big plus. Experience with handling Next Generation Sequencing data, population genomic data analysis and scripting/programming is also advantageous. Candidates must have excellent written and oral communication skills in English.

**\*How to apply\*:** Please email your application to Torsten Gi Günther (torsten 'dot' guenther 'at' ebc 'dot' uu 'dot' se). The email should use the subject line "CTS Postdoc application" and all documents should be attached as a SINGLE PDF file. The application should include a letter of intent describing your research interests and your suitability for the position. The application should also include a CV with a publication list and other relevant achievements. Please provide contact details for at least two references.

**\*The position\*:** Starting date is September 1st or according to agreement (but no later than December 2019). This position is funded by a tax-free two year stipend (23,000 SEK per month) awarded by Carl Tryggers Foundation. The regulations of the foundation require that the candidate is an incoming postdoc (i.e. the PhD degree should not be from Uppsala University).

Please contact Torsten Gi Günther (torsten 'dot' guenther 'at' ebc 'dot' uu 'dot' se) for informal inquiries. Reviewing applications will begin on May 1st 2019 and continue until a suitable candidate is found. The final candidate will have to be approved by the foundation.

More information: <https://gunther-lab.org/postdoctoral-fellowship-in-ancient-dna-and-population-genomics/> – Torsten Gi Günther Group Leader/Forskare Human Evolution Program Department of Organismal Biology Uppsala University Norbyvägen 18C 752 36 Uppsala, Sweden <https://gunther-lab.org/> Ni Är du har kontakt med oss på Uppsala universitet med e-post så innebär det att vi behandlar dina personuppgifter. För att bli medlem i vår lista för att få mer information om hur vi behandlar dina personuppgifter, se <http://www.uu.se/om-uu-dataskydd-personuppgifter/E-mailingUppsalaUniversity> means that we will process your personal data. For more information on how this is performed, please refer to our privacy policy <http://www.uu.se/en/about-uu-data-protection-policy> Torsten Gi Günther <torsten.guenther@ebc.uu.se>

---

## UppsalaU HumanPopgenHistoryAfrica

Postdoc in population genomics and human history in Africa

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our mission is to pursue top-quality research and education and to interact constructively with society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has 44.000 students, 7.100 employees and a turnover of SEK 7 billion.

The Department of Organismal Biology teaches and explores the evolution, development and function on the organismal level. For more information see [www.iob.uu.se](http://www.iob.uu.se). Duties/Project description: The potential for understanding human evolutionary history has taken great leaps in the last few decades with the rapid development in molecular genetics and population genetic theory. The postdoc project focuses on unveiling human evolutionary history in Africa using population genomics approaches. The project integrates population genomics, ancient DNA, and computational biology, and will work with genomic data already generated within the labs.

The research will be conducted as a joint project between the Jakobsson and the Schlebusch labs at the Human Evolution research program within the Department of Organismal Biology (Evolutionary Biology Center, Uppsala University). The Human Evolution research program at Uppsala University has a broad interest in population genetics and human evolution. There are ample opportunities to work closely with postdocs and PhD students that focus on related projects. The research environment is international with English being the working language. See our web pages for more information on the research and recent publications (<http://jakobssonlab.iob.uu.se/>, <https://www.iob.uu.se/research/human-evolution>, <https://www.iob.uu.se/research/human-evolution/schlebusch/>).

**Requirements:** The ideal candidate is highly motivated with thorough education and strong interest in evolutionary genetics/genomics, population genetics and human evolution. Previous and documented experience with large-scale genetic data analysis, bioinformatics, and



computational biology is a requirement.

To qualify for an employment as a postdoctor you must have a PhD degree or a foreign degree equivalent to a PhD degree in biology, genetics/genomics and/or bioinformatics. The PhD degree must have been obtained no more than three years prior to the application deadline. The three year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc.

Additional qualifications: Formal training and a degree in mathematics, computer science and/or statistics is advantageous.

Uppsala University strives to be an inclusive workplace that promotes equal opportunities and attracts qualified candidates who can contribute to the University's excellence and diversity. We welcome applications from all sections of the community and from people of all backgrounds.

Salary: Individual salary.

Starting date: As soon as possible or as otherwise agreed.

Type of employment: Temporary position according to central collective agreement. The position is 2 years.

Scope of employment: 100 %

For further information about the position please contact: Mattias Jakobsson, e-mail [mattias.jakobsson@ebc.uu.se](mailto:mattias.jakobsson@ebc.uu.se) or Carina Schlebusch e-mail [carina.schlebusch@ebc.uu.se](mailto:carina.schlebusch@ebc.uu.se)

Please submit your application by 1 May 2019, UFV-PA 2019/962 through the link below (no direct applications through email will be accepted)

<https://www.uu.se/en/about-uu/join-us/details/?positionId=260772> — This email has been checked for viruses by Avast antivirus software. <https://www.avast.com/antivirus> När du har kontakt med oss på Uppsala universitet med e-post så innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: <http://www.uu.se/om-uu/dataskydd-personuppgifter/>

E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/about-uu/data-protection-policy>  
[carina.schlebusch@ebc.uu.se](mailto:carina.schlebusch@ebc.uu.se)

---

## UQueensland EvolutionaryGenomics

A two-year postdoctoral position is available to work with Professor Steve Chenoweth on the evolution of gene expression. The position is based in the School of Biological Sciences at the University of Queensland. The school is one of the largest most productive Biology Departments in Australia with strengths in ecology, evolution, genetics, and conservation biology. Information about the School may be accessed: <http://www.biology.uq.edu.au/>. THE POSITION

The Chenoweth research group has a number of projects underway that aim to understand how gene expression evolves in species with two sexes. Our projects combine evolutionary quantitative genetic theory with genomic experiments conducted in fruit flies. Ongoing studies include 1) understanding the contributions of cis- and trans-regulatory mutations to adaptation of the two sexes, 2) developing new population genomic approaches for detecting natural selection - a collaboration with theoretical population geneticist Tim Connallon at Monash University, and 3) understanding how pleiotropy shapes the evolution of high-dimensional regulatory phenotypes. These projects are supported through quantitative genetic studies of natural variation in allele specific expression (ASE) in *Drosophila serrata*, an endemic found in rainforests along the east coast of Australia. Our group has recently performed extensive RNA-Seq assays of regulatory variation in F1 crosses created from panels of resequenced lines sourced from both natural populations and a mutation accumulation experiment.

We seek to recruit a postdoctoral researcher with an evolutionary background in either population, quantitative, or statistical genetics who has experience working with genomic data. The successful applicant will have the opportunity to contribute substantially to these projects and there are also opportunities to develop independent research projects.

### REMUNERATION

This is a full-time, fixed term appointment for two years at Academic level A. The remuneration package will be in the range \$67,542.89 - \$90,982.26 p.a., plus employer superannuation contributions of up to 17% (total package will be in the range \$79,025.18 - \$106,449.24 p.a.). The University of Queensland also offers other competitive options including salary sacrificing, on campus childcare, leave packaging and discounted private

health insurance as well as many other benefits.

ENQUIRIES To discuss this role please contact Steve Chenoweth at [s.chenoweth@uq.edu.au](mailto:s.chenoweth@uq.edu.au). To submit an application for this role, use the Apply button at the bottom of the page at <http://jobs.uq.edu.au/-caw/en/job/507180/postdoctoral-research-fellow-in-evolutionary-genomics> All applicants must supply the following documents: Cover letter Resume

Responses to Selection Criteria in the Position Description (available at: <http://jobs.uq.edu.au/-caw/en/job/507180/postdoctoral-research-fellow-in-evolutionary-genomics>).

Applications close: 23 Apr 2019 (11:55 PM) E. Australia Standard Time

Steve Chenoweth Professor, School of Biological Sciences University of Queensland St. Lucia, QLD 4072 Australia

<https://researchers.uq.edu.au/researcher/1091>  
[https://scholar.google.com.au/citations?user=egHKf\\_oAAAAJ&hl=en&oi=ao](https://scholar.google.com.au/citations?user=egHKf_oAAAAJ&hl=en&oi=ao) Steve Chenoweth  
[<s.chenoweth@uq.edu.au>](mailto:s.chenoweth@uq.edu.au)

---

## UToronto BacterialEvolutionaryGenomics

\*Postdoctoral Position in Evolutionary Genomics of Host-Pathogen Interactions\*

A postdoctoral position for a computational biologist is available to study how bacterial pathogens evolve in the lungs of cystic fibrosis patients over the course of disease development and treatment. The project is in the laboratory of David S. Guttman in the Department of Cell & Systems Biology at the University of Toronto, Canada.. The specific project employs genomic data from >2000 longitudinal-collected strains of *Pseudomonas aeruginosa* to understand evolutionary dynamics, identify causative mutations, and predict antimicrobial susceptibility. The candidate will focus on computational analyses using evolutionary and comparative genomic, genome-wide association, and machine learning methods. There is also potential for metagenomic and microbiome investigation depending on the candidate's interests. The position is part of a multi-institution Collaborative Health Research Project funded by the Canadian Institutes of Health Research and the Natural Sciences and Engineering Research Council of Canada.

Interested applicants should have a Ph.D. (or be very close to completion) in population, evolutionary, or statistical genetics or genomics. A strong background is evolutionary biology, mathematics and / or statistics is preferred. Some computational experience is necessary. The positions is available for a minimum of two years, subject to annual review, and can be started immediately.

The Guttman lab is a highly energetic and diverse group broadly focused on bacterial evolution in the context of host-microbe interactions. The lab aims to understand how bacterial pathogens adapt to changes in disease state or treatment over very short time scales in the CF lung; the evolution of host specificity and virulence and the emergence of new pathogens using the plant pathogen *Pseudomonas syringae*; and the role of microbial communities (microbiomes) in both human and plant health and disease. The Guttman lab is also closely associated with the Centre for the Analysis of Genome Evolution & Function (CAGEF), which is a genome centre with particular expertise in microbial and plant genomics and metagenomics. The genomic and bioinformatic resources afforded by CAGEF make the Guttman lab a particularly good place to work.

To apply, please send: 1) a cover letter outlining your research interests, career goals, and previous experience; 2) a CV; and 3) contact information for three references to \*[david.guttman@utoronto.ca](mailto:david.guttman@utoronto.ca) <[david.guttman@utoronto.ca](mailto:david.guttman@utoronto.ca)>\*

More information can be found at Guttman laboratory: <https://guttman.csb.utoronto.ca/>  
<https://scholar.google.ca/citations?user=SjuNdP0AAAAJ&hl=en> The Centre for the Analysis of Genome Evolution & Function: <http://www.cagef.utoronto.ca/> Department of Cell & Systems Biology: <https://csb.utoronto.ca/> The University of Toronto is the top university in Canada and ranked within the top 20 world-wide. It provides an outstanding scientific environment with a highly interactive community of researchers. The Guttman lab and University of Toronto are strongly committed to diversity and especially welcomes applications from racialized persons, persons of color, women, Indigenous / Aboriginal People, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. Toronto is a diverse, vibrant, and cosmopolitan city; one of the most desirable in the world in which to work and live.

David S. Guttman Ph.D. Professor & Associate Chair for Research, Department of Cell & Systems Biology Director, Centre for the Analysis of Genome Evolution & Function University of Toronto Toronto, Ontario,

Canada

David Guttman <david.guttman@utoronto.ca>

---

## UWisconsinMadison PopulationGenomics

[Note - reposted due to formatting issues with a previous version, with new due date of May 15]

The research group of John Pool at the University of Wisconsin - Madison invites applications for a postdoctoral research position. There are multiple opportunities for projects to work on, with an overarching theme of addressing big questions in population/evolutionary genetics. I'd like to give the successful candidate for this position a strong voice in shaping their research direction in the lab.

Potential research areas could include:

\* 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. We are also looking at the roles of epistasis and cryptic variation in the adaptive process. We focus on local adaptation among *Drosophila melanogaster* populations from contrasting natural environments, which provides a powerful and efficient system for addressing these questions.

\* The Genetic Architecture of Reproductive Isolation Perhaps surprisingly, both viability and reproductive incompatibilities exist between African and European populations of *D. melanogaster*, which diverged only ~10 kya but now occupy very different environments. We are developing this largely untapped system as a prime model for the evolution of reproductive isolation, with an interest in both mapping specific incompatibilities and estimating genome-wide parameters relevant to this partial isolation.

\* Fundamental Population Genetics We are interested in leveraging big data (such the >1000 genomes from our *Drosophila* Genome Nexus) 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, the relative occurrence of hard and soft sweeps

on autosomes versus the X chromosome, and estimating the total number of adaptive differences between two populations.

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](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 statement of research interests (up to 1 page) addressing the intersection between your own scientific interests and the Pool lab's research, and potential projects of interest, along with a CV and contact info for 3 references.

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. Salary follows the NIH scale. Individual or family health insurance is offered.

Applications are due May 15. 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](mailto:jpool@wisc.edu)

---

## Vairao Portugal GoatMicrobiome

AgriGenomics group is currently accepting applications to fill a 30 months contract for a PhD researcher on the topic of Genome Characterization of Native Portuguese Domestic Goat and sheep and its ruminar microbiome, at CIBIO-ICETA- Research Centre in Biodiversity and

Genetic Resources, Porto, Portugal.

Preferred candidates must possess a PhD, and

a) Demonstrated scientific and/or professional experience in the area of Population Genetics/Genomics, and/or metagenomics. b) Experience in the bioinformatics analysis of next-generation sequencing (NGS) data (genomics and/or transcriptomics), including bash, R and/or python programming languages.

Please see more details using the link:

<http://www.eracareers.pt/opportunities/-index.aspx?task=global&jobId3607> The applications are formalized at the electronic address

<http://www.cibio.pt>

with following documents in a digital form, in PDF format:

i) Curriculum vitae; ii) Motivational Letter; iii) Qualifications Certificate; iv) Other relevant documentation

\*Deadline for application submission is May 3rd, 2019\*.

Albano Beja-Pereira, Principal Researcher CIBIO - Research Centre in Biodiversity and Genetic Resources Campus Agrario de Vairao, Rua Padre Armando Quintas 4485-661 Vairao, Portugal

Lucia Perez <luca@cibio.up.pt>

---

## VLIZ Belgium BioinformaticsMarineSystemsBiol

The Flanders Marine Institute (VLIZ) in Ostend, Belgium has a vacancy for a researcher. Employment can start immediately after the selection procedure and ideally not later than 1st of October 2019. Deadline for applications is 15th of May. Read full job posting here: <http://www.vliz.be/en/vacancy/14-new-research-positions-2019> Project description: Natural ecosystems are often too complex to study them under controlled laboratory conditions. Organisms interact with their environment in multifaceted ways. Our understanding of how species traits, species interactions and evolu-

tion of individual species contribute to ecosystem functions is therefore still very fragmentary. Nevertheless, we urgently need better insights in the functioning of ecosystems to predict how they will change under anthropogenic pressures such as global warming or ocean acidification.

In this research line, VLIZ aims to unravel important processes in natural plankton communities such as ecosystem functions, and mutualist and antagonistic interactions among different species using an ecosystems biology approach. Specifically, VLIZ wants to use high throughput sequencing to describe the composition (metagenomics) and functions (meta-transcriptomics) of plankton communities. This information will be used to model relevant ecosystem processes such as biogeochemical cycling. VLIZ is furthermore interested to investigate how such processes will alter under various scenarios of global change.

The study area is primarily the southern North Sea, where field surveys can readily be conducted to cover seasonal and spatial dynamics of plankton communities. Next to the regional focus, we will encourage collaboration in international consortia to work on global datasets. Within this context, VLIZ wants to address the following research questions: 1) How are plankton communities composed and which factors define their spatial and temporal dynamics? 2) Which key species and key traits can we identify using gene expression profiles? 3) How can we use meta-transcriptomics data in ecosystem models (e.g. to investigate biogeochemical processes)? 4) Can we use these models to predict the effect of anthropogenic change (e.g. global warming or ocean acidification)?

This project will be organised in collaboration with one or more Flemish university research groups. There will be a focus on high throughput sequencing and bioinformatics analysis. Mathematical modelling in a systems biology context will form another core of this research project. This research will be performed in close collaboration with a post-doctoral researcher working on the same research line.

For questions, please contact Pascal Hablutzel, head of the research unit Nature Changes & Solutions, [pascal.hablutzel@vliz.be](mailto:pascal.hablutzel@vliz.be), +32 (0)59 34 14 16

Pascal Hablutzel <[pascal.hablutzel@vliz.be](mailto:pascal.hablutzel@vliz.be)>

---

## Workshops Courses

Barcelona IntroductionToGWAS,Nov25-29 . . . . . 117	125
Barcelona PhylogeneticAnalysis Oct14-18 . . . . . 118	Naples-Italy ProteinEvolution Jul24-26 . . . . . 126
Berlin Biogeography Nov4-8 . . . . . 118	Ploen EvolutionaryBiol Sep15-17 . . . . . 126
Berlin BioinformaticsEpigenomics Oct21-25 . . . . . 119	Ploen TransgenerationalInheritance Nov6-8 . . . . . 126
Berlin BioinformaticsWithBashAndPython Oct14-18 119	Portugal PopulationGenetics May13-17 . . . . . 127
Berlin CrisprGenomeEditing Oct28-30 . . . . . 120	QuebecCity GWAS Sep9-13 . . . . . 128
Berlin IntroductionMachineLearning Jun3-7 . . . . . 121	QuebecCity SpeciationGenomics Sep2-6 . . . . . 129
Cyprus MetageneticsBiodiversity Oct2-8 . . . . . 121	SCBI Virginia ConservationBioinformatics Oct9-18 129
Edinburgh BioinformaticsWorkflowsWithSnakemake May30-31 . . . . . 122	UFlorida PositiveSelection Jul22-24 . . . . . 130
Katoomba Australia EvolutionaryGenomics Aug4-9 122	UNewcastle EvolHumanBehavior Jul29-Aug2 . . . . . 131
LakeheadU Canada aDNA May27-Jun6 . . . . . 123	UWashington ConservationGenetics Jul8-10 . . . . . 131
Madrid IntroductionToNGS Jul1-5 . . . . . 123	Venice EvoDevo Aug26-30 CallApplications . . . . . 132
Madrid StatisticalPhylogenetics Jun10-19 RegMay1 124	YaleU SustainingBiodiversityInfrastructure Jun12-14 132
Modica BioinformaticsForNGS Jul22-26 . . . . . 125	Yunnan Metabarcoding Oct15-26 . . . . . 133
Modica VideoAnalysisInvertebratesMovement Jun24-28	

---

### Barcelona IntroductionToGWAS,Nov25-29

Dear colleagues,

Transmitting Science is offering a new course:

Introduction to GWAS (Genome-Wide Association Studies), November 25th-29th, 2019, Barcelona (Spain). Instructor: Gerard Muntan (Universitat Rovira i Virgili, Spain).

Course overview:

Genome-wide association studies have become increasingly popular to identify associations between genetic risk factors and phenotypic traits.

This introductory course is addressed to medical students, social scientists, and biologists without formal training in the field. The aim of the course is to provide a guideline for conducting genetic analyses. In addition to the illustration of the standard GWAS process, we will also show how to perform functional enrichment and apply polygenic risk score (PRS) analysis in order to provide individual level scores of genetic risk.

A mix of theoretical background and hands on experience

will walk students through a series of increasingly complex data manipulation and visualization tasks. These exercises will be based on PLINK, PRSice, and R, among others, which are commonly used, freely available software tools that are accessible for novice users.

More information and registration: <https://www.transmittingscience.org/courses/genetics-and-genomics/introduction-to-genome-wide-association-studies/> Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science [www.transmittingscience.org](http://www.transmittingscience.org)  
soledad.esteban@transmittingscience.org

---

## Barcelona Phylogenetic Analysis Oct14-18

Dear Colleagues,

Registration is open for the sixth edition of the course PHYLOGENETIC ANALYSIS USING R, October 14th-18th, 2019.

INSTRUCTORS: Dr. Emmanuel Paradis (Institut de Recherche pour le Développement, France) and Dr. Klaus Schliep (University of Massachusetts, USA).

More information: <https://www.transmittingscience.org/courses/evolution/-phylogenetic-analysis-using-r/> This course is for biologists dealing with the analysis of multiple molecular sequences at several levels: Populations, species, clades, communities. These biologists address questions relative to the evolutionary relationships among these sequences, as well as the evolutionary forces structuring biodiversity at different scales. The objectives are: (i) to learn the theoretical bases phylogenetic analysis, (ii) to know how to choose a strategy of molecular data analysis at the inter or intraspecific levels, (iii) to be able to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The software used for this course will be centered on the R language for statistics. This will include the use of specialized packages particularly ape, phangorn, and adegenet.

PLACE: Capellades, Barcelona (Spain).

Organized by: Transmitting Science and the Research School in Biosystematics (ForBio).

Other Transmitting Science courses: <https://www.transmittingscience.org/courses/> With best regards

Sole

Soledad De Esteban-Trivigno, PhD Scientific Director  
Transmitting Science [www.transmittingscience.org](http://www.transmittingscience.org)

Soledad De Esteban Trivigno  
<soledad.esteban@transmittingscience.org>

---

## Berlin Biogeography Nov4-8

Course: Big data Biogeography V Species occurrences through space and time

When: 4-8 November 2019

Where: Free University of Berlin (Germany)

Summary: The public availability of large-scale species distribution data has increased drastically over the last ten years. In particular, due to the aggregation of records from museums and herbaria, and citizen science in public databases such as the Global Biodiversity Information Facility (GBIF). This is leading to a big data revolution in biogeography, which holds an enormous but still poorly explored potential for understanding large scale patterns and drivers of biodiversity in space and time.

Objectives: After this course, students will be able to:

Obtain and prepare large scale species occurrence records from public databases in R (including data mining, data cleaning and exploration) Apply novel methods for handling and processing big data in biogeographic research, including area classification, bioregionalization and automated conservation assessments

Reconstruct species ancestral ranges based on species occurrences and phylogenetic trees, using different evolutionary models Understand the potential and caveats of fossil based biogeography, and be familiar with novel methods to estimate ancestral ranges and evolutionary rates from ranges of extinct and extant taxa

For the full program, please see: (<https://www.physalia-courses.org/courses-workshops/-course48/curriculum48/>)

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](mailto:info@physalia-courses.org)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto:info@physalia-courses.org) <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> "info@physalia-courses.org"

<info@physalia-courses.org>

---

## Berlin Bioinformatics Epigenomics Oct21-25

Epigenomic Data Analysis 21-25 October 2019

Free University of Berlin (Germany)

( <https://www.physalia-courses.org/courses-workshops/course31/> )

This course will introduce researchers and technical workers to the bioinformatic analysis of large epigenomic data sets obtained using Next-Generation Sequencing (NGS) technologies, with a focus on ChIP-seq, RNA-seq and DNase-seq / ATAC-seq. The course will cover the theoretical foundations of the most widely adopted algorithms and analysis pipelines, a targeted introduction to scripting in bash and R/BioConductor, and extensive hands-on tutorials using publicly available NGS data sets. At the end of this course, the students should be able to efficiently analyze their own data and identify common pitfalls of genomics data analyses.

The course is aimed at researchers moving the first steps in epigenomic data analysis and / or interested in learning more about this subject. The course will offer a balanced mixture of lectures and hands-on practical tutorials using popular tools and R/BioConductor packages. Previous knowledge of genomics data formats from Illumina sequencers and exposure to bioinformatics is beneficial but not a necessary prerequisite.

For the full program, please see: ( <https://www.physalia-courses.org/courses-workshops/course31/curriculum-31/> )

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](mailto:info@physalia-courses.org)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto:info@physalia-courses.org) <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> “[info@physalia-courses.org](mailto:info@physalia-courses.org)”  
<[info@physalia-courses.org](mailto:info@physalia-courses.org)>

---

## Berlin Bioinformatics With Bash And Python Oct14-18

Course: Bioinformatics with Bash and Python

Where: Free University of Berlin (Germany)

When: 14-18 October 2019

Instructor: Dr. Martin Jones (founder, Python for biologists)

Overview:

A fundamental part of bioinformatics (in contrast to simply computational biology) is the idea of scaling and automation. We want to arrange our tools into pipelines which can be executed with minimal supervision. Reliable automation of this type is key to many of the things that we want from our analyses; chiefly the ability to reproduce our results, and to extend them to other datasets.

In this course we will examine two different systems for automating bioinformatic analyses. For situations where we are mostly running existing command line tools, bash scripting will allow us to build pipelines with minimal overhead. We'll start with simple command lines and see how the Linux environment - though not designed with biology in mind - is well suited to the type of automation we need.

For situations where we don't have an existing tool available, and hence need to implement our own logic, bash quickly becomes unwieldy - it's theoretically possible to write complex programs in bash, but the experience is painful! It's much better to use a more modern programming language, and for most biological tasks Python fits the bill.

PROGRAM

Monday 14th V Classes from 09:30 to 17:30

Session 1 V connecting to the server and basic Linux commands

Session 2 V assembling Linux commands into pipelines

Tuesday 15th V Classes from 09:30 to 17:30

Session 3 V introduction to bash scripting and variables

Session 4 V flow control in bash, aliases and paths

Wednesday 16th V Classes from 09:30 to 17:30

Session 5 V introduction to Python, text and files

Session 6 V lists and loops in Python

Thursday 17th V Classes from 09:30 to 17:30

Session 7 V conditions in Python

Session 8 V writing functions in Python

Friday 18th V Classes from 09:30 to 17:30

Session 9 V paired data and dicts in Python

Session 10

The afternoon of Friday 18th is reserved for finishing off the next-gen workflow exercise, working on your own datasets, or leaving early for travel.

For more information, please visit the course website: <https://www.physalia-courses.org/courses-workshops/course1/> Here is the full list of our courses and Workshops: [ <https://www.physalia-courses.org/courses-workshops/> ]( <https://www.physalia-courses.org/courses-workshops/> )

Should you have any questions, please feel free to contact us: [info@physalia-courses.org](mailto:info@physalia-courses.org)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto: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](mailto:info@physalia-courses.org)”  
[<info@physalia-courses.org>](mailto:info@physalia-courses.org)

## Berlin CrisprGenomeEditing Oct28-30

Course: Approaches and Computational tools for CRISPR Genome editing

Where: Free University of Berlin (Germany)

When: 28-30 October 2019

Instructors:

1) Dr. Luca Pinello (( <http://pinellolab.org/> )Harvard Medical School, USA)

2) Dr. Kendell Clement (( <http://pinellolab.org/> )Harvard Medical School, USA)

OVERVIEW

Clustered regularly interspaced short palindromic repeats (CRISPR) genome editing has revolutionized the ability to modify a genome of interest in a targeted and programmable way. This system has accelerated biological discovery and clinical treatments and new genome editing variants with different editing properties are being introduced at a rapid pace. A variety of computational tools have been developed to address key challenges in the design and analysis of genome editing experiments. In this course we will introduce common design and analysis strategies, as well as state-of-the-art methods and tools that attendees can use to address their own genome editing needs.

### TARGETED AUDIENCE & ASSUMED BACKGROUND

This course is aimed at researchers and technical workers who are designing CRISPR genome editing experiments or will be analyzing genome editing data. The material is suitable both for experimentalists who want to learn more about data analysis as well as computational biologists who want to learn about genome editing design and analysis methods.

The requirements for this course are:

Working knowledge of CRISPR genome editing techniques, including genome-wide screens and tiling screens.

Also a working knowledge of basic laboratory processes such as PCR, next-generation sequencing, etc.

Some experience running simple commands on a terminal (Linux, Windows, or OSX)

Please visit our website to have more information about the course content: ( <https://www.physalia-courses.org/courses-workshops/course53/> )

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](mailto:info@physalia-courses.org)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto:info@physalia-courses.org) <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> [info@physalia-courses.org](mailto:info@physalia-courses.org)



---

## Berlin IntroductionMachineLearning Jun3-7

Dear all,

we have the last 5 places available on our course “Introduction to Machine Learning” which will take place at the Free University of Berlin (Germany) from the 3rd to the 7th of June 2019.

The registration deadline is soon approaching : May 14th, 2019.

Instructor:

Prof. Paolo Frasconi (University of Florence, Italy)

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 be 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.

For more information, please visit the course 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> )

Should you have any questions, please feel free to contact us: [info@physalia-courses.org](mailto:info@physalia-courses.org)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto: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](mailto:info@physalia-courses.org)

---

## Cyprus MetageneticsBiodiversity Oct2-8

Analysis of metagenetic data for macroecology workshop

Where: University of Cyprus, Nicosia, Cyprus

When: 2nd-8th October 2019

Fees: FREE for all participants

[www.metagenecol.eu](http://www.metagenecol.eu) Workshop overview:

New sequencing methods are rapidly changing the analysis of biodiversity. Metagenetics of community, ingested or environmental samples generates high-resolution data on composition, diversity and evolutionary history in a fraction of the time of traditional methods. However, using the great flood of DNA data for macroecology requires new bioinformatics and statistical skills. This course will teach procedures for the bioinformatic processing of major types of genetic data for species composition and phylogeny. Statistical analysis of the resulting biodiversity data will then be explored for community analysis and patterns of diversity distribution. The course is unique in that it takes students from the basics of bioinformatics and data handling to advanced topics in the use of large-scale DNA data in evolutionary and ecological analysis. The course will comprise 5 days of guided practicals using real-world data, supplemented by short talks and thematic lectures. There will be open time for discussions around issues in metagenetics, with the particular aim of discussing participant queries and ideas.

Instructors:

The instructors are prominent evolutionary biologists and ecologists, who have developed many of the protocols and methodologies used in the analysis of metagenetic data for macroecology: Prof. Alfred P. Vogler (Imperial College London and the Natural History Museum, UK), Dr. Carola Gómez-Rodríguez (University of Santiago de Compostela, Spain) and Dr. Thomas J. Creedy (Natural History Museum, UK). The local workshop organizers are Dr. Anna Papadopoulou and Dr. Vasilis Promponas (University of Cyprus).

Workshop details:

There will be no fees for participants as the workshop is organized within the framework of the iBio-Gen project under the Horizon 2020 Twinning funding scheme ([www.ibiogen.eu](http://www.ibiogen.eu)). Free coffee breaks and lunch

during weekdays, as well as a free excursion on the weekend, will be offered to all participants. However, travel and accommodation costs should be covered by the participants themselves.

The course is aimed at graduate students and early-career researchers interested in applying novel DNA-based methods to macroecological questions. The course focuses on bioinformatic and analytical methods, and participants are expected to have a working knowledge of R for linear parametric statistics and basic community data analysis. Some prior experience with the linux command line is also preferred, although pre-course on-line study materials will be available to all attendees to ensure a common starting point. An understanding of phylogenetics would be useful to get the most out of some sessions. For applications, please send a Curriculum Vitae and a short motivation letter to [ibigen.project@gmail.com](mailto:ibigen.project@gmail.com) by the 30th of May 2019.

More details can be found on the website:

[www.metagenecol.eu](http://www.metagenecol.eu) Anna Papadopoulou  
<[a.papadopoulou05@alumni.imperial.ac.uk](mailto:a.papadopoulou05@alumni.imperial.ac.uk)>

---

### Edinburgh Bioinformatics Workflows With Snakemake May 30-31

Bioinformatics Workflows with Snakemake <http://genomics.ed.ac.uk/services/bioinformatics-workflows-snakemake> Where: Edinburgh Genomics (University of Edinburgh, Kings Buildings Campus)

When: 30-31 May 2019

About: Researchers needing to implement data analysis workflows face a number of common challenges, including the need to organise their tasks, make effective use of compute resources, handle unexpected errors in processing, and document and share their methods. The Snakemake workflow system provides effective solutions to these problems. By the end of this course, you will be confident in using Snakemake to tackle complex workflow problems and in your day-to-day research.

Fees: £400

Instructors: Tim Booth - Bioinformatician and Software Developer, Edinburgh Genomics

Hywel Dunn-Davies - Bioinformatician and Software Developer, Edinburgh Genomics

Katie Emelianova - Bioinformatician and Data Analyst, Edinburgh Genomics

Who should attend: This course is intended for researchers who need to automate data analysis tasks for biological research involving next-generation sequence data, for example RNA-seq analysis, variant calling, CHIP-Seq, bacterial genome assembly, etc. Attendees must have a working knowledge of how to use the Linux BASH command line. The language used to write Snakemake workflows is Python-based, but no prior knowledge of Python is required or assumed.

For more information on this and other courses see our website <https://genomics.ed.ac.uk/services/training> or get in contact with our training team at [edge-training@ed.ac.uk](mailto:edge-training@ed.ac.uk)

Kind Regards

Nathan Medd

Training and Outreach Manager - Edinburgh Genomics  
G.06, Ashworth Laboratories, Charlotte Auerbach Road,  
The King's Buildings, The University of Edinburgh, EH9  
3FL, Edinburgh, Scotland

Edinburgh Genomics' Privacy Notice can be viewed at: <http://genomics.ed.ac.uk/about-us/privacy-notice> This email and any attachments are confidential and intended solely for the use of the recipient(s) to whom they are addressed. If you have received it in error, please destroy all copies and inform the sender.

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

TRAIN [edgenomics-training](mailto:edgenomics-training@ed.ac.uk) <[edge-training@ed.ac.uk](mailto:edge-training@ed.ac.uk)>

---

### Katoomba Australia Evolutionary Genomics Aug 4-9

Workshop: Workshop on Ecological and Evolutionary Genomics

Where: Katoomba, Blue Mountains (Australia)

When: August 4th-9th 2019

Website: <https://www.weeg2019.com/>  
<<https://protect-au.mimecast.com/s/7ApzCYW86Es69EPBI9rNZd?domain=protect-au.mimecast.com>>

Overview: The Workshop on Ecological and Evolutionary Genomics will be held in the stunning Blue

Mountains of New South Wales, within the heart of the historical town of Katoomba 1.5hrs from Sydney, Australia. Topics covered will include landscape genomics, detecting selection, genomic structural variants, and DNA metabarcoding. Each day of the workshop is dedicated to a particular topic, with international and national academic presenters. Participants will gain theoretical knowledge combined with analytical skills to produce results that are relevant for conservation biology and understanding evolutionary processes. The workshop is open to PhD and Masters students, post-docs, and all levels of faculty. The workshop assumes a basic understanding and working knowledge of population and evolutionary genetics and modern sequencing technologies.

Keynote presenters:

Ary Hoffman (University of Melbourne, VIC) Brenna Forester (Colorado State University, USA) Niko Balkenhol (University of Goettingen, Germany) Maren Wellenreuther (University of Auckland/ Plant and Food Research, New Zealand) Michael Bunce (Curtin University, WA)

Registration is via application only. A statement of interest and a brief 1-page CV is required (details: [www.weeg2019.com](http://www.weeg2019.com)). Applications are to be sent to [weeg2019@mq.edu.au](mailto:weeg2019@mq.edu.au) by the CLOSING DATE APRIL 26th. Successful applicants will be invited to register within 1-2 weeks of the closing date.

This workshop is funded by the NSW Chief Scientist Conference Sponsorship Grant, The Centre for Biodiversity Analysis (ANU/CSIRO), [evomics.org](http://evomics.org) and supported by Macquarie University Workshop director: Dr Rachael Dudaniec (Macquarie University); Contact: [weeg2019@mq.edu.au](mailto:weeg2019@mq.edu.au)

[rachael.dudaniec@mq.edu.au](mailto:rachael.dudaniec@mq.edu.au)

---

## LakeheadU Canada aDNA May27-Jun6

Practical DNA Training Program:

A two-week (9 business days) intensive laboratory-based training program designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training program is offered at various times through-

out the year and we will work with you to find a suitable time for training. The cost of the training program is now \$2500.00.

The next scheduled times for the Practical DNA Training Program is: May 27 - June 6, 2019 June 17-27, 2019 July 8-18, 2019 August 6-16, 2019

For more information please contact us at 807-343-8877 or email [paleodna@lakeheadu.ca](mailto:paleodna@lakeheadu.ca) or visit our website at [www.ancientdna.com](http://www.ancientdna.com) and click on 'Training Programs'.

Thank you.

Karen.

Karen Maa Administrative Assistant

Mailing Address: Paleo-DNA Laboratory 955 Oliver Road Thunder Bay, ON P7B 5E1

Physical Address: Paleo-DNA Laboratory 1294 Balmoral Street, Suite 300 Thunder Bay, ON P7B 5Z5

Telephone: 1-866-DNA-LABS

Karen Maa <[kmaa@lakeheadu.ca](mailto:kmaa@lakeheadu.ca)>

---

## Madrid IntroductionToNGS Jul1-5

Summer course available "INTRODUCTION TO NEXT-GENERATION SEQUENCING: APPLICATIONS IN ECOLOGY AND EVOLUTION" in Madrid (Spain) July, 1st to 5th.

Dear EvolDir Community,

You can find below the information about the summer course "INTRODUCTION TO NEXT-GENERATION SEQUENCING: APPLICATIONS IN ECOLOGY AND EVOLUTION" which will take place in the Summer School of Rey Juan Carlos University, Madrid, from 1st to 5th, July. The Fundacion General CSIC and the EVOLTREE network also support the course.

The course is aimed at graduates, postgraduates and PhD students on Evolutionary Biology and related sciences, interested in knowing the new tools and the potential that is being developed with the new techniques of massive parallel sequencing. Senior researchers with aim to be introduced in NGS applications are also welcome. No specific training in bioinformatics is necessary.

The main objective of this course is to show a battery of potential applications of the NGS by researchers who are currently working with this technological approach. As an introductory course, the main purpose is not looking

for a complex or deep training in a specific technique, but to give a broad view of the available approaches.

The assistant to this course should end with the feeling of knowing the techniques and their applications, with the purpose of being able to assess which ones may be interesting for their research or on which to deepen in later stages.

The specific objectives are:

1. To present an updated information on the different NGS techniques and their applications, potential and complexity.
2. To provide basic training in the main software for each of the techniques, as well as in data processing, and give tips on how to expand knowledge. This includes from the quality analysis, edition and analysis of the files to the interpretation of results. We aim that, with this basic knowledge, the student can be trained later if he is interested in a specific aspect of the ones addressed (for example, attending specialized courses or self-taught).
3. To favour the contact between students interested in specific techniques with teachers and specialized personnel, for possible collaborations or training.

Course fees range from 10€(in house staff) to 120€(students and unemployed) - 150€(standar).

Please visit our website to have more information about the course, grants, content and online enrolment: <https://uverano.urjc.es/33221/detail/introduction-to-next-generation-sequencing.-applications-in-ecology-and-evolution.-iv-edition.html> Deadline: 30/05/2019

Alfredo García Fernández <alfrex1@gmail.com>

---

## Madrid StatisticalPhylogenetics Jun10-19 RegMay1

MADPHYLO 2019: Madrid Workshop in Statistical Phylogenetics

Where: Real Jardin Botanico (CSIC), Madrid, Spain

When: 10th-19th June 2019

[www.madphylo.com](http://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&codA&len=es> SYNTHESYS plus If you work in an EU country or a country associated with the EU Framework Pro-

grammes 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>

---

## Modica BioinformaticsForNGS Jul22-26

Where: Modica, Sicily, Italy What: Bioinformatics for Next-Generation Sequencing When: 22-26 July 2019

Outline:

Next-Generation Sequencing (NGS) has become an essential tool in genetic and genomic analysis. It is increasingly important for experimental scientists to gain the bioinformatics skills required to assess and analyze the large volumes of sequencing data produced by next-generation sequencers.

Advantages and disadvantages of current sequencing technologies and their implications on data analysis will be discovered.

This course will provide an introduction to the technology, analysis workflows, tools and resources for Next-Generation Sequencing data analysis. The content will provide insights into how biological knowledge can be derived from genomics experiments and explain different approaches to analyzing such data.

Themes:

-NGS ABCs -R-python workflow -data visualization - from code to interpretation

Instructor:

Giorgio Giurato, Ph.D. University of Salerno, Italy V Senior Bioinformatician Genomix4life V Co-founder

For more info regarding the course, please visit: <https://www.hybleatraining.com/course/bioinformatics-for-next-generation-sequencing/> or get in touch with us at: [info@hybleatraining.com](mailto:info@hybleatraining.com)

Best regards,

Pierluigi - - - HYBLEA TRAINING Pierluigi Colangeli & Silvia Lechthaler [www.\\*hybleatraining.\\*com](http://www.hybleatraining.com) [info@hybleatraining.com](mailto:info@hybleatraining.com)

pierluigi colangeli <[pierluigi.colangeli@gmail.com](mailto:pierluigi.colangeli@gmail.com)>

---

## Modica VideoAnalysisInvertebrates-Movement Jun24-28

Where: Modica, Sicily, Italy What: Video analysis of invertebrates movement When: 24-28 June 2019

Outline: In this course you will learn how to analyse the movement and behavior of invertebrates from videos. The aim is to offer you a new analytical tool to study causes and consequences of movement in small organisms, ranging from insect to zooplankton. The course will cover all the salient aspects of video analysis, starting with basic and advanced video filming techniques (data acquisition), experimental design, and analytical pipelines for testing movement and behavior under different environmental conditions, and at population and community level. Original data will be collected and analysed, plus an original dataset (<https://www.doi.org/10.4228/ZALF.DK.92>) will be explored during the course.

Themes: - filming techniques and video setup - experimental design - data extraction with R and ImageJ (BEMOVI package) - data cleaning and visualization - statistical methods of movement analysis

Audience: Biologists, zoologists, behavioral and movement ecologists, ecotoxicologists. Researchers that want to implement the study of behavior and movement in their experiments. Ideally, the attendee should have basic knowledge of R and ImageJ, however, the inexperienced users will be able to run the pipeline successfully.

Instructor: Pierluigi Colangeli, PhD candidate at BioMove (<https://www.biomove.org/>) Hyblea Training co-founder

For more info regarding the course, please visit: <https://www.hybleatraining.com/course/video-analysis-of-invertebrates-movement/> or get in touch with us at: [info@hybleatraining.com](mailto:info@hybleatraining.com)

Best regards,

Pierluigi - - - HYBLEA TRAINING Pierluigi Colangeli & Silvia Lechthaler [www.\\*hybleatraining.\\*com](http://www.hybleatraining.com) <<http://www.hybleatraining.com>> [info@hybleatraining.com](mailto:info@hybleatraining.com) +39 3405621514

pierluigi colangeli <[pierluigi.colangeli@gmail.com](mailto:pierluigi.colangeli@gmail.com)>

---

## Naples-Italy ProteinEvolution Jul24-26

Greetings from the International Summer School on °Protein Evolution: from Environmental Adaptations to Biotechnological Applications±!

We would like to introduce the upcoming edition of International Summer School on Protein Evolution (SSPE 2019) to be held at Stazione Zoologica Anton Dohrn from 24th to 26th July 2019 in the charming city of Naples. Please take a look at the preliminary programme: <https://summerschool2019.wixsite.com/-sznproteinevolution> This course is designed for PhD students and early-career researchers aiming at acquiring an interdisciplinary understanding of concepts and methods for the investigations of protein structure, function, and evolution, with insights into environmental adaptations and their potential biotechnological applications. Admission to the course will be made on a first come, first served basis and the number of participants will be limited to 22.

The course program integrates theoretical lectures with hands-on practical tutorials on molecular evolution, sequence data manipulation and alignment, protein structure, molecular modelling, docking analysis, and molecular evolution. Participants are particularly encouraged to work on their own laptop.

Attending the SSPE at the Stazione Zoologica Anton Dohrn in Naples, you will have the benefit of enjoying an exciting experience in a highly stimulating research environment and in one of the most inspiring city in the world.

Detailed information on the program of our course and online registration form for the SSPE 2019 are available at the following link: <https://summerschool2019.wixsite.com/-sznproteinevolution> Looking forward to having you as a host, please do not hesitate to contact us at [sspe1@szn.it](mailto:sspe1@szn.it) if you need any further assistance.

the SSPE 2019 Scientific Committee

Sergio Stefanni, PhD Dept. of Biology and Evolution of Marine Organisms (BEOM)Stazione Zoologica Anton Dohrn Villa Comunale 80121 - Naples Italy email: [sergio.stefanni@szn.it](mailto:sergio.stefanni@szn.it) / [ss Stefanni@gmail.com](mailto:ss Stefanni@gmail.com) office: +39 081 5833228 mobile: +39 328 9078617 skype: wkdsurfer

°Viaggiar descnta ma se ti parti mona te torni mona±  
(proverbio veneto)

Sergio Stefanni <[sstefanni@gmail.com](mailto:ssstefanni@gmail.com)>

---

## Ploen EvolutionaryBiol Sep15-17

Dear all,

I am sending this email to advertise the workshop which will be held in MPI for evolutionary biology.

The title is “Evolution of interacting populations”. In this workshop, we assemble scientists studying evolving ecological systems from mathematics and physics perspective to discuss the directions that evolution can take and how to model such systems.

Confirmed invited speakers are: Tobias Galla, Jeff Gore, Silvia De Monte, Andrew Morozov, Wenying Shou, Kalin Vetsigian. More detailed information is available at <https://workshops.evolbio.mpg.de/event/15/> . Deadline of Registration is April 30th. So, please singed up now if you are interested in our workshop!

Looking forward to seeing you in Plon (Germany).

on behalf of the organizing committee Hye Jin Park

Hye Jin Park <[hjpark@evolbio.mpg.de](mailto:hjpark@evolbio.mpg.de)>

---

## Ploen TransgenerationalInheritance Nov6-8

Dear colleagues,

This is a reminder for our meeting on “Causes and Consequences of Inclusive Inheritance”, which will take place at the Max Planck Institute for Evolutionary Biology in Plön, Germany, between the 6th and 8th of November 2019. The abstract submission is open until April 30th.

Meeting Description: Parental effects occur when the phenotype of one or both parent(s) affects the phenotype of offspring beyond the direct effects of genetic inheritance. Effects can be maladaptive, for instance, when offspring lifespan and/or reproductive success are reduced because of transgenerational senescence, or adaptive, for example, when parasite exposure of parents primes the

immune responsiveness of offspring. From a mechanistic perspective, the question which processes underlie transgenerational inheritance remains open. Moreover, from an evolutionary point of view, the fitness consequences of transgenerational inheritance and its impact on adaptation to changing environments are also mostly unknown. In this meeting, we aim to discuss examples of transgenerational inheritance in natural populations of non-model organisms, potential mechanisms underlying such patterns, as well as its evolutionary underpinnings and consequences.

Plenary speakers: Sandra Bouwhuis (Institute of Avian Research, Germany), Alexei Maklakov (University of East Anglia, UK), Eric Miska (University of Cambridge, UK), Pat Monaghan (University of Glasgow, UK), Bram Kuijper (University of Exeter, UK) & Tobias Uller (Lund University, Sweden).

Format: Plenary talks are scheduled for 30 min (25 + 5 min for questions), classic talks for 15 min (12 + 3 min for questions). Poster presenters are invited to give a 3 min flash talk at the start of the meeting to advertise their poster prior to the poster session.

Costs: We do not charge a registration fee. A limited number of travel grants will be available on a competitive basis. To apply, please explain your funding situation, indicate your motivation for joining the meeting and send your abstract and CV to [transgenin@evolbio.mpg.de](mailto:transgenin@evolbio.mpg.de).

Registration: Abstract submission is open until April 30th, registration until October 21st. We will inform participants about the outcome of abstract selection by early June. For registration and abstract submission, please use our website: <https://workshops.evolbio.mpg.de/event/14/> We are looking forward to meeting you in Plön! Kind regards, Britta Meyer (MPI, Plön), Miriam Liedvogel (MPI, Plön), Melanie Heckwolf (GEOMAR, Kiel) & Sandra Bouwhuis (Institute of Avian Research, Wilhelmshaven)

Inclusive Inheritance Workshop  
<[transgenin@evolbio.mpg.de](mailto:transgenin@evolbio.mpg.de)>

Transgenerational Inheritance Workshop  
<[transgenin@evolbio.mpg.de](mailto:transgenin@evolbio.mpg.de)>

## Portugal Population Genetics May13-17

Course Announcement / Reminder PGDH19 Population Genetics and Demographic History: model-based approaches

with Mark Beaumont, Lounès Chikhi, Willy Rodriguez, Vitor Sousa and Armando Arredondo

Key terms: Model-based Population Genetics

IMPORTANT DATES for this Course Deadline for applications: May 7th 2019 Course date: May 13th - May 17th 2019

The GTPB is proud to announce that the above referenced hands-on training course is open for applications

Admission: Candidates with adequate profile will be accepted in the next 72 hours after the application until we reach 20 participants. Course description Genetic and genomic data are increasingly used by ecologists and evolutionary biologists in general. It has thus become important for many biologists with different levels of experience to produce and analyse genetic (and genomic) data. In this course we will take a practical approach to the analysis of genetic and genomic data, but we will also provide some of the theoretical background required to understand the outputs of the software used. This course will be organised so as to mix lectures where important notions are introduced with practicals where freely available software will be used. While this will not be the focus of the course, we will also introduce and discuss genealogical (coalescent-based) simulation methods and those based on forward-in-time simulations. Altogether this will allow to discuss the potentialities and limitations of the tools available to the community.

In this five-day course we will introduce the main concepts that underlie many of the models that are frequently used in population genetics. We will focus on the importance of demographic history (e.g. effective sizes and migration patterns) in shaping genetic data. We will go through the basic notions that are central to population genetics, insisting particularly on the statistics used to measure genetic diversity and population differentiation. The course will also cover a short introduction to coalescent theory, Bayesian inference in population genetics and data simulation. We will also introduce methods that have been recently developed to analyse genomic data such as the PSMC method of Li

and Durbin that reconstructs the demographic history of a species or population with the genome of a single individual.

Most theory will be put into practice in practical sessions, analyzing real and/or simulated datasets. In these sessions, we will look at measures of genetic diversity and differentiation and use methods to infer demographic history. We will learn how to perform coalescent simulations of genetic/genomic data (using mainly Richard Hudson's ms program). We will also show how to simulate data for PSMC analyses. This will allow users to compare the PSMC obtained with real data to those obtained for the models they used. We will also look at how habitat fragmentation can be simulated using an in-house program. Some exercises will make use of R scripts (R being a freely available statistical program). Basic R knowledge is a pre-requisite but we will provide a short introduction to R. The R statistical package is a very powerful tool to analyse data outputs from many population genetics software, and can also be used to simulate genetic data under simple demographic scenarios.

More information at the GTPB website, <http://gtpb.igc.gulbenkian.pt/bicourses/2019/PGDH19/> Hoping that this course meets your interests,

Pedro Fernandes

The Gulbenkian Training Programme in Bioinformatics  
Pedro L. Fernandes, Organiser Instituto Gulbenkian de  
Ciência Rua da Quinta Grande, 6 2780-156 OEIRAS  
Portugal

“Pedro L. Fernandes” <pfern@igc.gulbenkian.pt>

---

## QuebecCity GWAS Sep9-13

Course: Introduction to genome-wide association studies (GWAS)

When: 9-13 September

Where: Institut de Biologie Intégrative et des Systèmes (IBIS); Université Laval Québec (Québec), Canada

Instructors: Dr. Filippo Biscarini (Italian National Research Council, Italy) and Eric Normandeau (Université Laval and Ressources Aquatiques Québec, Canada).

( <https://www.physalia-courses.org/instructors/t54/> )

Overview

This course will introduce students, researchers and

professionals to the steps needed to build an analysis pipeline for Genome-Wide Association Studies (GWAS). The course will, on one hand, describe all the necessary steps involved in a typical GWAS study; on the other hand, we will build a reusable and reproducible GWAS pipeline.

Format

The course is structured in modules over five days. Each day will include introductory lectures with class discussions 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, results will be interpreted and discussed in group.

Assumed Background

The course is aimed at students, researchers and professionals interested in learning how to build a structured pipeline for semi-automated and reproducible GWAS analyses. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of GWAS and bioinformatics pipeline building, progressively describing all steps and putting them seamlessly together in a general workflow. Attendees should have a background in biology, specifically genetics; previous exposure to GWAS experiments would also be beneficial.

Learning Outcomes Understanding the different steps involved in a typical GWAS analysis and how to build them together in a general workflow / bioinformatics pipeline

—  
Please visit our website to have more information about the course content: ( <https://www.physalia-courses.org/courses-workshops/course49/> )

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](mailto:info@physalia-courses.org)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto:info@physalia-courses.org) <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> “[info@physalia-courses.org](mailto:info@physalia-courses.org)”  
<[info@physalia-courses.org](mailto:info@physalia-courses.org)>



---

## QuebecCity SpeciationGenomics Sep2-6

Course: Speciation Genomics

When: 2-6 September

Where: Institut de Biologie Intégrative et des Systèmes (IBIS); Université Laval Québec (Québec), Canada

Instructors: Dr. Mark Ravinet (CEES, Univeristy of Oslo, Norway) and Dr. Joana I. Meier (University of Cambridge, UK).

( <https://www.physalia-courses.org/instructors/t54/> )

Overview

This course will provide a thorough introduction to the growing field of speciation genomics. The course aims to take students from the initial steps required for handling raw sequencing data to demographic modelling and inference of genome-wide signatures of selection and introgression. Through a combination of lectures covering key theoretical and conceptual topics, alongside hands-on exercises, participants will learn the most important computational approaches used in speciation genomics. This will include a heavy emphasis on data visualization and interpretation. After completing of the course, the participants should be able to begin using NGS data to shed light on the genomic aspects of speciation in their study system of choice.

Format

This course is designed for researchers and graduate students with strong interests in applying novel high-throughput DNA sequencing technologies to study the population genomic basis of speciation. The course will mainly focus on the analysis of NGS data for study systems for which a reference genome is available. We will provide theoretical lectures and hands-on exercises drawing on examples of whole-genome resequenced and RAD-sequencing data. Participants will make use of the UNIX command line, R and Python throughout the course.

Assumed Background

The participants should have some basic background in evolution and genomics. No programming or scripting expertise is required. Previous experience in UNIX-based command line and R is an advantage but a standard introduction will be provided. All hands-on ex-

ercises will be run in a Linux environment on remote servers. Statistical analyses will be run in R using RStudio.

Learning Outcomes

Handling NGS data from raw reads to genetic variants

Applying basic population genetic statistics

Visualizing the genetic structure

Inferring demographic history

Identifying regions under divergent selection or barriers to gene flow

Understanding the potential and limitations of different methods to detect regions under selection

—

Please visit our website to have more information about the course content: ( <https://www.physalia-courses.org/courses-workshops/course37/> )

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: ( <mailto:info@physalia-courses.org> )

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto:info@physalia-courses.org) <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> “[info@physalia-courses.org](mailto:info@physalia-courses.org)”  
[<info@physalia-courses.org>](mailto:info@physalia-courses.org)

---

## SCBI Virginia ConservationBioinformatics Oct9-18

Bioinformatics Analysis for Conservation Genomics October 9-18, 2019 Smithsonian-Mason School of Conservation, Front Royal, VA, USA

<https://smconservation.gmu.edu/programs/-graduate-and-professional/bioinformatics-analysis-for-conservation-genomics/> This course is designed to provide attendees at any career stage with a theoretical understanding of the methods used in conservation genomics along with the practical skills necessary to design and carry out the analysis component of a conservation genomics study. While an introduction to the theoretical aspects of each of the analytical

steps will be given, the emphasis of the course will be on hands-on training, enabling the participants to complete the analysis steps behind a conservation genomics study. Thus, the course will follow the format of short lectures introducing each analytical step, followed by hands-on activities during which students will complete the corresponding analysis. The course will begin with an overview of conservation genomics, comparison of different next generation sequencing platforms, and the analytical factors to consider when beginning a conservation genomics study. The rest of the course will focus on the bioinformatics analysis behind a conservation study, including: genome assembly (trimming, assembly techniques, quality assessment), genome annotation, mapping low coverage genome data to a reference genome, SNP calling, demographic analysis, and estimation of genome-wide diversity. These steps will all be accomplished with real data used in a recent conservation genomics study and performed on the Smithsonian High-Performance Computing Cluster (SI/HPC). By the end of the course, attendees will have acquired the necessary background and applied knowledge to implement genomic analyses for the conservation of endangered species.

The Smithsonian-Mason School of Conservation is a partnership between George Mason University and the Smithsonian Conservation Biology Institute (SCBI). All courses are intensive residential programs hosted in a sustainably-built Academic Center on the grounds of SCBI in Front Royal, Virginia, USA. All courses offer continuing education credits (CEUs) and some can be taken for graduate credit. Limited scholarships are available for eligible applicants. See our upcoming offerings below and check out our website (<http://SMConservation.gmu.edu>) for more course details and pricing.

Rebecca Dikow (dikowr@si.edu)

---

## UFlorida PositiveSelection Jul22-24

NSF-funded Workshop: Testing for Positive Selection in a Phylogenetic Framework using NGS-based datasets: July 22-24.

A three-day workshop will be held at the Whitney Laboratory for Marine Bioscience (University of Florida) during July 22-24, 2019. The workshop organizers, Drs. Scott Santagata and Joseph Ryan, will lead participants through a series of computational exercises having the

following goals:

Â We will provide supplementary training on aspects of Orthologous gene assignments (OrthoFinder), removing paralogous genes to establish single-copy orthologous gene alignments (PhyloPYPPruner), and multi-gene phylogenetic relationships (RAxML).

Â We will establish collaborative research groups to test for genes under positive selection from diverse organisms and habitats (e.g., polar, terrestrial, marine, tropical) using genomic and transcriptomic datasets.

Â We will evaluate current analytical methods for determining positive selection (e.g., PAML, HyPhy) and their statistical significance.

Participants are encouraged to work with their own NGS-based datasets, but sample datasets will also be provided and analyzed using a Docker-based bioinformatics platform. Applicants with transcriptomic datasets that span ecological boundaries (e.g. high vs. low latitudinal habitats, marine vs. freshwater habitats, deep vs. shallow water habitats, etc.) will be given priority. However, anyone who is interested in learning these techniques is encouraged to apply.

Lodging will be provided in the Research Village Cabins at the Whitney Laboratory (<https://www.whitney.ufl.edu/support/research-village-at-whitney-laboratory/>) at no cost to participants. Funds will also be provided to offset the costs of round trip travel based on the number of participants and demonstrated need. Participants should plan to arrive during the afternoon of July 21st and leave in the afternoon/evening of the 24th.

To apply please email [scott.santagata@liu.edu](mailto:scott.santagata@liu.edu) (due date: 06/01/19) with one attached PDF document containing: A) Current CV, B) One-page description detailing your research experiences and how this workshop fits into your overall career goals, and C) Estimated funds needed for round trip travel. Graduate students, post-doctoral researchers, and early career investigators from underrepresented groups are encouraged to apply. Applications may be accepted after the due date depending on the number of applicants and amount of available funds.

Scott Santagata, Associate Professor Department of Biology Life Sciences Building, Room 261 Long Island University-Post 720 Northern Blvd. Greenvale, NY 11548-1300 Phone:516-299-3029 Website: <https://sites.google.com/site/scottsantagata/Labpage> Researchgate: <https://www.researchgate.net/profile/Scott.Santagata> Scott Santagata <[Scott.Santagata@liu.edu](mailto:Scott.Santagata@liu.edu)>

---

## UNewcastle EvolHumanBehavior Jul29-Aug2

Dear researchers,

We are excited to announce the upcoming ALIFE Workshop on Evolution of Human Behaviour: Using Theory to Address Societal Challenges.

This workshop will explore how research on the evolution of human behaviour can be moved beyond the theoretical realm to address societal challenges. It is part of the ALIFE conference hosted in Newcastle (29th July V 2nd August).

The workshop will be organised in two parts. The first 1.5 hours will focus on the state-of-the-art theoretical and modelling work. The second 1.5 hours will discuss how this knowledge on the evolution of human behaviour can contribute to (i) improve human societies, (ii) design artificial societies, and (iii) develop the interface between them. The workshop will emphasize the role of new technology which can either conflict with previous behavioural adaptations or shape our cultural evolution. It includes topics such as:

P From the evolution of morality to ethical artificial intelligence

P From the evolution of social behaviour to sustainable socio- technical systems

P From the evolution of social learning to trustworthy media

P From the evolution of institutions to democratic societies

The committee now welcome submissions for contributed talks (10 min + 5 min question) on either the theoretical or the practical part of the workshop.

Submissions are extended abstracts (<500 words) and can describe published or novel work. The work submitted does not have to directly apply to humans but its relevance to the field of the evolution of human behaviour has to be clearly stated. Accepted abstracts will be published in a booklet hosted on this website. Submissions should be send as a single file, in PDF format only, to [ehbalife@gmail.com](mailto:ehbalife@gmail.com). The deadline for submission is Friday 14th June.

More information can be found on the website: <https://ehbalife.github.io> Looking forward to receive your

contribution,

The organising committee,

Cedric Perret, James Borg, The Anh Han, Tom Lenaerts, Simon Powers.

“Perret, Cedric” <[C.Perret@napier.ac.uk](mailto:C.Perret@napier.ac.uk)>

---

## UWashington ConservationGenetics Jul8-10

We are pleased to advertise the Conservation Genetics module of the Summer Institute of Statistical Genetics at the University of Washington. This module runs July 8-10, 2019 with instructors Dahlia Nielsen and Nadia Singh. More information on the module, including instructions for how to register, can be found at: <https://www.biostat.washington.edu/suminst/sisg2019/modules/SM1904> This new module provides training in conceptual foundations and practical aspects of data analysis to understand conservation and management of species. It will introduce the principles and applications of conservation genetics, from assessing the genetic health of individuals and whole populations to deciding on species and sub-species divisions. Students will learn foundational models in population and evolutionary genetics, as well as core methods used in genetics and genomics. Topics covered will include genetic variation, dynamics of small populations, effective population size, population fragmentation and gene flow, phylogeography, inbreeding and inbreeding depression, natural selection, ancient DNA and resurrecting extinct organisms. The module will also cover methods for developing genomic resources with an emphasis on next generation sequence data generation and analysis (RAD-seq, whole genome sequencing, transcriptome sequencing).

Dahlia Nielsen is an Associate Professor of Biological Sciences and a resident member of the Bioinformatics Research Center at North Carolina State University. Her research focuses on methods development and applications in identifying genes underlying complex traits, including gene expression responses and molecular signaling between hosts and pathogens. She has been engaged in various projects to develop genomic resources for non-model species.

Nadia Singh is an Associate Professor of Biology and a member of the Institute for Ecology and Evolution at the University of Oregon. Her research focuses on

the causes and consequences of variation in fundamental genetic processes for evolution. She is particularly interested in phenotypic plasticity in recombination and the molecular mechanisms underlying this phenomenon.

Nadia Singh <nsingh@uoregon.edu>

---

### Venice EvoDevo Aug26-30 CallApplications

Dr. Johannes Jaeger Guest Lecturer, Dept of Mol Evol & Dev, University of Vienna Associate Faculty, Complexity Science Hub (CSH) Vienna +43 664 216 02 43

Call for applications: Venice Summer School in Evo-Devo, 26-30 August 2019 <http://meetings.embo.org/-event/19-evodevo> \*Topic\*: \*Mechanism in development and evolution\*

\*Description\*: Understanding organismal development and evolution has been one of the greatest challenges for biology since its beginnings. The central aim of developmental biology is to uncover the mechanisms underlying pattern formation and morphogenesis. By extension, evolutionary developmental biology (evo-devo) is considered to be a “mechanistic” science. But what exactly is meant by “mechanism” in these contexts? What is a developmental mechanism, and how do these mechanisms cause evolutionary change?

This summer school gathers a group of world-leading empirical investigators and theoreticians from the fields of developmental biology and evo-devo together with modelers and philosophers of biology to investigate the notion of developmental mechanism and its role in the integration of developmental and evolutionary biology. This integration lies at the heart of modern biology. Its relevance goes beyond the scope of evo-devo, since an understanding of the mapping from genotype to phenotype through metabolism, physiology, and development is crucial in other fields, such as the genetic study of complex disease and organismal behaviour.

This EMBO|FEBS Lecture Course is mainly aimed at early-stage (PhD or postdoc) empirical and theoretical researchers with a general background and interest in developmental and/or evolutionary biology. More senior investigators are welcome to apply as well. Exceptions can be made for motivated masters students. Applicants from non-biology fields who have some familiarity and interest in evolutionary-developmental biology are encouraged to apply.

\*Speakers\*: Ingo Brigandt (Alberta) Graham Budd (Uppsala) James DiFrisco (Leuven) Scott Gilbert (Swarthmore) Verônica Grieneisen (Cardiff) Johannes Jaeger (CSH Vienna) Antónia Monteiro (National University of Singapore) Fred Nijhout (Duke) Virginie Courtier-Orgogozo (Institut Jacques Monod) Mihaela Pavlicev (Cincinnati Children’s Hospital) James Sharpe (EMBL Barcelona) Berta Verd (Cambridge) Günter Wagner (Yale)

Registration and abstract submission deadline: \*15 April 2019\* Notification of decision: 15 May 2019 Registration fee: 650 EUR Apply here: <https://www.conference-service.com/febs19-41/access.html> For more information please consult the event website <<http://meetings.embo.org/event/19-evodevo>>, where you can find the program, details about the application and venue, and contacts for any further questions.

Johannes Jaeger <yoginho@gmail.com>

---

### YaleU SustainingBiodiversityInfrastructure Jun12-14

Application Deadline May 17th: 3 days that will change the course of your project: Discover SBI this June

Join the NSF funded, ESA organized, Sustaining Biological Infrastructure course and discover success for your lab, field station, collection, or research program!

Spend 3 days getting hands-on experience with financial management, strategic planning, and communication skills and building your “success toolbox” to make your project more successful and sustainable.

Our alumni have shared that bringing a colleague who is working on the same project is an invaluable way to get even more out of the program. To support that, we offer a colleague discount- the second person gets \$200 off their registration.

Join us this June 12-14 at Yale University! We’re also co-located with the 3rd Annual Digital Data in Biodiversity Research Conference. Join for the whole week and save 50% on your conference registration.

The deadline is approaching: May 17th, but book early for great hotel deals.

To learn more about the course and how to apply, visit [www.esa.org/sbi/how-to-apply](http://www.esa.org/sbi/how-to-apply) Emily Mastrianni <emily@esa.org>

## 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@mail.kiz.ac.cn

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

- Kristine Bohmann (Natural History Museum of Denmark) - Frdric Boyer (LECA, CNRS, France) - Anthony Chariton (Macquarie University, Australia) - Shyam Gopalakrishnan (Natural History Museum of Denmark) - Min Tang (China Agricultural University) - Shanlin Liu (Natural History Museum of Denmark) - Douglas Yu (Kunming Institute of Zoology; University of East Anglia, UK) - 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 notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

## Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.