
E v o l D i r

June 1, 2020

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

Foreword

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

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

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



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Conferences

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MarineEvolution Postponed

Dear friends and colleagues,

It is with great regret that we must inform you of our decision to postpone (NOT CANCEL!!) Marine Evolution 2020. As you will guess, this is due to the various uncertainties we all face in the current COVID-19 situation.

At this point, we can only say that our intention is to postpone the meeting until 2021, probably around the same time of year. We'll maintain the website (<https://ccmar.ualg.pt/en/page/marine-evolution-2>) active and endeavour to provide more information as soon as we can in the coming months.

We hope that you and your loved ones are all staying safe at this time.

With best wishes from the organizing committee,

Gareth Pearson Rita Castilho Regina Cunha Andreia Pinto

Rita Castilho <rcastil@ualg.pt>

Online Choanoflagellates

Dear colleagues and friends,

We write to invite you to the 2020 Virtual Choanoflagellates-and-Friends Meeting to be held May 26/27 via Zoom. This online meeting follows on a long-running series of international choanoflagellate workshops and the online format was inspired by the recent (and very successful) Electronic Symposium on Protistology (<https://protist.online/>).

Whether you are a major fan of choanoflagellate research or just mildly curious and want to find out what all the fuss is about, please join us. There will be something for everyone – evolutionary cell biology, animal origins, tool development, microbial ecology, comparative genomics, biophysics – and special appearances from a number of “friends,” including animals, diverse holozoan protozoa, *Chlamydomonas*, and even a virus or two. We're a welcoming community and hope you'll all come join the science and fun.

Please be sure to register by May 22: <https://sites.google.com/view/virtualchoanocon2020/home>
 Choanoflagellately yours, Nicole King and Thibaut Brunet (co-organizers) University of California, Berke-

ley / Howard Hughes Medical Institute Department
of Molecular & Cell Biology nking@berkeley.edu |
t.brunet@berkeley.edu <https://kinglab.berkeley.edu/>
"tlinden@berkeley.edu" <tlinden@berkeley.edu>

Online Demographics 2

Dear Colleagues,

Please see the announcement for turning the SMTDA2020 International Conference and Demographics2020 Workshop in Barcelona into a web-conference the same dates and with the same program but via the facilities of the web conferences.

We already have done the appropriate provisions for a successful event. More information in the web at <http://www.smtda.net/>.

The deadline for Abstract submissions is set to May 15, 2020, see at <http://www.smtda.net/-abstractsubmission.html> and <http://www.smtda.net/-registrfeesexcursions.html> We already invite papers for the conference proceedings and further publications in books and journal issues. Sent submissions to secretariat@smtda.net

On behalf of the Conference Committee,
Prof. Christos H Skiadas, Conference Chair

Over the years several Books from leading publishers emerged from the SMTDA and ASMDA Conferences and events. I am happy to inform you that the basic details of the 2 collective volumes we have edited for iSTE WILEY as a result of the SMDTA2018 Conference in Chania, are now available online.

Data Analysis and Applications 3, ISBN : 9781786305343, Publication Date : April 2020 <http://www.iste.co.uk/book.php?id=1630> Data Analysis and Applications 4, ISBN : 9781786306241, Publication Date : April 2020 <http://www.iste.co.uk/book.php?id=1635>
>From ASMDA2019 in Florence, Italy Demography of Population Health, Aging and Health Expenditures. ISBN : 978-3-030-44695-6 : Vol 50 of The Springer Series on Demographic Methods and Population Analysis, Springer Nature Switzerland AG, 2020 <https://www.springer.com/gp/book/9783030446949>
"secretar@smtda.de" <secretar@smtda.de>

Online EvolutionEcol Jun1-5

Dear EvolDir,

Join us for the next week of our successful and popular online seminar series in Evolution and Ecology.

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

Now that many departmental seminar talks and conferences have been cancelled or postponed, we believe there is a great opportunity to replace that otherwise missing stimulus, and to keep our international research community connected. To that end, we are inviting some of the most exciting scientists in the community to share their research.

When: 5-6PM BST / 9-10AM PDT, up to 3 seminars/week Mon, Wed, Fri

Where: talks live-streamed to our YouTube channel <https://www.youtube.com/channel/UCMsYvoHLNVm4rbcTLj162zQ>, post your questions for our speakers via Slack

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (<https://twitter.com/EvoEcoSeminars>)

How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/-shared_invite/zt-ev4fe0io-M7B~D6p74bIV_ZRcDtmAcg
Our talks this coming week are:

Mon 1 June: No talk- Whit/Pentecost Monday

—
Wed 3 June: "C. elegans parental experiences regulate a critical decision made by the progeny"

Prof. Oded Rechavi (Dept. of Neurobiology, Tel-Aviv University, Israel)

—
Fri 5 June: "The evolution of iridescent structural colour in Heliconius butterflies"

Dr. Nicola Nadeau (Dept. of Animal & Plant Sciences, University of Sheffield, UK)

—
Please follow our Twitter feed and join the Slack group

for details of future upcoming talks.

Hope that you can join us! Feel free to circulate to anyone who may be interested!

Many thanks,

Dr. Elizabeth Duxbury Dr. Andreas Sutter Dr. Iulia Darolti Dr. Wouter van der Bijl

—
Dr. Elizabeth Duxbury Senior Postdoctoral Research Associate Prof. Alexei Maklakov Group School of Biological Sciences University of East Anglia Norwich Research Park UK

“E.Duxbury@uea.ac.uk” <E.Duxbury@uea.ac.uk>

Online EvolutionEcol May11-15

Dear EvolDir,

Our successful and popular online seminar series in Evolution and Ecology is now into its fifth week and we would like to invite you to join the online community of evolutionary biologists and ecologists, for our upcoming talks.

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

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Our talks this week are:

Mon 11 May: “How and why do sex chromosomes evolve?” Prof. Catherine Peichel (Institute of Ecology & Evolution, University of Bern, Switzerland)

—
Wed 13 May: “Ancient genomic history of dogs, wolves and humans” Dr. Pontus Skoglund (The Francis Crick Institute, London, UK)

— Fri 15 May: “The evolution of aging, the great transition, and the increasing risk of chronic disease” Prof. Stephen Stearns (Dept. of Ecology & Evolutionary Biology, Yale University, USA)

—
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Dr. Elizabeth Duxbury Senior Postdoctoral Research Associate Prof. Alexei Maklakov Group School of Biological Sciences University of East Anglia Norwich Research Park UK

Online EvolutionEcol May25-29

Dear EvolDir,

Join us for the next week of our successful and popular online seminar series in Evolution and Ecology.

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Our talks this coming week are:

Mon 25 May: "The secret of a long, fecund life: Why termite queens can live so long"

Prof. Judith Korb (Institute of Biology, University of Freiburg, Germany)

Wed 27 May: "Darwin's Question revisited: How and why species multiply"

Prof. Rosemary Grant (Dept. of Ecology & Evolutionary Biology, Princeton University, USA)

Fri 29 May: Title TBC Prof. Nicole King (Dept. of Molecular & Cell Biology, University of California Berkeley, USA)

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"E.Duxbury@uea.ac.uk" <E.Duxbury@uea.ac.uk>

Online EvolutionEcology May18-22

Dear EvoDir,

Join us for the sixth week of our successful and popular online seminar series in Evolution and Ecology.

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

Now that many departmental seminar talks and conferences have been cancelled or postponed, we believe there is a great opportunity to replace that otherwise missing stimulus, and to keep our international research community connected. To that end, we are inviting some of the most exciting scientists in the community to share their research.

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Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (<https://twitter.com/EvoEcoSeminars>) How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-dtvmr4s5-IA7td3IfBPx2JNvHWd2swg Our talks this week are:

Mon 18 May: "Evolution of genomic oddities: Making sense of transposons, satellites and germline/soma genome differences in birds"

Dr. Alexander Suh (School of Biological Sciences, University of East Anglia & Department of Organismal Biology, Uppsala University, Sweden)

Wed 20 May: "Sexual dimorphism in lifespan: the role for diet and nutrient-sensing in shaping ageing and longevity in males and females"

Dr. Jennifer Regan (Institute of Immunology & Infection Research, University of Edinburgh, UK)

Fri 22 May: "Epistasis, the spice of evolution: Insights from the plant immune system"

Prof. Detlef Weigel (Max Planck Institute for Developmental Biology, University of Tuebingen, Germany)

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“Elizabeth Duxbury (BIO - Staff)”
<E.Duxbury@uea.ac.uk>

Online Evolution Ecology May4-8

Dear EvoDir,

Our successful and popular online seminar series in Evolution and Ecology is now into its fourth week and we would like to invite you to join the online community of evolutionary biologists and ecologists, for our upcoming talks.

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

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Our talks this week are:

Mon 4 May: “Ghosts of oceans past: What can data on historical parasite burdens tell us about the future of marine disease?”

Prof. Chelsea Wood (School of Aquatic and Fishery Sciences, University of Washington, USA)

—
Wed 6 May: “The evolution of individual recombination rates in the wild”

Dr. Susan Johnston (Institute of Evolutionary Biology, University of Edinburgh, UK)

— Fri 8 May: “Darwin meets the antibiotic crisis: Can we control bacterial drug resistance evolution?”

Prof. Hinrich Schulenburg (Dept. of Evolutionary Ecology & Genetics, University of Kiel; Max Planck Institute for Evolutionary Biology, Plön, Germany)

—
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Many thanks,

Dr. Elizabeth Duxbury Dr. Andreas Sutter Dr. Iulia Darolti Dr. Wouter van der Bijl

— Dr. Elizabeth Duxbury

Senior Postdoctoral Research Associate Prof. Alexei Maklakov Group School of Biological Sciences University of East Anglia Norwich Research Park UK

“Elizabeth Duxbury (BIO - Staff)”
<E.Duxbury@uea.ac.uk>

Online Microbial Evolution Aug12-14

Dear evoldir readers,

We are organising a virtual conference from August 12th-14th to increase interactions in microbial ecology and evolution, and to support the growing cause of reducing conference carbon emission via remote conferencing. We had originally planned this conference to be entered around 5 hubs globally, but are likely to go fully virtual now, spanning multiple time-zones.

The topic of the conference will be centred around 5 themes: 1. Ecology and evolution of infection and the environment 2. Ecology and evolution of synthetic or-

ganisms 3. Quantitative impact of spatial structure
4. Cooperation, communication and conflict 5. Eco-
evolutionary dynamics in microbial communities

More information can be found on our website: <https://www.meevirtual.org/> Abstract submission deadline: June 15th Registration deadline: August 5th Conference dates: August 12-14th

Best wishes, David Baltrus (University of Arizona) Sam Brown (Georgia Tech) William Harcombe (University of Minnesota) Sara Mitri (University of Lausanne) Wolfram Möbius (University of Exeter)

sara.mitri@unil.ch

Snowbird Utah GenesAsEnvironment Nov15-18

AGA2020 REDUX!

Genes as Environment: Indirect Genetic Effects in Evolution, Agriculture, and Medicine

The American Genetic Association 2020 President's

Symposium has been rescheduled to take place Nov 15-18, 2020. We will still hold the meeting in Snowbird, Utah, but instead of spring flowers, anticipate snow on the mountaintops!

Early Registration will remain open until August 31st. Student and postdoc AGA members receive free registration if they submit a poster abstract by then, and have the chance to be selected for an oral presentation and \$300 travel award. Poster abstracts from all registrants will be accepted. AGA members receive significant discounts on symposium registration.

We hold the friendliest symposia - small meetings in lovely settings that provide great opportunities to interact with the best in the field.

Key Distinguished Lecturer Allen J Moore will open the meeting with his address, *Why we need to understand indirect genetic effects*

Invited speakers include: Nathan Bailey Amelie Baud Piter Bijma Butch Brodie Nancy Chen Niels Dingemans Kathleen Donohue Courtney Fitzpatrick Maren Friesen Andrew McAdam Joel McGlothlin Stephanie Porter David Rand Julia Saltz Michael Wade Alastair Wilson

Join us in Snowbird! <https://www.theaga.org/agatwentytwenty.htm> theaga@theaga.org

GradStudentPositions

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CityULondon CancerEvolution	9	UBergen PoLiMeRBioinformatics	15
Israel EvolutionSociality	9	UCLouvain MicrobialEvolution	15
Krakow OutbreakInsectGenomics DeadlineSoon	9	UdePau IslandMacroEvolution	16
LaRochelleU SusceptibilityAndPesticides	10	UFZ-Halle PlantPopGenetics SeedTransferZones ...	17
MemorialU CommunityPhylogenetics	11	UKonstanz 2 BirdSociality	18
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Princeton EvolutionaryBiol	13	UNEuchatel HostParasiteInteractions	19

UPorto COVID19evolution	20	UTours EvolutionSignallingProteins	23
UQueensland UExeter HostParasiteCoevolution ...	20	UZurich PlantEvolution	23
UQueensland UExeter ReproductiveInvestment	21	Vienna PopulationGenetics	24
URoehampton London EcolEvolutionBehaviour ...	22		

BarIlanU EvolutionAging

We are seeking for outstanding, highly motivated, independent, creative and enthusiastic Ph.D students for exiting research on the evolution of aging.

The research at our lab combine molecular biology and multiple omics methods. We offer strong and positive research environment with excellent opportunities for future scientific career.

Please send your application to Prof. Haim Cohen.
Faculty of Life Sciences Bar Ilan University, Israel

Haim.Cohen@biu.ac.il

Haim Cohen <Haim.Cohen@biu.ac.il>

Berlin MaxPlanck 2 MicrobialEvolution

Title: Within person evolution of infectious pathogens during disease

PI: Felix M. Key

Place: Max Planck Institute for Infection Biology, Berlin, Germany

Deadline: May 24th 2020

Lab: <http://www.mpiib-berlin.mpg.de/2003543/key-lab> Application webform: <http://www.mpiib-berlin.mpg.de/1912770/application> Description:

The human microbiome comprises trillions of bacteria that generate billions of mutations every day ' an enormous adaptive potential. While poorly understood, commensal bacteria might exploit this adaptive potential to translocate into new niches of the human microbiome where they contribute to disease. Using whole-genome sequencing cultured bacterial isolates from clinical samples combined with computational inference methods the project aims to reconstruct the within person evolution of commensal bacterial species during the initiation

and progression of infection, which can provide new strategies for intervention or treatment.

We are looking for a motivated student to work at the interface of microbiology (incl. robotic automation) and computational genetics in our new lab. The ideal candidate has a background in microbiology, genetics, bioinformatics, evolutionary biology or neighboring disciplines. Knowledge/interest in wet lab microbiology, robotic automation, and programming (python, bash, R etc.) is strongly desired.

Title: Deep evolutionary history of microbial pathogens using ancient DNA

PI: Felix M. Key

Place: Max Planck Institute for Infection Biology, Berlin, Germany

Deadline: May 24th 2020

Lab: <http://www.mpiib-berlin.mpg.de/2003543/key-lab> Application webform: <http://www.mpiib-berlin.mpg.de/1912770/application> Description:

Uncovering the deep evolutionary history of infectious microbes intertwined with human prehistory is critical for our understanding about disease emergence and the development of successful strategies for prevention and intervention. Ancient DNA provides a unique resource that allows to trace the evolution of microbial pathogens directly back in time. Using ancient DNA and big data repositories combined with evolutionary inference methods, the project aims to reconstruct genomes from infectious pathogens thousands of years old, which we leverage to understand the timing and genetic changes associated with disease emergence and spread.

We are looking for a motivated student who has a background in bioinformatics, genetics, computer science, microbiology, evolutionary biology or neighboring disciplines. Knowledge in programming (python, bash, R etc.) as well as high-throughput sequencing is strongly desired. The interdisciplinary nature of the project requires a keen interest in archaeology, anthropology and human history.

Felix-Michael Key <fkey@mit.edu>

CityU London Cancer Evolution

Two funded PhD positions are available to join the research group led by Rob Noble in the Department of Mathematics at City, University of London.

The group uses mathematical and computational models to investigate the evolution and ecology of cancer, in collaboration with experimental biologists and clinicians. Students will be funded by, and will become members of, the international Arizona Cancer Evolution Center (<http://cancer-insights.asu.edu>), which unites cancer evolution experts in London, the US, Switzerland and elsewhere. More details are available at <https://robjohnnoble.github.io>. Candidates should have (or will soon have) a good honours degree in mathematics, physics, computational biology or another scientific discipline that has equipped them with strong analytical skills, and who are enthusiastic about applying those skills to answering important biological and clinical questions. Demonstrated mathematical modelling capability, relevant biological knowledge, and programming experience (e.g. in C, Python or Matlab) are highly desirable.

Interested candidates should email a cover letter (one page), CV, transcripts, and the names of two references to robjohnnoble@gmail.com.

The positions will remain available until filled, with an initial application deadline of 5th June 2020.

The preferred starting date is October 2020.

Robert Noble <robjohnnoble@gmail.com>

Israel Evolution Sociality

The evolutionary basis of sociality

We are looking for an enthusiastic PhD student (that already has an MSc degree) for a multidisciplinary project on the evolution of cooperation in Arabian babblers. The project involves capturing, marking, sampling, observing, recording, and carrying out manipulation experiments in the Sheizaf Nature Reserve, in the Arava, Israel. The ideal applicant has a strong background in

behavioural ecology and endocrinology, field experience handling birds, and an ability to work both independently, and as part of a team. Financial support includes a scholarship from Bar Ilan University, tuition, and TAship. For more information, please contact Dr. Lee Koren (Lee.Koren@biu.ac.il). Please include a CV and a cover letter with field experience and interests. Start date: October 2020.

Thanks and best wishes, Lee

Lee Koren, PhD The Mina and Everard Goodman Faculty of Life Sciences Bar-Ilan University Ramat Gan, 5290002 Israel

Institute of Nanotechnology and Advanced Materials (Building 206) Office B-940; Lab B-935 (9th floor) Telephones: office +972-3-7384371 lab +972-3-7384372 Skype: leezik Lee.Koren@biu.ac.il <https://leekoren.wixsite.com/korenlab> <http://dsi.biu.ac.il/-team/prof-lee-koren/> Lee Koren Lab (Facebook page) @LeeKoren2 (Twitter)

Lee Koren <Lee.Koren@biu.ac.il>

Krakow Outbreak Insect Genomics Deadline Soon

PhD Student position in Population genomics of outbreaks - deadline for application approaching!

We are seeking a motivated PhD Student to join the project "Genomics of population outbreaks in an emerging model system - neutral and adaptive evolution in the spruce bark beetle", funded by the Polish National Science Centre (NCN) SONATA BIS grant.

About the project

A major goal in evolutionary biology is to understand which processes shape genetic diversity observed in natural populations. Classic population genetic theory provides a solid mathematical framework to study genetic variation and predict efficacy of natural selection relative to drift in equilibrium conditions, for example under constant population size. However, the majority of natural populations often experience large size fluctuations that make prediction less straightforward. The main purpose of this project is to test how extreme fluctuations in population size of outbreaking species affect the dynamics of neutral and adaptive genetic variation. Many pests experience epidemic outbreaks characterized by sudden changes in population size, often spanning

orders of magnitude. Such outbreaks are known from ecological studies of closely monitored species of economic importance. However, little is known about how genetic variation changes during outbreak cycles. Specifically, the rate of adaptive evolution during relatively short periods of large population size remains unknown. This can be studied in species which experience extreme fluctuations of population size, such as spruce bark beetle (*Ips typographus*). Spruce bark beetle is the most destructive pest of Norway spruce forests because under specific conditions (e.g. storms) populations may outbreak, causing mass mortalities of spruce stands. We will compare populations of spruce bark beetle that have experienced frequent, recent outbreaks and populations that did not experience outbreaks in the recent past. By combining existing knowledge on biology and ecology of the species with newly generated, large-scale genomic data, we will address specific questions about the relationship between genome-wide variation and fluctuating effective population size: How outbreaks affect species genetic structure? Are adaptations in frequently outbreaking populations mainly driven by soft sweeps? How demographic history of the spruce bark beetle and historical fluctuations of effective population size over time affect current patterns of neutral and adaptive variation and more.

The PhD student will be working with large, whole genome resequencing data obtained from several populations and >500 individuals. The samples are being collected and the sequencing is planned for autumn 2020. Thus, the student will be able to work with the data shortly after he/she starts his/her PhD studies. The PhD student will analyse whole-genome variation patterns including differentiation, divergence and recombination rate variation along the spruce bark beetle genome. The PhD student will also infer spruce bark beetle's demographic history using coalescent-based simulations. The PhD student will gain a wide range of scientific experience including genome-wide sequence data analysis as well as demographic history modelling and will be encouraged to develop his/hers own projects using extensive datasets available.

About the place and salary

The student will be based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe - Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland (www.eko.uj.edu.pl/en_GB). Krakow is a beautiful city with a dynamic cultural life (European City of Culture 2000; more than 100 festivals and other events organized every year; modern museums, cinemas, theaters, restaurants etc). It has good access to outdoor activities (biking, hiking and more) and is well-connected to the rest of Europe.

The PhD student will be supported by a 48-month, tax-free research stipend: 4500 PLN (~1050 EUR) per month. This stipend may be combined with the standard PhD program scholarship (for those that will pass the entrance exam to PhD graduate school at Institute of Environmental Sciences, approximately 2200 - 3500 PLN). Note that in Poland, the living costs are relatively low (check out a cost-of-living calculator such as www.numbeo.com) and even without additional funding from graduate school the salary is more than enough to fully enjoy life in Krakow.

Requirements

The successful candidate will have an M.Sc. degree in a relevant field by October 2020. We are looking for a student with strong interest in Evolution, Molecular Ecology, Population Genetics and/or Genomics as well as experience with, or a keen interest in learning, Bioinformatics and Computational Biology; and strong English language, communication, 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>

LaRochelleU Susceptibility And Pesticides

General information

Reference : UMR7372-FREANG-002 Workplace : VILLIERS EN BOIS Date of publication : Monday, May 04, 2020 Scientific Responsible name : Frédéric Angelier, Clémentine Fritsch, François Brischoux Type of Contract : PhD Student contract / Thesis offer Contract Period : 36 months Start date of the thesis : 1 October 2020 Proportion of work : Full time Remuneration : 2 135,00 euro gross monthly

Description of the thesis topic

What is the role of pesticides in the susceptibility of vertebrates to pathogens?

The concept of “One Health” is based on an integrative approach to human, animal and environmental health. It stems from the fact that the majority of emerging diseases are of animal origin and result from ecological imbalances. In this context, the study of the impact

of pesticides on ecosystems, wildlife and human health takes on its full meaning. Indeed, it is now obvious that pollutants, by disturbing ecological balances, impact the dynamics of various diseases. Moreover, these pollutants are often major endocrine and immune disruptors that can therefore increase susceptibility to these diseases.

In this context, this thesis project aims to improve the understanding of the processes and practices responsible for the emergence of resistance in pathogens, taking the example of aspergillosis in birds and the use of fungicides as phytosanitary products. It thus aims to define situations at risk of emergence and spread of resistant infectious pathogens to wildlife and humans. This thesis project will test the hypothesis that environmental fungicide contaminations in agroecosystems increase the presence and occurrence of resistant strains of aspergillosis in the environment. It will examine whether fungicides adversely affect the health of common birds by weakening their physiological systems and increasing the emergence of resistant strains of aspergillosis. This thesis project will be based on an interdisciplinary approach linking ecotoxicology, physiology, functional ecology, environmental and analytical chemistry, and molecular biology. The two objectives of the thesis will be the following:

Obj. 1: Degree of fungicide contamination and resistant strains in anthroposystems The objective will be to identify within anthroposystems (1) the degree of fungicide contamination and (2) the occurrence of aspergillosis and resistant strains. The fieldwork will take place in wine-growing and urban areas where fungicide treatments and the occurrence of aspergillosis are important. A dozen viticultural, urban and forest sites with a gradient of fungicide use will be selected. On these sites, non-lethal blood samples will be taken from common birds. These measurements will make it possible to measure the degree of contamination of the ecosystem and relate it to the occurrence of aspergillosis and resistant strains.

Objective 2: Experimental study of the influence of triazoles on pathogen resistance The objective will be to understand the additional risk that fungicide contamination may pose to organisms exposed to pathogens. For this purpose, captive birds kept in experimental aviaries at the CEBC will be exposed to environmental doses of triazoles while other unexposed birds will form a control group. Following this exposure, the functioning of the physiological systems involved in pathogen resistance will be examined (immunity, hormonal axes) in order to detect the potential for endocrine and immune disruption of fungicides. This experiment will be conducted in adult birds, but also in developing chicks to test the potential deleterious effect of these fungicides on the

ontogeny of these key physiological systems.

Financial support and valorization The thesis project is part of the PEPSAN (PI: C. Fritsch, MITI, Mission pour l'interdisciplinarité du CNRS) and BIODITOX (PI: F. Brischoux, ANSES) projects which will provide financial support for the missions and analyses related to this thesis. The project will rely on the expertise of the thesis directors in ecophysiology and ecotoxicology and on the means made available at the CEBC (biological analysis platform, experimental aviaries). The work will be promoted through scientific publications in international journals and participation in conferences. The results will also be transmitted to decision-makers via the network of supervisors.

Work Context

The student will be part of the Evolutive Ecophysiology team of the Centre d'Etudes Biologiques de Chizé (UMR 7372, CNRS, La Rochelle University, 79360 Villiers en Bois) where he will be based. It will be attached to the Euclide Doctoral School (La Rochelle University). The student will carry out his thesis under the supervision of F. Angelier (CEBC), C. Fritsch (LCE, Chrono-Environnement laboratory, Besançon) and F. Brischoux (CEBC). The fieldwork will be done in connection with CEBC (CNRS, Chizé),

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

MemorialU CommunityPhylogenetics

I am seeking a motivated MSc or Ph.D. student to conduct a study that aims to understand the phylogenetic diversity of the flora of Newfoundland, and the phylogenetic structure of different habitat types in this island of the north Atlantic. Knowledge of how phylogenetically diverse the flora is in different areas will inform conservation actions in the province. The role of plant traits on the historical assembly of these plant communities could also be addressed, and other hypotheses of the student's interest. The student will reconstruct a species-level phylogeny of the 1,300 native plants of Newfoundland using publicly available DNA sequences. The student will work under the mentorship of Dr. Julissa Roncal,

and collaborate with Dr. Michael Burchinski and Dr. Susan Meades. Check out the Flora of Newfoundland website <https://newfoundland-labradorflora.ca/> Student's qualifications: - A BS degree with Honours or MSc degree in a related discipline (e.g. biology, botany, conservation, ecology, molecular biology, bioinformatics) - Strong knowledge of phylogenetic and phylogenetic comparative methods, ability to code in R. - Experience in organismic botany, ecology, and conservation 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 2020 or January 2021. The MSc and Ph.D. program comprises two and four years with an annual stipend of \$19,000 and \$20,500, respectively. If GPA is >85% student can get an additional \$5,000. The student is expected to assist in teaching laboratories for 60 hours during the fall and winter semesters, but not in the spring/summer. 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. Position fully funded by NSERC.

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. Only students who are short listed will be contacted for a skype interview. For more information on the research group visit: <https://julissaroncal.wordpress.com/about-me-2/> For instructions on how to apply to Memorial's graduate program visit: <http://www.mun.ca/become/graduate/apply/-index.php> - Julissa Roncal, Ph.D. Associate Professor and Curator of the Ayre Herbarium Department of Biology Memorial University of Newfoundland 232 Elizabeth Avenue St. John's, NL, A1B 3X9, Canada Office SN4102, phone (709) 864 2241 Laboratory SN4096-4097, phone (709) 864 2093 Ayre herbarium (709) 864 6233 Mobile: (709) 351 6771 <http://julissaroncal.wordpress.com/> she/her

Julissa Roncal <jroncal@mun.ca>

Poland MIZ CanidEvolGenomics

A fully-funded PhD position is available in a research group led by dr Malgorzata Pilot at the Museum and Institute of Zoology, Polish Academy of Sciences. The group specialises in mammalian evolutionary genomics, and the PhD project will be focused on hybridisation between representatives of the genus *Canis*. The position is available for four years, with the start date of 1st of October 2020. The research group is based at the Research Station of the Museum and Institute of Zoology in Gdańsk, and maintains strong links with the main research facilities of the MIZ in Warsaw.

Required skills and qualifications - MSc degree in biological sciences or a related area, awarded or to be awarded before October 2020 - Good theoretical knowledge of population genetics - Experience with molecular genetics labwork and the analysis of DNA sequence data - Good knowledge of English - Knowledge of programming will be an advantage

Scope of work - Laboratory work to prepare DNA for the SNP genotyping and Next Generation Sequencing (including DNA extraction and quantification, preparation of libraries, operation of the Pacific Biosciences sequencer) - Population genetic analyses of the data produced to characterize the hybridisation patterns - Preparation of research papers describing the study results and contribution of the work on research papers as a team member - Participation in lectures and other activities being part of the PhD studies curriculum

Enrollment conditions The PhD student will be based at the Research Station of the Museum and Institute of Zoology in Gdansk. The PhD studentship will commence on the 1st October 2020 and is expected to be completed with the thesis submission within 4 years. A tax-free stipend is available for the 4 years of the PhD studies and is not extendable. The stipend is sufficient to cover life expenses of a single person and assures a good standard of life in Poland. The successful candidate will be enrolled as a PhD student in the Bioplanet Doctoral School of the Polish Academy of Sciences. The School does not charge tuition fees. The School provides obligatory and optional classes for PhD students, which are run in English. Travelling from Gdansk to Warsaw will be required to attend the classes. The classes are scheduled so as to minimize the number of travels required.

Research environment The research at the MIZ is focused on a broad range of themes in animal biology, including systematics, biogeography, evolutionary biology, ecology and population genetics. Małgorzata Pilot's research group is part of the Laboratory of the Molecular and Biometric Techniques led by Prof. Wiesław Bogdanowicz, grouping researchers focused on population genetics, phylogeography and evolutionary genomics of a broad range of animal taxa. MIZ laboratories contain modern equipment for genomic analyses, including Pacific Biosciences RSII long-read sequencer and Illumina MiSeq System. The state-of-the-art ancient DNA laboratory carries out work on mammalian palaeogenetics. The Museum's zoological collection is among the largest and most valuable in Europe.

How to apply The following documents are required in the application: - MSc degree certificate, or a document confirming your enrollment in a MSc programme together with a letter from the MSc supervisor stating the expected completion date. - CV including the list of publications and/or manuscripts in preparation, with the following statement provided at the end and signed:

"I give my consent to the processing of personal data provided in my application documents by the Museum and Institute of Zoology PAS for the purpose of the recruitment process, pursuant to the Personal Data Protection Act of 10 May 2018 (Journal of Laws 2018, item 1000) and in agreement with Regulation (EU) 2016/679 of the European Parliament and of the Council of 27 April 2016 on the protection of natural persons with regard to the processing of personal data and on the free movement of such data, and repealing Directive 95/46/EC (General Data Protection Regulation; L 119 from 04.05.2016)". Applications that do not include this statement will not be considered.

- Motivation letter (no longer than one A4 page) - Contact details of two persons who can be contacted for references.

These documents should be sent to the project supervisor, Dr Malgorzata Pilot (mpilot@miiz.waw.pl) no later than 4 June 2020. The title of the message should be "Application for a PhD position in canid genomics". Informal inquiries can be also addressed to Małgorzata Pilot.

Selection procedure The candidates will be assessed based on the information in the submitted documents. The shortlisted candidates will be invited for an interview, which will be carried out via Skype. The selected candidate will be requested to submit the application to the Doctoral School and attend the oral entry exam (via Skype or in person).

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Princeton Evolutionary Biol

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 8-10, 2020 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 June 15th. 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.

Webinars offering information on the EEB Scholars program, including guidance on the application process, will be held on May 19th 2020 and June 2nd at 1:30pm EST. Click here to register < <https://forms.office.com/Pages/ResponsePage.aspx?id=-FgH2LzF0XUK1rwd9d5G9pJZG14jvNndEtdb6ac1DMTBUNldZTTc2S> >

Please direct any questions to EEB.Scholars@princeton.edu.

Cheers,

Beth Leman Program Administrator Department of Ecology and Evolutionary Biology (EEB) B15@princeton.edu 609-258-2798 (o) 973-610-1428 (m)

"Beth E. Leman" <b15@princeton.edu>

TexasAMU Computational Genomics

A computational systems biology lab (<https://www.genomezoo.net/>) at Texas A&M University, College Station, has an opening for a PhD student.

You will be working on developing machine learning tools for single-cell data analyses—They will teach you how to do it.

They are looking for:

Motivated candidates with expertise in evolutionary genetics, functional genomics, bioinformatics, translational medicine, or a related field. or Motivated candidates with expertise in machine learning, computer science, data science, statistics, or a related field.

To apply, please email Dr. James Cai (jamescai@genomezoo.net) with your information and GitHub handle.

James Cai, Ph.D. Associate Professor Department of Veterinary Integrative Biosciences Department of Electrical & Computer Engineering (affiliated) Texas A&M University College Station, TX 77843-4458 Tel (979) 458-5482 | Fax (979) 847-8981 jcai@tamu.edu

James Cai <jamescai@genomezoo.net>

UBergen PoLiMeR

PhD position in experimental and computational sciences for the Marie-Curie Innovative Training Network “PoLiMeR”

Start date: Negotiable, position open until filled

Host: Department of Biomedicine, University of—Bergen, Norway (<https://www.uib.no/en/biomedisin>)

The PoLiMeR consortium (Polymers in the Liver: Metabolism and Regulation) has identified the inherited, liver-related diseases of glycogen and lipid metabolism as the ideal starting point for innovative research training in personalised ‘Medicine’. These diseases are life-threatening for children. Since each specific disease is rare, research efforts are diluted. Our system-based perspective opens possibilities for the application of novel

drugs and diagnostic tools to a range of different diseases. For more details, see: <http://polimer-itn.eu/> Activities and responsibilities The project for this position investigates the interplay between coenzyme and energy metabolism in fatty-acid oxidation defects. The host organization is the Department of Biomedicine at the University of Bergen, Norway. The PhD student will experimentally study NAD and CoA coenzyme metabolism in patient-derived and genetically engineered cell lines using advanced mass-spectrometry-based techniques.

Qualification profile Eligible candidates for a PhD position in the PoLiMeR training network should have the following qualifications: A master’s degree in a discipline relevant to this PhD position (at the time of application, the thesis must be submitted) Strong background in biochemistry of metabolism and motivation for scientific research in an interdisciplinary and international environment Excellent English presentation and writing skills Good organizational and communication skills, being a team-player

Successful candidates must fulfil the criteria defined by the European Commission: As an Early Stage Researcher, you have to be in the first four years of your research career and have not been awarded a doctoral degree at the time of recruitment. At the time of recruitment by the host organization, researchers must not have resided or carried out their main activity (work, studies, etc.) in the country of their host organisation for more than 12 months in the 3 years immediately prior to the reference date.

Applicants should send a motivation letter, CV and documentation of their degree(s)

We offer As a PhD student in this project you will be part of a highly international consortium of young researchers. You will have your individual research project at your host organization, focusing on your discipline of interest. To complement your specialized training, you will do internships at a complementary PoLiMeR partner organization. In addition, you will follow advanced interdisciplinary courses by leaders in the field of Systems Medicine. Thus, you will be trained to become a Systems-Medicine expert, with expertise in computational and wet-lab techniques, who can collaborate between clinical, academic, and industrial environments.

Send application to info@polimer-itn.eu

Project Info: Prof. Mathias Ziegler mathias.ziegler@uib.no

UBergen PoLiMeRBioinformatics

PhD position in experimental and computational sciences for the Marie-Curie Innovative Training Network “PoLiMeR” (Bioinformatics)

Start date: Negotiable, position open until filled

This is one of two PhD positions currently advertised.

Host: Department of Biomedicine, University of—Bergen, Norway (<https://www.uib.no/en/biomedisin>)

The PoLiMeR consortium (Polymers in the Liver: Metabolism and Regulation) has identified the inherited, liver-related diseases of glycogen and lipid metabolism as the ideal starting point for innovative research training in personalised ‘Medicine’. These diseases are life-threatening for children. Since each specific disease is rare, research efforts are diluted. Our system-based perspective opens possibilities for the application of novel drugs and diagnostic tools to a range of different diseases. For more details, see: <http://polimer-itn.eu/>

Activities and responsibilities The project for this position investigates the interplay between coenzyme and energy metabolism in fatty-acid oxidation defects. The host organization is the Department of Biomedicine at the University of Bergen, Norway. The PhD student will use bioinformatics tools to identify alterations of NAD and CoA coenzyme metabolism in patient-derived and genetically engineered cell lines. Experimental data needed for the analyses are generated in the host group and throughout the consortium. Qualification profile Eligible candidates for this PhD position should have the following qualifications: A master’s degree in a discipline relevant to this PhD position (at the time of application, the thesis must be submitted) Strong motivation for scientific research in an interdisciplinary and international environment Excellent English presentation and writing skills Good organizational and communication skills, being a team-player

Successful candidates must fulfil the criteria defined by the European Commission: As an Early Stage Researcher, you have to be in the first four years of your research career and have not been awarded a doctoral degree at the time of recruitment. At the time of recruitment by the host organization, researchers must not have resided or carried out their main activity (work, studies, etc.) in the country of their host organisation for more than 12 months in the 3 years immediately

prior to the reference date.

Applicants should send a motivation letter, CV and documentation of their degree(s)

We offer As a PhD student in this project you will be part of a highly international team of young researchers. You will have your individual research project at your host organization, focusing on your discipline of interest. To complement your specialized training, you will do internships at a complementary PoLiMeR partner organization. In addition, you will follow advanced interdisciplinary courses by leaders in the field of Systems Medicine. Thus, you will be trained to become a Systems-Medicine expert, with expertise in computational and wet-lab techniques, who can collaborate between clinical, academic, and industrial environments.

Send application to info@polimer-itn.eu

Project Info: Prof. Mathias Ziegler mathias.ziegler@uib.no

UCLouvain MicrobialEvolution

PhD position in Microbial Ecology, Evolution, and Physiology

We are looking for a highly motivated candidate to apply for a PhD position, funded through UCLouvain, in the labs of Profs Bertanne Visser, Caroline Nieberding (UCLouvain, <https://visserlab.be>; <https://nieberdinglab.be/>) and Ellen Decaestecker (KU Leuven, www.kuleuven-kulak.be/aquaticbiology/-EllenDecaestecker).

Fat synthesis and associated pathologies have recently been linked to the gut microbiota in humans. Surprisingly, little is known about the role gut microbiota play in fat synthesis of insects. Using the parasitic wasp *Nasonia vitripennis* as a model, this project aims to test the hypothesis that gut microorganisms affect fat synthesis in wasps. We will use laboratory and field-collected populations to determine to what extent there is plasticity in fat synthesis (using stable isotope tracing and Gas Chromatography-Mass Spectrometry). We will further use molecular techniques to characterize the microbial community, as well as comparative metagenomics (using Next Gen Sequencing) to identify the genes that affect fat synthesis in the host.

The ideal candidate for this position will have a strong background in ecology and evolution, as well as an inter-

est in molecular biology and physiology. The candidate will be able to obtain skills in collecting host wasps from the field, rearing and manipulating host wasps and their endosymbionts, molecular techniques (DNA extraction, PCR amplification, analyzing DNA sequences), physiological measurements (determining fat content, stable isotope tracing and analyzing fatty acid profiles obtained with mass spectrometry), planning and designing experiments, as well as writing and presenting research findings.

The deadline for applications is July 1st 2020. The position will start September 1st 2020 (with some flexibility, but at the latest October 1st 2020) and the applicant should have obtained a MSc diploma no later than September 1st, 2020. Current funding is available to hire the PhD candidate for a duration of 15 months. The candidate is expected to actively contribute in obtaining additional funding sources for the remainder of the PhD project, with help of the PhD supervisors, for which several national funding options are available.

The salary will be around 2000 euro net per month, including benefits (e.g., health insurance), which are included in the Belgian system. Our Universities are Equal Opportunity/Affirmative Action Employers, in both the French and Dutch-speaking regions of Belgium, but the language for meetings and scientific interactions is English. For background information about our universities, see <https://uclouvain.be/en/index.html> and <https://www.kuleuven.be/kuleuven/>. Applications should be sent to Bertanne Visser (bertanne.visser@uclouvain.be) and must include 1) a motivation letter, including a statement of interests; 2) full CV, including list of publications, if available; 3) Contact details of at least 2 referees.

Prof. Dr. Bertanne Visser, F.R.S.-FNRS Research Associate Evolution and Ecophysiology group Biodiversity Research Centre Earth and Life Institute UCLouvain Croix du Sud 4 1348 Louvain-la-Neuve Belgium bertanne.visser@uclouvain.be <https://visserlab.be> We support the Peer Community In. Check us out at <https://peercommunityin.org/> “bertanne.visser@uclouvain.be” <bertanne.visser@uclouvain.be>

UdePau IslandMacroEvolution

PhD Project: Emerging Macroecological and Macroevolutionary Patterns of Island Radiation: A Global Assessment.

Understanding the origin and maintenance of biodiversity is a key issue in macroecology and macroevolution. In this quest, islands along with the exceptional species radiations (rapid episodes of diversification from a common ancestor) they harbor have always served as testing ground for ecological/evolutionary theories. Despite recent accumulation of data for islands, we still lack a synthetic view of what island radiations are and no formal extensive comparative analysis across island systems and lineages has been yet achieved. By means of meta-analysis, this PhD intends to perform a first global assessment of island radiation in order to estimate the tempo and mode of diversification among lineages and archipelagos and to further examine the relationships between diversification patterns, emerging community structure and biogeographic processes. At first, the project will focus on oceanic archipelagos (islands formed over oceanic plates and never connected to continental landmasses) since they harbor most of the spectacular radiations reported in the literature. In the course of the research project, other types of islands or island-like systems (continentals, mountains tops) might be taken into consideration. Overall, we expect this project to provide strong baseline information regarding the eco-evolutionary processes structuring island communities.

The Université de Pau et des Pays de l'Adour (UPPA) is a leading research and teaching university, among the top 20 universities in France, located in the beautiful, culturally rich and highly diverse area of the Atlantic Pyrenees (<https://www.pau-pyrenees.com>). UPPA has been recently labeled as Université d'Excellence as part of the Future Investments program launched by the French government with the core scientific domain spanning over all areas of Energy and Environment (<http://www.e2s-uppa.eu>). Within UPPA, the laboratory IPREM is Joint Research Unit CNRS / UPPA (UMR 5254) with members interesting in the development of fundamental knowledge in chemistry, microbiology, environmental and ecological sciences, in relation to applications concerning the management of the environment in a context of global change. The PhD supervisor (Assistant Professor in Biostatistics/Community Ecol-

ogy - STEE/IPREM) is an ecologist with broad interests in island biogeography, community ecology, macroecology and biostatistics. He is also an external collaborator of the Centre for Ecology, Evolution and Environmental Changes (cE3c) of the University of Lisbon. The PhD project will also capitalize on long-term, and ongoing, collaborations established between the PhD supervisor and several close collaborators in the field of island ecology, specifically in the Universidad Autónoma de Madrid, Finnish Museum of Natural History, University of Azores, Oxford, Birmingham and Athens. In the course of the PhD project, the student will be able to apply for International Doctoral Mobility Grants in UPPA to undertake collaborative work with researchers aboard for up to 6 months.

The deadline for applications is 15th June 2020, with a possible start date from October 2020 onwards. The student will receive a monthly gross salary of 1768 euro + extra gratification for teaching duties 32 hours per year. Applicants from all countries are eligible. An MSc or equivalent is required as well as good knowledges of ecological, evolutionary and biogeographical processes.

Desirable: - Experience with ecology, evolution and/or biogeography. - Prior experience with data analysis in R - Prior experience with phylogenetic inference software will be advantageous - Very good spoken and written English communication skills For more information, please contact françois.rigal@univ-pau.fr

To apply please send one document comprising a CV, Cover letter, Copy of the diploma, Candidate's MSc or equivalent (marks and ranking), Letters of recommendation, Contact details for two references to françois.rigal@univ-pau.fr

frigal001 <françois.rigal@univ-pau.fr>

UFZ-Halle PlantPopGenetics SeedTransferZones

The Helmholtz Centre for Environmental Research (UFZ) with its 1,100 employees has gained an excellent reputation as an international competence centre for environmental sciences. We are part of the largest scientific organisation in Germany, the Helmholtz association. Our mission: Our research seeks to find a balance between social development and the long-term protection of our natural resources.

The UFZ's Community Ecology— Department is offering a PhD position in the project RegioDiv to investigate genetic variation of grassland plant species used in regional seed production systems. To this end, we are seeking an enthusiastic person for the following topic.

PhD position (m/f/x) Genetic variation of plant species for regional seed production - Project RegioDiv Working time: 65% (25.35 hours per week), limited to 3 years Your tasks:

From March 2020 onwards the use of native origins is mandatory according to §40 BNatSchG if plants are established in the wild. Seeds from regional seed production ("Regiosaatgut") is often used, which is produced in 22 regions of origin. The regions of origin were defined without considering empirical data on spatial genetic structure of plant species. The project will establish empirical knowledge about genetic variation of grassland plant species and will draw conclusions for the system of regional seed production.

You will analyse 25 representative plant species used in regional seed production. In each of the regions of origin several populations will be assessed. You will contribute to plant collection including coordination of sampling by volunteers. You will genotype plant samples with SNP markers using next-generation sequencing techniques and ddRAD protocol. Based on the broad sample, population genetic structure will be analysed for each species. Across species you will analyse whether spatial-genetic differentiation shows general, species-group specific or species-specific patterns and which biogeographic and environmental factors are likely causal. Moreover, the congruence of spatio-genetic groups with the regions of origin will be assessed. Ultimately we will consider which practically relevant suggestions can be drawn from the results with respect to legal specifications concerning the use of native seed.

Your profile: -Master's degree or equivalent in biology, geocology, or geography, or a related field -Solid knowledge of population genetics/genomics of plants -Knowledge of central European grassland plant species. -Data analysis skills, including bioinformatics analysis of NGS data -Knowledge of scripting languages like R— is an advantage -Proficiency in German to manage sample collection with volunteers -Proficiency in English -Ability to work in an interdisciplinary team, organising abilities and willingness to collaborate with national and international partners

We offer: -Top level interdisciplinary research at a research centre which enjoys an excellent reputation within Germany as well as internationally - Excellent technical facilities -Work in inter-disciplinary and multinational teams -Excellent links to national and international research networks -Support and optimal training courses by our graduate school (HIGRADE) -Remuneration in accordance with the TVöD public-sector pay grade 13 (65%)

The UFZ has a strong commitment to *diversity* and actively supports *equal opportunities* for all employees regardless of their origin, religion, ideology, disability, age or sexual identity. We look forward to applications from people who are open-minded and enjoy working in diverse teams.

Your contact for any questions you may have about the job: Walter Durka walter.durka@ufz.de

Please submit your application via our online portal with your cover letter, CV (please omit your photo, age, or marital status) and relevant attachments.

Closing date for applications: 31.05.2020

Place of work: Halle (Saale)

More information about jobs at the UFZ: www.ufz.de/career < <http://www.ufz.de/career> > Helmholtz-Zentrum für Umweltforschung GmbH - UFZ Permoserstraße 15 04318 Leipzig, Germany

Walter Durka <walter.durka@ufz.de>

UKonstanz 2 BirdSociality

The drivers and consequences of social relationships in birds

1 PhD position is available at the Department of Biology, University of Konstanz (Germany) in the lab of Michael Griesser to study the drivers and consequences of social

relationships in Siberian jays. The fulltime position is funded for 3 years, starting September 2020.

The project combines field experiments with long-term data, and will use Siberian jays as system. This family living bird species does live in stable groups, but does not breed cooperatively. The fieldwork for the project will take place in Swedish Lapland in late winter and autumn, and involves fieldwork on cross-country ski and on foot, with temperatures ranging from -30C to +30C. The candidate will benefit from a strong interest in experimental field biology and social evolution.

The Griesser lab is attached to Prof Iain Couzin's Chair of Biodiversity and Collective Behaviour and has links to the Centre for the Advanced Study of Collective Behaviour. The University of Konstanz one of the nine "elite universities" in Germany, and is located a short ride outside the city of Konstanz, overlooking Lake Constance and the Alps. The University of Konstanz focuses on excellence in research, and the successful applicant will benefit from outstanding infrastructure, opportunities for training, and a highly collaborative, diverse, and international research environment. Our working language is English; applicants must therefore be fluent in this language; no knowledge of German is required.

The University of Konstanz is committed to increasing the number of individuals with disabilities in their workforce and therefore we encourage applications from such qualified individuals. Furthermore, we seek to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply. We offer extensive support to help researchers balance professional and home life, including assistance with childcare and support of the elderly, and flexibility in how employees arrange working hours.

Required qualifications: 1) MSc in behavioural ecology, evolutionary biology or similar 2) Field experience of behavioural observations and experimental work 3) Bird handling experience (including mist netting) 4) Highly motivated and sociable personality 5) Project management skills and ability to work independently 6) Driver's license 7) Basic knowledge of skiing (X-country or downhill)

Applications received before 6 July 2020 will be given full consideration.

If you wish to apply, send a motivation letter, CV, publication list, two contacts for references and short summary of your current research (as a single PDF) to michael.griesser@gmail.com

Michael Griesser Department of Biology University of Konstanz 78457 Konstanz, Germany

The endocrinological mechanisms of bird sociality

1 PhD position is available at the Department of Biology, University of Konstanz (Germany) in the lab of Michael Griesser to study the endocrinological mechanisms of sociality in Siberian jays. The fulltime position is funded for 3 years, starting September 2020.

The project combines field experiments and endocrinological methods, and will use Siberian jays as system. This family living bird species does live in stable groups, but does not breed cooperatively. The fieldwork for the project will take place in Swedish Lapland in late winter and autumn, and involves fieldwork on cross-country ski and on foot, with temperatures ranging from -30C to +30C. The candidate will benefit from a strong interest in field endocrinology, lab work, and behavioural ecology.

The Griesser lab is attached to Prof Iain Couzin's Chair of Biodiversity and Collective Behaviour and has links to the Centre for the Advanced Study of Collective Behaviour. The University of Konstanz one of the nine "elite universities" in Germany, and is located a short ride outside the city of Konstanz, overlooking Lake Constance and the Alps. The University of Konstanz focuses on excellence in research, and the successful applicant will benefit from outstanding infrastructure, opportunities for training, and a highly collaborative, diverse, and international research environment. Our working language is English; applicants must therefore be fluent in this language; no knowledge of German is required.

The University of Konstanz is committed to increasing the number of individuals with disabilities in their workforce and therefore we encourage applications from such qualified individuals. Furthermore, we seek to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply. We offer extensive support to help researchers balance professional and home life, including assistance with childcare and support of the elderly, and flexibility in how employees arrange working hours.

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

ULondon InvasiveBeetles

PhD project developing evolutionary and ecological analysis to identify species which threaten to become invasive pests.

We have funding for fees (and a full stipend of ~17k pa for for a EU or UK student). It would suit a student with a first degree, or comparable background, in a Biology or Bioinformatics discipline.

The project includes a placement within Defra's Risk and Horizon Scanning Team: <https://bit.ly/2WRK6fC> is a collaboration between Royal Botanic Gardens, Kew (Dr Laura Kelly) and Queen Mary University London (Prof. Richard Nichols)

will focus on Agrilus, a genus of more than 3000 species of wood-boring beetles.

Several Agrilus species have become major pests of trees and shrubs species with a devastating impact on plant health; yet some of them were previously known as minor infestations that caused minimal damage to their natural hosts. We will use phylogenetic methods to predict Agrilus host range expansions and to assess future risk to plant species that have not yet come into contact with these beetles.

Details of the application process and further information can be found here: <https://bit.ly/3e9tlCq> If you have specific questions do not hesitate to contact me

Richard Nichols (r.a.nichols@qmul.ac.uk)
Professor of Genetics <https://www.qmul.ac.uk/sbcs/staff/richardnichols.html>
richard.alan.nichols@googlemail.com

UNeuchatel HostParasiteInteractions

A PhD position on the evolutionary and resource ecology of host-parasite interactions is available for up to 4 years in Prof. Jacob Koella's lab at the University of Neuchâtel, Switzerland.

I am looking for an enthusiastic, motivated, and independent biology graduate whose MSc degree has a

strong component in evolution, ecology or parasitology. The PhD project will be within the context of an SNF grant, of which the general context is described below.

The position will require some teaching of biology labs for undergraduate (in French) and graduate (in English) students, and there will be opportunities to supervise student projects.

Neuchâtel is an attractive city in the French part of Switzerland with a high quality of life. It is located on the shore of Lake Neuchâtel with the Jura mountains to the North and a view of the Bernese alps to the South. It is an excellent area for outdoor activities such as biking, hiking, climbing or skiing.

If you are interested in the position, please send me (jkoella@gmail.com) a 1-2 page cover letter indicating your research background, your CV, and two letters of reference (or the names of two people whom I could ask for a letter). I will review applications continuously until I have found a suitable candidate. The position is available immediately, and I hope to find someone to start before October 1.

Context of SNF project Most of our ideas about the evolution of host-parasite systems are based on epidemiologically relevant traits - the rate of parasite-induced mortality, transmission rate and recovery rate - and on assumptions about their interactions. While this has given a useful framework that lets us formulate and test new ideas, it remains unsatisfying that we generally assume, rather than understand, the processes of the infection that underlie these traits and thus that determine epidemiology. One way towards this understanding is to consider how the host's limited resources are used for the parasite's growth and for the host's defense against parasites and its development, thereby letting disease-induced mortality and other traits emerge naturally from the parasite's dynamics.

Using **theory and experiments** with the microsporidian *Vavraia culicis* and its host, the mosquito *Aedes aegypti*, this proposal takes two approaches to look at the effects of resources on the dynamics of a parasite within its host. In a **quantitative** approach, it considers resources as a source of energy and studies how the energy budget within hosts influences the link between the parasite's growth and the host's mortality. In a **qualitative** approach, it asks whether the relative contributions of different nutrients (focusing on proteins and sugars), in addition to the energy content, influence the parasite's development and the host's response, and whether the host's preference for nutrients lessens the damaging impact of the parasite.

Jacob Koella

Institut de Biologie Université de Neuchâtel rue Emile-Argand 11 2000 Neuchâtel Switzerland

Jacob Koella <jkoella@gmail.com>

UPorto COVID19evolution

PhD Students Proposals

Call for PhD competition on COVID-19 for Portuguese students - Portugal.

The position is contingent on competition approval.

Applicants: Portuguese citizens

Requirements:

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

Candidates should possess a Master's degree and English proficiency. Applicants should be Portuguese citizens.

Research project and laboratory: The PhD candidate will develop the awarded project in CI-MAR, Porto, Portugal, under the Evolutionary Genomics and Bioinformatics group Head by Prof. Agostinho Antunes (<http://orcid.org/0000-0002-1328-1732> and <https://www.scopus.com/authid/detail.uri?authorIdq02537544>) in collaboration with several international institutions. Topic of research would range from COVID-19 Adaptive evolution, comparative genomics, and related host-immunity molecular genomics, etc.

Candidates should send the CV and copies of their graduation and Master's degrees (including final grades) to Prof. Agostinho Antunes (aantunes@ciimar.up.pt) till 11 May 2020 (first come first served chance).

Agostinho Antunes <aantunes777@gmail.com>

UQueensland UExeter HostParasiteCoevolution

A fully funded PhD position is available on host-parasite coevolution, jointly supervised by Dr Jan Engelstaedter at The University of Queensland, Australia, and Dr Ben

Longdon at the University of Exeter, UK. The student will spend time at both partner institutions and will graduate with a joint degree from both universities.

About the project Pathogens are an inevitable part of every ecosystem. In humans as well as in livestock and natural systems, the majority of pathogens have only arrived in their host species relatively recently, by switching from a different host species. In addition to the epidemiological processes of within- and between-host species transmission, pathogens also often evolve very rapidly. Their genomes change as they adapt to their host through processes such as mutation, natural selection and random genetic drift. To complicate things further, their hosts also undergo evolutionary change, and evolution in hosts and pathogens can be tightly linked: hosts evolve resistance to pathogens and in turn pathogens evolve to overcome this resistance, resulting in continuous coevolutionary arms races.

Evolutionary biologists have long been fascinated by host-pathogen coevolution and a large body of literature is devoted to understanding the dynamics and patterns of resistance and susceptibility arising through time and space, as well as the underlying infection genetics. However, the scope of these studies is almost exclusively restricted to a single pair of host and pathogen species. In this project we will combine theoretical and experimental approaches to investigate more realistic systems in which coevolution between multiple pathogen and multiple host species are considered. For the theoretical part, to be conducted at The University of Queensland under the supervision of Dr Jan Engelstaedter, mathematical models will be constructed and analysed in which host species may interact with each other through various processes (e.g., competition or predation), and pathogens may switch more or less rapidly between host species. Both analytical methods and computer simulations will be used to assess how coevolution impacts the ability of pathogens to undergo host shifts and how in turn host shifts affect coevolution. In the experimental part of the project, to be performed at the University of Exeter under Dr Ben Longdon's supervision, these theoretical predictions will be scrutinised by using a system of bacteria as hosts (several *Staphylococcus* species) and a range of viruses (bacteriophages) as their pathogens. This system is ideally suited to study host shifts in a high-throughput manner, and the experiments will be the first to interrogate the interplay between coevolution and the ability of pathogens to jump between host species. The results from this project are expected to have wide-ranging implication in several fields, including ecosystem stability, emerging infectious diseases, and agriculture.

About the QUEX scheme The University of Queensland

and the University of Exeter are seeking exceptional students to join a world-leading, cross-continental research team tackling major challenges facing the world's population in global sustainability and wellbeing as part of the recently launched QUEX Institute. The joint PhD programme provides a fantastic opportunity for the most talented doctoral students to work closely with world class research groups and benefit from the combined expertise and facilities offered at the two institutions. This prestigious programme provides full tuition fees, stipend, travel funds and Research Training Support Grants to the successful applicants. Fully-funded scholarships are available for the best applicants. This select group will have the chance to study in the UK and Australia, and will graduate with a joint degree from The University of Queensland and the University of Exeter.

About the scholarship These scholarships include a living stipend of AUD \$28,092 (2020) tax free, indexed annually, tuition fees and Overseas Student Health Cover (where applicable). A travel grant of AUD \$8,500 per annum, and a training grant of AUD \$3,000 are also available over the program.

Online application: <https://scholarships.uq.edu.au/-scholarship/quex-phd-scholarship> Application deadline: 15 June 2020

For further information, please contact Jan Engelstaedter (j.engelstaedter@uq.edu.au) or Ben Longdon (B.Longdon2@exeter.ac.uk).

j.engelstaedter@uq.edu.au

UQueensland UExeter ReproductiveInvestment

Fully funded PhD position on Female reproductive investment and ageing: an evolutionary perspective on age-related disease available at the University of Queensland, Australia and the University of Exeter, UK.

The student will be joint supervised by Dr Marina Fortes, University of Queensland and Dr Barbara Tschirren, University of Exeter, will spend time at both partner institutions, and will graduate with a joint degree from the University of Queensland and the University of Exeter.

The project Some individuals age faster than others, experience age-related diseases earlier and ultimately live a shorter life. Understanding the biological basis of individual variation in ageing trajectories remains one of the big challenges for science. Genomic constraints and

resource-based trade-off between reproductive investment and healthy ageing probably underlie individual susceptibility to age-related decline. However, these hypotheses remain experimentally untested.

This project uses a unique avian life history model, explicitly created to study the links between reproduction and ageing, to address these knowledge gaps. Using an artificial selection approach, we have created replicated genetic lines of quails (*Coturnix japonica*) that differ in their ageing trajectories. Birds selected for high reproductive investment age quickly and live shorter, whereas birds selected for low reproductive investment age slowly and live longer. This experimental model is thus ideally suited to test the consequences of reproductive investment for the development of age-related disease. Genomes and transcriptomes of these quail will be scrutinized using systems biology methods to unravel the molecular basis of ageing processes, targeting the discovery of genes and pathways that affect reproduction, ageing and the development of age-related disease.

This project combines the complementary skills and expertise of researchers in veterinary science, evolutionary biology, genomics, bioinformatics and systems biology from the University of Queensland, Australia, the University of Exeter, United Kingdom and the Institute of Avian Research, Germany. This is a unique PhD research and training opportunity for a student with a background in evolutionary biology interested to gain bioinformatics and systems biology skills, or a student with a bioinformatics, veterinary or systems biology background and an interest in evolutionary biology. In addition to available (phenotypic, WGS, transcriptomic) datasets, the student will have the opportunity to conduct experimental work to test the potential of nutritional interventions in buffering genetic susceptibility to age-related disease.

This cross-disciplinary and synergistic project will provide novel and essential insights into molecular constraints involved in the processes of reproduction that impact on healthy ageing and have broad implications for evolutionary biology, animal breeding and welfare, and human health.

The QUEX Scheme The University of Queensland and the University of Exeter are seeking exceptional students to join a world-leading, cross-continental research team tackling major challenges facing the world's population in global sustainability and wellbeing as part of the QUEX Institute. The joint PhD scholarship program provides a fantastic opportunity for the most talented doctoral students to work closely with world class research groups and benefit from the combined expertise and facilities offered at the two institutions.

Scholarship value These scholarships include a living stipend of AUD \$28,092 (2020) tax free, indexed annually, tuition fees and Overseas Student Health Cover (where applicable). A travel grant of AUD \$8,500 per annum, and a training grant of AUD \$3,000 are also available over the program.

Online application <https://scholarships.uq.edu.au/-scholarship/quex-phd-scholarship> **Deadline:** June 14th 2020

Contact b.tschirren@exeter.ac.uk for more information.

B.Tschirren@exeter.ac.uk

URoehampton London EcolEvolutionBehaviour

Masters by Research in Ecology, Evolution and Behaviour at the University of Roehampton, London, UK

We are excited to announce the Masters by Research (MbyRes) in Ecology, Evolution and Behaviour starting at the University of Roehampton in September 2020. The course offers students the opportunity to develop, design and conduct a substantial independent research project for the duration of the course (1 year full-time, 2 years part-time) with the support of a dedicated supervisor. Further details about the course can be found here < <https://eur02.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.roehampton.ac.uk%2Fpostgraduate-courses%2Fecology-evolution-and-behaviour%2F&data=02%7C01%7CAntonia.Ford%40roehampton.ac.uk%7C8876f85127dd4dfABXSd3iYPhrRjHfSHmmUx3qyCcFUnQ4%2BmRk0a8bmryk%3D&re0> >.

Examples of animal behaviour research project opportunities (and the supervisor) include:

- §Division of labour and sexual differences in bone robusticity in hunter- gatherers and farmers (Lia Betti)
- §The behavioural physiology of air-breathing divers (Lewis Halsey)
- §Social integration: causes, consequences and ontogeny (Julia Lehmann)
- §Life-history strategies in cooperative breeding banded mongooses (Harry Marshall)
- §Multimodal individual recognition of humans by goats (Alan McElligott)
- §Social organisation and collective nest building in ants

(Andrea Perna)

§Contagion of affiliative social behaviour in primates
(Stuart Semple)

A fuller list of potential project topics can be found here
< <https://eur02.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.roehampton.ac.uk%2Fresearch-centres%2Fcentre-for-research-in-ecology-evolution-and-behaviour%2Fpostdoctoral-and-phd-opportunities%2F%23masters&data=02%7C01%7CANTONIA.FORD%40ROEHAMPTON.AC.UK%7C8876F85127DD4DFA80B08D7F8B3BCD2%7C5FE650635C3747FBB4CCE42659E607EDXNVSN55Z65ENRQAXFNJHI7FT1GYFVRXJDQVBGEORRESEARCHPROJECT> >. Please get in touch with Harry Marshall (harry.marshall@roehampton.ac.uk) for more details. Please disseminate this to anyone who may be interested.

Antonia Ford Lecturer in Zoology Centre for Research in Ecology, Evolution, and Behaviour | Department of Life Sciences Whitelands College | Holybourne Avenue University of Roehampton | London | SW15 4JD

Antonia Ford <Antonia.Ford@roehampton.ac.uk>

UTours EvolutionSignallingProteins

Dear administrator,

A thesis grant is offered at the University of Tours (funding is acquired) on “THE SYSTEMIC STUDY OF THE MOMENT OF APPEARANCE AND DISAPPEARANCE IN THE TREE OF THE LIFE OF GENES ENCODING PROTEINS INVOLVED IN INTRACELLULAR SIGNALLING PATHWAYS - Approach compared to the previous study of the moment of appearance and disappearance of the ligand / receptor pairs”. I attach the corresponding document on this subject.

This three-year thesis will start in October 2020. The registration deadline for the doctoral school competition is June 10, 2020 (SSBCV doctoral school at the University of Tours). Student with solid skills in evolutionary biology, and especially in bioinformatics tools to study the evolution of genes (positive selection ...), Python programming, R language ...

Kind regards, Philippe Monget

pmonget <philippe.monget@inra.fr>

UZurich PlantEvolution

PhD position in plant evolutionary biology, University of Zurich. University of Zurich, Dept. of systematic and Evolutionary Botany

RESEARCH PROJECT: Genetic basis of hornwort carbon-concentrating mechanisms.

Biophysical carbon concentrating mechanisms (CCMs) operating at the single-cell level have evolved independently in some eukaryotic algae and a single lineage of land plants, the hornworts. An essential component for an efficient biophysical CCM is a pyrenoid, which represents a specialized compartment inside chloroplasts that mainly comprise the CO₂-fixing enzyme RuBisCO. Hornworts with pyrenoids fix significantly more carbon than their relatives without pyrenoids. Given the repeated gains and losses of pyrenoids in hornworts during the last 50 million years, we may assume that their assembly is potentially controlled by a few master regulators of eco-evolutionary relevance. In a joint effort, we will combine comparative -omics with reverse genetics tools to study the genetics, function, and molecular basis of pyrenoid-based CCM in hornwort plastids under different environmental conditions. Guided by ultrastructure-based monitoring of the pyrenoid assembly in hornworts, we aim to identify the genetic toolkit of biophysical CCM in hornworts through two interdependent approaches: First, we aim to predict candidate CCM components in silico through a set of homology searches that compare the hornwort gene set with algal CCM component. Second, we employ an exploratory gene and protein (co)expression profiling of isolated plastids collected under low vs. high CO₂ concentrations and under flooding. A strength of our experimental design is that we contrast up to three pairs of pyrenoid bearing and pyrenoid lacking hornwort species. Finally, we will investigate pyrenoid functionality under various environmental conditions. Specifically, we aim to conduct localization and functional validation analyses for a core set of genes discovered in our CCM gene prediction approaches. These experiments are possible through our recent advances to establish *Anthoceros agrestis* and other hornwort species as a tractable model system. Together, our collaborative project will not only allow a comparison of the mechanisms of pyrenoid assembly between algae and hornworts, but also reveal general principles and species-specific innovations in the evolution of carbon-concentrating plastids. Above that,

focusing on and understanding the basis of land plant CCM instead of only the algal form could eventually contribute to efficiently engineer pyrenoid assembly and boost photosynthetic efficiency of crops. Relevant publications: <https://www.nature.com/articles/s41477-020-0618-2>, <https://doi.org/10.1016/j.tplants.2017.02.002>. This project is funded (initially for three years) by the German National Science Foundation (DFG) MadLand (<https://madland.science/>) program to Peter Szovenyi and Susann Wicke. The project requires collaborative work including frequent visits to Germany and to the USA (Fay-Wei Li's lab at Cornell).

The Dept. of Systematic Botany hosts research groups working on the evolutionary and ecological drivers of biodiversity, on the macroevolution of plants, on plant-insect interactions/pollination, on the evolution of mating systems, hybridization and speciation. The Dept. of Plant and Microbial Biology hosts many groups working on plant molecular and developmental biology, epigenetics, community genomics and plant adaptation. Both institutes are housed in the beautiful Botanical Gardens and host a diverse community of researchers in plant biology.

Ideal candidates will have an MSc in biology with a specialization in evolution, developmental genetics and/or bioinformatics. This position primarily involves reverse genetic, microscopy, gas exchange measurements and bioinformatic work and requires advanced skills in handling, analyzing and interpreting high-throughput next-generation sequencing data. Good skills in assembling vectors, carrying out genetic transformations and microscopy are also required. Previous experience with *Chlamydomonas* pyrenoids is a plus but not necessary. In case not all these skills are covered, the willingness to quickly acquire them is absolutely necessary. The student will closely work together with the second PhD student/postdoctoral associate in Germany on this grant. Students should be willing to work both in the wet lab and in the office doing computational work. The position is initially for three years. Selected candidates will be enrolled in one of the two affiliated PhD schools in evolution or plant sciences.

CLOSING DATE: The position is opened until filled, but all application material including CV, a summary of research experience, a letter of

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Vienna PopulationGenetics

Reminder: Call for PhD students in Population Genetics is open: apply by May 31, 2020

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 love for evolutionary research and a background in one of the following disciplines: evolutionary genetics, functional genetics, theoretical or experimental population genetics, bioinformatics, mathematics, statistics.

Topics include:

- Temperature adaptation in *Drosophila*: phenotypic adaptation.
- Understanding polygenic adaptation.
- Inference of selection signatures from time-series data.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 31, 2020 will be considered. Two letters of recommendation need to be sent directly by the referees.

Depending on the project, PhD degrees will be awarded either in genetics, mathematics or statistics. PhD students will receive a monthly salary based on currently EUR 2.205,60 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 – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator

www.popgen-vienna.at <https://twitter.com/PopGenViennaPhD> c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

<http://www.vetmeduni.ac.at/en/population-genetics/> <https://twitter.com/PopGenVienna>
julia.hosp@gmail.com

Jobs

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ClemsonU TeachingEvolution 25	UGreifswald ResAssist Digitisation 30
KULeuven EcolEvolGenomics 26	UKansas Tech EvolutionaryBiochemistryMicrobiology 31
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TexasAMU LabTech Genomics 28	Vienna TechAssist HostMicrobe 33
UCalifornia Davis Tech FlowerEvolution 29	
UFreiburg ForestGenomics 29	
UFribourg Switzerland Biodiversity 30	

Ken Hayes <hayes.ken@gmail.com>

BishopMuseum DirectorOfInformatics

Bernice Pauahi Bishop Museum is seeking a Director of Informatics to lead a major effort to consolidate, expand, and enable the Museum's digital assets, including databases as well as tens of terabytes of digital images, videos, audio files and documents. The Director will oversee the architecture, development, testing, and implementation of a robust infrastructure for managing and sharing digital information at Bishop Museum in support of collections, research, data sharing and public outreach, such that the resulting infrastructure will improve efficiency and effectiveness of future data creation and maintenance into perpetuity.

For more information and to apply visit <https://www.bishopmuseum.org/Careers/> – Kenneth A. Hayes

Bishop Museum

T: 808.847.8217

On View Now < https://www.bishopmuseum.org/exhibits/#_blank >

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*Bishop Museum inspires our community and visitors through the exploration, celebration**, and perpetuation of the extraordinary history, culture, and environment of Hawai**É»**i and the Pacific.*

ClemsonU TeachingEvolution

Lecturer in Biological Sciences The Department of Biological Sciences at Clemson University is seeking a full-time, 9-month Lecturer in Biological Sciences with expertise in ecology and/or evolutionary biology to begin Fall 2020. We seek someone who will contribute innovative teaching and student-centered learning in our BA and BS degrees in Biological Sciences and online MS in Biological Sciences for Science Educators. The Department supports faculty development at all ranks, and promotion through instructional ranks will be expected for this renewable, non-tenure track position. Salary level will be commensurate with education and experience and a benefits package is included.

Teaching responsibilities will include: 1) undergraduate lecture and lab courses, such as introductory biology, ecology, evolution or others within the candidate's area of expertise and 2) online MS courses, such as ecology, evolution, scientific writing, animal biology, plant biology, or teaching pedagogy/experimental design and analysis. There are summer salary opportunities available for teaching on-campus, online, and study abroad.

Department Description The Department of Biological Sciences at Clemson University harnesses faculty expertise across the areas of ecology, evolution, and organismal biology; microbiology; molecular, cellular and developmental biology; and environmental toxicology to

advance the University's discovery mission and provide strong educational programs at both the undergraduate and graduate levels.

The Department, located within the College of Science, is home to 50+ full-time faculty, including 14 lecturers, supporting research and degree programs in Biological Sciences, Microbiology and Environmental Toxicology. The department's student population includes ca. 70 graduate students in MS and PhD programs in Biological Sciences, Microbiology, Environmental Toxicology and 300 in the online MS program in Biological Sciences for Science Educators. There are 1650+ undergraduate students in BA and BS degree programs in Biological Sciences and Microbiology.

For more information about the Department of Biological Sciences at Clemson University, visit the Department's website at <http://www.clemson.edu/science/departments/biosci/>. Qualifications Successful candidates will have a PhD in biological sciences or a related discipline at the time of appointment. Ideal candidates will have demonstrated successful experience teaching university-level biology lecture and laboratory courses, as well as have a strong interest in online teaching and undergraduate study abroad experiences.

How to Apply Applicants should submit the following items through Interfolio <http://apply.interfolio.com/75823> (1) cover letter, (2) curriculum vitae, (3) statement of teaching philosophy, experience, and interests, (4) course evaluations or other evidence of past teaching performance, (5) statement describing teaching strategies currently used or planned to use to foster diversity and inclusion, and (6) names and contact information for three professional references.

Inquiries should be directed to Dr. Michael Childress, chair of the search committee (mchildr@clemson.edu).

For full consideration, applications should be submitted by May 20, 2020. Review will continue until the position is filled.

*Note: References will not be contacted until final stages of the interview process.

mchildr@clemson.edu

KULeuven EcolEvolGenomics

Assistant/Associate Professor in Ecological and Evolutionary genomics at KU Leuven, Belgium

The Division 'Ecology, Evolution and Biodiversity Conservation' at the Department of Biology at the KU Leuven (Belgium) is seeking candidates for a faculty position in Ecological and Evolutionary genomics starting 1 October 2021.

We encourage applications by outstanding candidates with a research program at the intersection of ecology and evolution which addresses fundamental research topics using a genomics toolbox with aquatic organisms. The successful candidate will be expected to build her/his own independent research group and further integrate and strengthen collaborations across research groups within the Division. The new faculty member will also have responsibility for part of the teaching in ecology, evolution and genomics. After a pre-selection step by the Division, the successful candidate will be expected to continue the selection procedure at the university level for one of the two 'BOFZAP' categories of research professorships: junior BOFZAP for a researcher with high research potential proven by internationally recognized scientific publications, or Senior BOFZAP for a highly internationally recognized researcher in the field. Key selection criteria for BOFZAP positions is excellence in research reflected in both the scientific achievements and the research plan for the next five years. We aim for candidates with a research profile at the level of successful ERC applicants. Candidates should master up-to-date molecular and bioinformatic methods. Candidates are expected to teach students at all academic levels, including supervision of PhD students and postdocs. Candidates will be appointed in an academic staff position (ZAP) with a rank depending on the candidate's qualifications. BOFZAP researchers receive a BOF start-up grant. In addition the department of Biology provides a PhD fellowship of 4 years.

Information about the Division 'Ecology, Evolution and Biodiversity Conservation' can be found at <https://bio.kuleuven.be/eeb>. KU Leuven is a research-intensive, internationally oriented university that was elected Europe's most innovative university by Reuters and consistently ranks and features in Europe's top-15 universities within the Times Higher Education ranking < <https://www.timeshighereducation.com/world>

[university-rankings/ku-leuven#ranking-dataset/589595](https://www.university-rankings/ku-leuven#ranking-dataset/589595) >. Leuven is a historic, dynamic and lively city located in the heart of Belgium, within 20 minutes from Brussels, the capital of the European Union, and less than two hours from Paris, London and Amsterdam.

For the pre-selection step by the Division please submit a motivation letter (max. 1 page), short CV (max. 2 pages), a scientific achievements track-record (max. 2 pages) including a list of five most important publications, and a first outline of a research plan for the coming 5 years (max. 2 pages). Please refer to potential collaborations within the Division in your research plan.

Questions can be directed to the Head of the Division, Professor Robby Stoks (robbystoks@kuleuven.be). The application must be sent as a single PDF by email to Conny.coeckelberghs@kuleuven.be with as subject 'Eco-Evo Genomics faculty position'. The closing date for applications is June 25th 2020.

Robby Stoks <robbystoks@kuleuven.be>

MaxPlanck Yale MapOfLife

The Map Of Life and the Max Planck Yale Center for Biodiversity Movement and Global Change is hiring a full time software engineer.

Position Focus:

Map of Life (MOL) and the Max Planck 'V Yale Center for Biodiversity Movement and Global Change (MPYC) are seeking a Software Engineer who is interested developing new technologies to support effective global biodiversity education, monitoring, research and decision-making by assembling and integrating a wide range of knowledge about species distributions and their dynamics over time. Built on a scalable web platform geared for large biodiversity and environmental data, MOL provides best-possible species distribution information together with a range of information and biodiversity indicator products. MOL leads the data integration and mapping efforts of the Half-Earth Project that aims to identify and prioritize target areas for global biodiversity conservation. Responsibilities and tasks will include:

Developing responsive web applications using HTML5 and CSS3 on modern JavaScript frameworks and Python, documenting through GitHub and workflow optimization, working in Unix-based systems. Supporting and building backend API services. Supporting and building frontend interfaces with frameworks like An-

gular, React, etc. Receiving and providing feedback on code, incorporating user feedback directly into products. Assessing and meeting technical and stakeholder needs. Conducting written and oral presentations that summarize the analysis of data, interpret findings, and provide conclusions and recommendations. Solving problems in an organized and logical manner.

The Max Planck Yale Center supports research and training around the use of new technologies such as GPS tracking and remote sensing to address questions in ecology, behavior, and global change. Flagship Center projects include the Icarus initiative, a space station-based near-global GPS animal movement observation system, Movebank, which supports the management and integration of movement data, and Map of Life.

Please go to the following link to apply:

https://sjobs.brassring.com/TGnewUI/Search/Home/Home?partnerid=25053&siteid=5248#jobDetails=-1412308_5248 Meg Blake Currently Working Remotely Senior Administrative Assistant: Faculty and Research Support Yale University

The Yale Center for Biodiversity and Global Change
Cell: 860-227-0516 Email: Megan.Blake@Yale.edu Pronouns: She/Her/Hers

"Blake, Megan" <megan.blake@yale.edu>

OakRidgeNatILab StaffFellowship

Applications to the Oak Ridge National Laboratory Distinguished Staff Fellowship (<https://www.ornl.gov/-careers/distinguished-fellowships>) program are being accepted through Friday, May 29, 2020 (5:00 p.m. EST). The program includes the Liane B. Russell Fellowships, focusing on broad areas of biological sciences, biomolecular chemistry, computational biology, and environmental and ecosystem sciences. The program cultivates future scientific leaders by awarding outstanding early-career scientists and engineers—who demonstrate success within their academic, professional, and technical— areas with resources and enriching research opportunities.

Interested candidates may apply via this link: <https://career4.successfactors.com/-sfcareer/jobreqcareer?jobId=3090&company=-utbattelleP&username=ORNL> (ORNL (<https://www.ornl.gov/>) is the largest and most diverse science and energy laboratory in the US Department

of Energy (DOE) system. Distinguished Fellows represent a broad range of disciplines and are expected to establish the foundation for a long-term career at ORNL, while program mentors facilitate each Fellow's integration into ORNL's scientific community and alignment of their research activities with Laboratory and DOE missions.

Russell Fellowship candidates must demonstrate their ability to contribute to DOE missions in one (or more) of the following research areas: . Artificial intelligence and machine learning . Complexity in biological and environmental systems . Quantitative biology and genome security

Applicants must have received their PhD in a STEM field before they begin their fellowship and can be no more than 5 years beyond receiving their highest technical degree when they apply. Current ORNL postdoctoral researchers and ORNL staff members are not eligible to apply. ORNL's DSF program continues to play a vital role in ensuring the accomplishment of the Laboratory's mission of delivering scientific discoveries and technological breakthroughs needed to realize solutions in energy and national security and provide economic benefit to the nation.

For more details, please visit the program website at <https://www.ornl.gov/careers/distinguished-fellowships>. Potential fellows are strongly encouraged to contact current ORNL staff to discuss alignment between their research interests and DOE/ORNL research priorities.

Josh Michener Staff Scientist, Biosciences Division Oak Ridge National Laboratory michenerjk@ornl.gov michenerlab.org

Sidney Montana InsectPopDynamics

Research Entomologist or Ecologist

Insect pest population dynamics or applied geospatial modeling The USDA Agricultural Research Service is seeking a permanent, full-time Entomologist or Ecologist as lead investigator in one of the following two areas: 1) Applied modeling, spatial analysis, and forecasting of rangeland and crop insect pest distribution, outbreak dynamics, population growth, and/or risk analysis; OR 2) Plant-insect pest population dynamics with a strong quantitative focus. Candidates with geospatial modeling expertise or strong programming skills

in a language such as R or python are encouraged to apply. The position is at the Northern Plains Agricultural Research Laboratory in Sidney, MT. We expect the selected candidate to lead a research program that develops practical methods and strategies that improve forecasting, predictive modelling and risk assessment of key insects such as rangeland grasshoppers, Mormon crickets and wheat stem sawfly as part of developing more effective and ecologically sustainable approaches to pest management. Prior experience working with insects is preferred but not required. Our location houses a team of highly collaborative and enthusiastic scientists and support staff working in the fields of ecology, botany, entomology, pollinator resources, restoration, population genetics and agronomy. The position is advertised at the GS-12 level (\$76K starting salary), includes full government benefits, has promotion potential to GS-15 (up to \$160K), and is open to all U.S. Citizens and Nationals. Please apply on USAJobs (www.usajobs.gov; Job Announcement Number: 568113100). Ad runs from May 20 to June 17, 2020. Questions? Please contact Dr. John Gaskin (john.gaskin@usda.gov).

“Gaskin, John” <john.gaskin@usda.gov>

TexasAMU LabTech Genomics

The Marine Genomics Laboratory (MGL) at Texas A&M University Corpus Christi is seeking a highly motivated individual to join our team of researchers as a full-time laboratory technician. The successful applicant for this position (Research Specialist I) will be responsible for planning and performing laboratory work for several projects related to the genetics of cultured fish and shellfish.

Responsibilities include performing standard molecular biology techniques such as PCR and gel electrophoresis, constructing various kinds of genomic libraries for next-generation sequencing (NGS), developing and improving protocols for genomic lab techniques, and training and supporting students and research staff in the laboratory.

Candidates for this position must have (1) a Bachelor's or Master's degree in a related field and (2) at least four years experience with molecular biology techniques. Preferred qualifications include prior experience with next-generation sequencing library preparation or other genomic techniques.

To apply: https://tamus.wd1.myworkdayjobs.com/-en-US/TAMUCC_External/job/Corpus-Christi-

TAMUCC/Research-Specialist-1R-029353-1 For more information, please contact: Dr. Chris Hollenbeck
Email: christopher.hollenbeck@tamucc.edu

Christopher.Hollenbeck@tamucc.edu

UCalifornia Davis Tech FlowerEvolution

We –Jenny Gremer, Annie Schmitt, Sharon Strauss, and Julin Maloof– at UC Davis are looking to hire a technician to work on a collaborative project studying the evolution of the seasonal germination niche in a group of native wildflowers (*Streptanthus*). This is an ideal position for a recent graduate looking for research experience before graduate school.

Responsibilities include carrying out experiments in the field, lab, and controlled environment chambers, collecting field data and plant tissues, propagating plants and maintaining experimental populations. Field work will include plant surveys and collections of plant specimens and seeds. The technician will also oversee student assistants, manage databases, and perform basic statistical analyses, as well as coordinate supplies, equipment, and safety protocols.

Requirements: College-level course-work or equivalent experience/training in plant-related biological sciences or field biology. The applicant must possess excellent written and oral communication and strong organizational skills. Must be able to organize and coordinate lab, greenhouse, controlled chamber, and field research. Experience accurately recording, organizing, coordinating and curating data for analysis and reporting required, as well as skills to problem solve and trouble shoot, and ability to work independently and as a member of a research team. Research experience with plants, especially germination experiments, phenology, and field surveys preferred, as is experience using R software for data management and statistical analyses, experience working with herbarium specimens, and molecular biology lab experience working with DNA and/or RNAseq.

This is a full-time position. Starting date can be immediately or as soon as possible, with a proposed duration of one year with possibility of extension.

Application: Please go to the following link to access the UC Davis Human Resources application system and apply by June 6, 2020:

<https://careerspub.universityofcalifornia.edu/>-

http://ucdavis/EMPLOYEE/HRMS/c/-HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=-HRS_APP_JBPST&JobOpeningId=7869&PostingSeq=-1&SiteId=7&languageCd=ENG&FOCUS=Applicant

Please contact Annie Schmitt (jschmitt@ucdavis.edu) and/or Jenny Gremer (jrgremer@ucdavis.edu) for inquiries or additional information.

Sharon Y. Strauss Professor, Evolution and Ecology
2320 Storer Hall, One Shields Ave., Davis, CA 95616

Sharon Strauss <systrauss@ucdavis.edu>

UFreiburg ForestGenomics

The Faculty of Environment and Natural Resources of the University of Freiburg invites applications for a Full Professorship (W3) for Forest Genetics in the Institute of Forest Sciences to be filled by October 2020. Please find the complete job description at: <http://www.uni-freiburg.de/administration/-stellenboerse/00001038> This professorship represents the field of “Forest Genetics” in research and teaching. The main task of the professorship will be genetic and epigenetic analysis of DNA and RNA from trees using bioinformatic tools and methods from different research fields as well as the development of new bioinformatic tools. This includes genome research using molecular-biological, biotechnological and bioinformatic methods to identify relationships between the information stored in the genomes and plant attributes. Other possible research areas are ecological forest genetics including analyses of the effects of environmental factors and anthropogenic influences such as forest fragmentation and forest management on the genetic composition (and diversity) of tree populations and the assessment of plant diversity through genetic analyses such as bar-coding and metagenomics. A special commitment to teaching in forestry and environmental science programs is expected. The emphasis in teaching is on forest botany, genetic principles and ecological genetics, breeding and multiplication of trees, epigenetics.

Michael Bauder <michael.bauder@unr.uni-freiburg.de>

UFribourg Switzerland Biodiversity

The Faculty of Science and Medicine of the University of Fribourg (Switzerland) and the Department of Biology (<https://www3.unifr.ch/bio/en/>) invite applications for an open-rank position of a Professor in Environmental Biology.

Qualified applicants must have an outstanding track record of research in the field of fundamental ecological research with potential applied aspects using quantitative, state-of-the-art approaches, possibly including an evolutionary perspective. Topics of interest are, but are not limited to, agroecology, biological control, biodiversity, conservation biology, global change biology, or invasion biology.

The candidate will teach at the BSc level and contribute to the future MSc program “Environmental Biology” and/or the MSc program “Bioinformatics and Computational Biology”. Teaching experience at university level is expected.

The successful candidate will develop an internationally recognized competitive research program sustained by external funding.

The closing date for applications is 30 June 2020.

More information about the position can be found here: <https://www3.unifr.ch/scimed/positions> Prof. Thomas Flatt Department of Biology University of Fribourg Chemin du Musée 10 CH-1700 Fribourg Switzerland e-mail: thomas.flatt@unifr.ch phone: +41 26 300 8833 phone: +41 26 300 8850 (secretary) Web: <https://www3.unifr.ch/bio/en/groups/flatt/> European Drosophila Population Genomics Consortium: <http://droseu.net/> FLATT Thomas <thomas.flatt@unifr.ch>

UFribourg Switzerland Plant Evolution May31

The Faculty of Science and Medicine of the University of Fribourg (Switzerland) and the Department of Biology (<https://www3.unifr.ch/bio/en/>) invite applications for an open-rank position of a Professor in Plant Science.

Qualified applicants must have an outstanding track record of research in molecular and/or cellular aspects of plant development, physiology, or interaction with other organisms.

Potential areas of interest include, but are not limited to, plant disease, crop evolution, pest control, stress resistance, and food security. The candidate is expected to use modern approaches such as state-of-the-art genetics, high-throughput -omics, and/or bioinformatic approaches.

The candidate will teach at the Bachelor level and contribute to the future master program “Environmental Biology” and/or the master program “Bioinformatics and Computational Biology”. Teaching experience at university level is expected.

The successful candidate will develop an internationally recognized competitive research program sustained by external funding.

The closing date for applications is 31 May 2020.

More information about the open position on: <https://www3.unifr.ch/scimed/positions> . Prof. Thomas Flatt Department of Biology University of Fribourg Chemin du Musée 10 CH-1700 Fribourg Switzerland e-mail: thomas.flatt@unifr.ch

FLATT Thomas <thomas.flatt@unifr.ch>

UGreifswald ResAssist Digitisation

At the University of Greifswald’s Institute of Mathematics and Computer Science in the Faculty of Mathematics and Natural Sciences, there is a job vacancy expected to be available from 01/07/2020 or for earliest possible appointment, subject to budgetary regulations, for a full-time Research Assistant. The fixed-term contract shall end on 30/06/2022. The position is suitable for part-time employment. Payment will be made according to pay group 13TV-L Wissenschaft. The position on offer is being provided within the research consortium DIG-IT!- “Digitisation of natural complexity for the solution of socially relevant ecological problems”, as part of Mecklenburg-Vorpommern’s research excellence programme “Digitisation in Research”.

The DIG-IT! project: DIG-IT! seeks to advance digitisation, in particular deep learning, making it accessible for use in ecological sciences. For this purpose, DIG-IT! combines the developmental expertise for the au-

tomated analysis of image data (Fraunhofer Institute for Computer Graphics, Rostock and Biomathematics University Greifswald), as well as the mathematical expertise of the Biomathematics and Stochastics research group, with the application of the results for tackling urgent ecological questions (Botany / Landscape Ecology / Zoology University Greifswald). More information can be found here: <https://dig-it.uni-greifswald.de> Job description: DIG-IT! has been running since mid-2019, meaning that numerous digitisation tasks have already been concluded. The DIG-IT! consortium is thus able to access a broad variety of digitised data, ranging from bat images and bat sound recordings to tree cross-sections and pollen images and 3D root data. First analyses of this data has already been performed. The position advertised here, which belongs to the Biomathematics and Stochastics research group, shall now bring the understanding and findings gained from this data to a new level (“explorer” function). The postdoc shall ask and find the answers to new questions, which are only possible thanks to the new data: for instance, can the classification of bat image data be improved by also considering bat sound data or genetic data? Can 3D root growth be predicted if the distribution of nutrients in the soil is known? Can multidimensional data support the deep learning techniques in order to obtain useful presumptions?

There is an immense variety of mathematical, statistical and computer science questions in this project. The postdoc can therefore play an active role and make the most of his or her individual strengths and creativity in order to contribute to the level of knowledge gained by DIG-IT!. In particular, the postdoc is able to choose the mathematical and computer science tools and techniques used to tackle these questions in accordance with his/her strengths and interests.

The digitisation of image and acoustic data is not a core task of the position on offer. However, support with programme adjustment and possibly with the digitisation of some extra data are part of the job description. In particular, the successful candidate is expected to support PhD candidates with digital experience from the fields of both ecology and biomathematics with regard to aspects of machine learning.

Job requirements:

Completed PhD in (bio-)mathematics, bioinformatics, computer science or a closely related discipline Mathematical experience, e.g. in the areas of graph theory and mathematical modelling Sound knowledge of statistics Knowledge in the area of machine learning Mastery of at least one programming language; ideally Python Excellent knowledge of the English language (both written

and spoken) Willingness to collaborate in an interdisciplinary team Biological experience and German language proficiency are desirable, but not essential. We are seeking a highly motivated candidate with outstanding qualifications, who is an enthusiastic and experienced researcher, and willing to contribute to this joint project.

This advertisement is directed at all persons, irrespective of gender. The University would like to increase the proportion of women in areas in which they are underrepresented and thus applications from women are particularly welcome and will be treated with priority if they have the same qualifications and as long as there are no clear reasons which make a fellow applicant more suitable. Severely disabled applicants with the same qualifications will be considered with preference. In accordance with § 68(3) PersVG M-V, the Staff Council will only be involved in staff matters of the academic or artistic staff on request. Please only submit copies of original documents with your application as these cannot be returned. Unfortunately, application costs (e.g. travel expenses for interviews) will not be reimbursed by the state of Mecklenburg-Vorpommern. Applications comprising all usual documents (letter of motivation,

— / —

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>

UKansas Tech Evolutionary Bio-chemistry Microbiology

Assistant Researcher position in the Unckless Lab at the University of Kansas

The Unckless lab at the University of Kansas invites applications for an assistant researcher that will focus on the evolution of immune peptides. We recently found that several *Drosophila* antimicrobial peptides show signatures of balancing selection (the adaptive maintenance of multiple alleles). This position would involve dissecting the mechanisms of balancing selection on these peptides using a combination of approaches including microbiology (minimum inhibitory concentrations, zone of inhibition assays) and biochemistry (structural and functional studies using circular dichroism, NMR, etc.). The goal is to understand how balancing selection maintains alleles from the ecological to the biochemical level.

The successful candidate should have experience in some of the approaches listed above and would be able to develop skills in some of the other approaches. A bachelor's degree in biology or a related field is required.

The Unckless Lab studies evolutionary genetics in general with a focus on the evolution of immunity and selfish genetic elements. The University of Kansas is home to both the Department of Molecular Biosciences and the Department of Ecology and Evolutionary Biology and members of the lab interact directly with other labs spanning biochemistry, microbiology, genetics, genomics, evolution and ecology. Lawrence, Kansas is a vibrant college town with plenty of good food, cultural events and a wonderful downtown area. The cost of living is very reasonable. We are about 45 minutes from Kansas City.

For more details including required and preferred qualifications and directions about how to apply, please visit <https://employment.ku.edu/staff/17181BR> and/or inquire directly with Rob Unckless (unckless@ku.edu). Application review begins on May 25 and will continue until a qualified applicant pool has been identified. The estimated start date is August 3rd, 2020, but is flexible.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, retaliation, gender identity, gender expression and genetic information in the University's programs and activities. The following persons has been designated to handle inquiries regarding the non-discrimination policies and are the Title IX Coordinators for their respective campuses: Director of the Office of Institutional Opportunity and Access, IOA@ku.edu, Room 1082, Dole Human Development Center, 1000 Sunnyside Avenue, Lawrence, KS, 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses; Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

“Unckless, Robert L” <unckless@ku.edu>

UKonstanz EvolutionaryBiology

At the University of Konstanz in Germany we have an opening for an

Assistant Professor/Jr. Group leader in evolutionary biology (genomics of speciation and adaptation)

(starting date is on or around October 1st 2020)

The person we are looking for should be an evolutionary biologist who works on questions in either molecular evolution, and/or the genomics of speciation and adaptation. The position is intended for a Ph.D. biologist, ideally with prior postdoc experience, a strong publication record in evolutionary biology, and with expertise in evolutionary genomics. A total of three research groups two of which are headed by Junior Group Leaders make up the evolutionary biology group (20 members total in the lab), in the Department of Biology at the University of Konstanz:

<http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=172> Our taxonomic emphasis is on fish, particularly on cichlids fish, but also other fish model systems are used in our research on comparative and speciation genomics and comparative developmental biology. We are especially interested in the origins of (convergently evolved) adaptations, speciation, and phylogenomics of the cichlid fish adaptive radiations from Nicaragua and Africa. But, we are open to anyone investigating other interesting taxa. For publications of the lab see:

<http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=92> . Space in a modern fish facility is available and the exclusive support of a 50% technician will be provided to this new group. Wet lab space, equipment, departmental facilities, including core-facilities in proteomics and genomics, and annual financial support for research expenses and student support, are provided by the University of Konstanz. The lab has sufficient space and state-of-the-art equipment for research in genomics, molecular, and developmental biology.

The University of Konstanz and the Department of Biology are among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the southern border between Germany and Switzerland. The

position comes with a competitive salary, and excellent health and retirement benefits.

Appointments are initially for three years and are renewable for several years after that. Habilitation is possible, and a modest amount of teaching (in English at the BSc and MSc level) is required. The Assistant Professor is expected to acquire external funding and to supervise undergraduate, and graduate students as well as postdocs.

The University of Konstanz is an equal opportunity employer and tries to increase the number of women in research and teaching. The University of Konstanz is committed to further the compatibility of work and family life and has onsite child care facilities

<https://www.uni-konstanz.de/en/equalopportunities/-family/childcare/kinderhaus-knirps-co-child-care-centre/> . Additional information contact: a.meyer@uni-konstanz.de , phone: 49 7531 884163.

For our current research output see:

<https://scholar.google.com/citations?user=qf6eWtgAAAAJ&hl=en&oi=ao> Applications - including a statement of research interests, research plans, a full CV and names and email addresses of 3 referees - should be emailed to: a.meyer@uni-konstanz.de.

Applications should be received by June 15th, 2020.

Prof. Dr. Axel Meyer Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon 49 (0)7531 88 4163 fax 49 (0)7531 88 3018

secretary: Christiane.Weber@uni-konstanz.de tel. 49 (0)7531 88 3069

<http://www.evolutionsbiologie-uni-konstanz.com/> Axel Meyer <prof.dr.axel.meyer@gmail.com>

USDA Hawaii 3 Entomologist

Aloha!

The USDA Agricultural Research Service is currently accepting applications for three vacant positions within the Tropical Crop and Commodity Protection Research Unit in Hilo, Hawaii.

1 Research Entomologist/Research Biologist (GS 12-14, with promotion potential to GS 15): [https://](https://www.usajobs.gov/GetJob/ViewDetails/567739800)

www.usajobs.gov/GetJob/ViewDetails/567739800 2 Biological Science Technicians (GS 7-8, with promotion potential to GS 9): <https://www.usajobs.gov/GetJob/ViewDetails/568005900> <https://www.usajobs.gov/GetJob/ViewDetails/567322000> Note: the two technician positions are two separate announcements for two different jobs, so anyone interested should apply to both.

The positions are permanent and in the federal service.

All interested parties will find details relevant to the position in the announcements, and all applicants should apply directly through those links on USAJOBS.

Sheina B. Sim, Ph.D. Research Biologist USDA-ARS Daniel K. Inouye US PBARC 64 Nowelo Street Hilo, HI 96720 Phone: 808-932-2175

“Sim, Sheina - ARS” <sheina.sim@usda.gov>

USDA Hawaii BioSciTech InsectFunctionalGenomics

Technician position in Hilo (Term position) in insect functional genomics/genetics, details of position here: <https://www.usajobs.gov/GetJob/ViewDetails/569034400> Open & closing dates: 05/22/2020 to 06/05/2020

Thanks! Scott

Scott Geib PhD Research Scientist USDA-ARS Daniel K Inouye U.S. Pacific Basin Agricultural Research Center Hilo, Hawaii scott.geib@usda.gov 808-959-4335

“Geib, Scott” <scott.geib@usda.gov>

Vienna TechAssist HostMicrobe

Full-time Research Technician (40 hours/week) on Host-Microbe Interactions at the Department of Cell & Developmental Biology, Med. Univ. Vienna

A full-time Research technician (40 hours/week) position is available in the group of Wolfgang Miller at the Department of Cell and Developmental Biology of the Medical University of Vienna. The main focus of our group research is deciphering how host-microbe inter-

actions between *Drosophila*, endosymbiotic *Wolbachia* bacteria and other selfish genetic elements affect their life history traits. We are combining genetics, molecular & cellular biology and microbiology in conjunction with cutting-edge NGS technologies.

You will be integrated in our dynamic research team and will be responsible for *Drosophila* maintenance and genetics, and will assist in a variety of molecular, cell biological and genetic projects as well as high-throughput phenotypic assays. Moreover, you are also expected to help with laboratory management and organization.

This full-time post is expected to start July 1st, 2020 and is limited for 1-year with the possibility for further extension depending on successful evaluation.

The following responsibilities are expected from you:

1. Molecular genetics and cellular analyses, including isolation of DNA, RNA and proteins; standard, diagnostic and RT-PCR, primer design, NGS library preparation, cDNA synthesis and preferentially FISH and ISH techniques
2. *Drosophila* stock keeping, typing and crossing of sensitive lines
3. Lab organization and management

Your profile:

We are looking for a reliable, highly organized and motivated candidate with good social and communication skills and practical experience in at least three of the four skills mentioned above, who is fitting the following profile:

- Experienced technician with a Bachelor's degree in Biology, Genetics, Molecular Biology, or a related field

- Excellent understanding of the theoretical and technical principles of common techniques in genetics and molecular & cellular biology. Experience with the *Drosophila* system will be highly valued

- She/He should be willing to acquire further skills and contribute to the development of new analytic methods

- Excellent written and spoken English skills; Computer know-how and experience in Microsoft Word, Excel and PowerPoint is essential

In case of interest, please contact Wolfgang Miller (wolfgang.miller@meduniwien.ac.at).

The advertisement will be open until the position is successfully filled. For further information please visit the Lab page: <https://anatomieundzellbiologie.meduniwien.ac.at/zellbiologie/-developmental-biology/group-miller/>

Wolfgang J. Miller, PhD Lab Genome Dynamics, Dept Cell & Developmental Biology Center of Anatomy and Cell Biology, Medical University of Vienna, Schwarzschanerstr. 17,

Bauteil C, Hochparterre, Raum 36 A-1090 Vienna

AUSTRIA.

email: wolfgang.miller@meduniwien.ac.at

<http://anatomieundzellbiologie.meduniwien.ac.at/-zellbiologie/-developmental-biology/group-miller/> Tel. 0043 1 40160 37750

Fax 0043 1 40160 37790

Wolfgang Miller <wolfmanmiller@yahoo.com>

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Accurate hCoV19 alignments

Many evolutionary biologists try to help with COVID-19 and perform evolutionary studies. The very first step is multiple genome alignment, which is surprisingly difficult due to poor quality data. We implemented a profile HMM approach in a user friendly website: <https://covalign.pasteur.cloud/> and a manuscript is available on <https://www.biorxiv.org/content/10.1101/2020.05.25.114884v1> Thank you, best, Olivier

Directeur du DBC/C3BI - Directeur de Recherche au CNRS <https://research.pasteur.fr/en/member/olivier-gascuel/> Département de Biologie Computationnelle (DBC/C3BI) USR 3756 - Institut Pasteur et CNRS, Paris, France <https://research.pasteur.fr/en/department/computational-biology/> <https://c3bi.pasteur.fr/> Olivier GASCUEL <olivier.gascuel@pasteur.fr>

COVID and Biodiversity

Dear Colleague

We are writing on behalf of a COVID Task Force, a CETAF-DiSSCo joint action (CETAF = Consortium of European Taxonomic Facilities, <https://cetaf.org/>; DiSSCo = Distributed System of Scientific Collections, <https://www.dissco.eu/>).

As a group of researchers working in different fields, we recently established a COVID Task Force, with the aim to help clarify the links between biodiversity, human pressure and the origin and causes of coronaviruses and similar disease spill-over, as well as to identify the actions that should be put in place to complement the efforts made in other disciplines. This effort is equally important to anticipate and prevent the occurrence and propagation of zoonotic infectious diseases worldwide.

One of the first tangible actions we want to pursue is a horizon scanning exercise among stakeholders to identify priority questions that scientists should explore to reach a better understanding of pathogen origins, spill-over processes and their ecological correlates.

The answers to these questions are needed to clarify the role that certain animal species play with respect to the pandemics such as the current one, and the environmental conditions that may facilitate these phenomena, from wildlife trade and consumption to habitat loss or degradation. We aim to publish, in the peer-reviewed literature, a list of questions that would form the basis to steer future research work.

Given your expertise in the field, we would be most grateful if you could supply a list of questions that you see as priorities for research funding. The form has space for up to twenty questions but feel free to send as many as deemed important. Many thanks in advance for your important contribution.

Participation in the survey is on voluntary base and you are not obliged to answer all the questions. Your answers to the survey will be treated anonymously. The contribution of respondents will be acknowledged in the publication only if you leave your name.

We would also greatly appreciate if you could circulate this message to colleagues who you think might be interested. We apologise in advance for any cross-posting.

This is the link to the Google form:

https://docs.google.com/forms/d/e/1FAIpQLSfh7ZEPY60o0pByqYuoVtCt_eyeo6ikDXrNLWdoFPdyI2oEtC/viewform Best regards

For the CETAF-DiSSCo COVID Task Force

prof. Danilo Russo, University of Naples Federico II, Italy

prof. Sandro Bertolino, University of Turin, Italy

prof. Maarten Vanhove, Hasselt University, Belgium

Dr. Séverine Thys, Ghent University, Belgium

Maarten VANHOVE <maarten.vanhove@uhasselt.be>

marcos antezana <marcos.antezana@gmail.com>

DelawareStateU EvoDevo Consulting

The Charvet lab at Delaware State University is looking for consultants to work on research projects leading to publications in peer-reviewed articles. The consultant has the opportunity to work with a diverse team to integrating state of the art MR imaging with gene expression to study the evolution and development of human and non-human brains. The goal of this research is to integrate from genetics to neuroimaging to enhance translational work from model organisms to humans. This is an excellent opportunity to work collaboratively with diverse researchers and to gain experience working with methods that cut across scales of organization. We are looking for individuals who will perform statistical analyses with the programming language R, write manuscripts, analyze RNA sequencing data, and collect data from MR scans. If you are interested in working remotely in exchange for consulting fees and facilitate the completion of research projects leading to publications, contact Christine Charvet at ccharvet@desu.edu at Delaware State University.

Christine Charvet <charvetcj@gmail.com>

ForensicTricks Covid19

many non-sophisticated kit-addicted medical DNA labs around the world are accepting the ~8-16x pooling limit duly mentioned as non-hard by the researchers in the link below.

<https://www.medrxiv.org/content/10.1101/2020.03.26.20039438v1> ror

could the ancient- and forensic-DNA wet-bench experts in evoldir generate a list of their best and most extreme tricks for PCR-ig samples with very little target sequence?

including tricks for when one starts with lots of garbage non-target RNA and DNA?

btw, any tricks for field flash prepping a sputum sample hopefully w/o need for subsequent cold storage (direct dumping into a tube with phenol mix maybe)?

Lapland Sweden AvianFieldAssist

Expenses paid field assistant positions to assist fieldwork with Siberian Jays in Swedish Lapland

We are looking for 3 highly motivated expenses paid field volunteers to join our field project (main responsible Dr. Michael Griesser, University of Konstanz, Germany).

For the upcoming field season (15 Aug 'V 8 Nov 2020) we are looking for 3 assistants to assist in our work on social evolution in Siberian jays. The work of the assistants will be to help with catching and ringing birds, do behavioural observations, do field experiments, and data management. The work will be carried out in both pristine and managed boreal forests. Observe that temperatures in the end of the season can be as low as -15C, and that the fieldwork can be physically strenuous at times.

Qualifications: 1) Field work experience, involving behavioural observations and experiments 2) Preferably bird ringing and mist-netting experience 3) Ability to work in small teams and sociable personality 4) Driving license (manual transmission) 5) Fluent in English 6) Highly motivated

Applications received before 6 July 2020 will be given full consideration.

If you wish to apply, send a motivation letter, CV, publication list, two contacts for references and short summary of your current research (as a single PDF) to michael.griesser@gmail.com

Michael Griesser Department of Biology University of Konstanz 78457 Konstanz, Germany

Michael Griesser <michael.griesser@gmail.com>

LMU Munich Paleobiology

Dear EvolDir readers,

please find attached an announcement for our Master's program "Geobiology and Paleobiology" to forward to interested students.

With kind regards, Oliver Voigt

PD Dr. Oliver Voigt

Master's program in Geobiology and Paleobiology (MGAP)

Department of Earth- and Environmental Sciences, Palaeontology & Geobiology & GeoBio-Center LMU Ludwig-Maximilians-University Munich, Richard-Wagner-Str. 10, 80333 Munich, Germany

<http://www.mgap.geo.uni-muenchen.de>

mgap@geo.lmu.de

Applications invited for the Master's program "Geobiology and Paleobiology" (MGAP) at the Ludwig-Maximilians-Universität (LMU) Munich (Germany) for EU students until 30 June 2020

The Master's program "Geobiology and Paleobiology" (MGAP) is a consecutive, research-focussed, two-year Master of Science program at the Faculty of Geosciences of the Ludwig-Maximilians-Universität (LMU) Munich, in collaboration with researchers of the Bavarian Natural History Collections and the GeoBio-Center @ LMU. MGAP aims to provide students with a comprehensive introduction into the interdisciplinary research fields of geobiology and paleobiology.

The MGAP program is based on interdisciplinary, research-oriented courses in geo- and biosciences that address patterns and processes of evolutionary and environmental geobiology and paleobiology. The module-based curriculum provides an integrative approach facilitated by experts in different areas of expertise. Students will learn and acquire routines with a wide range of scientific methods such as modern techniques in molecular biology, fieldwork, collection management, comparative morphology, phylogeny, bioinformatics, statistics and (paleo-) biodiversity assessments. Students will learn independent scientific work in individual and intensively supervised research projects at early stages of the curriculum.

MGAP in brief

- International Master's program in Geobiology and Paleobiology (Master of Science, M.Sc.) at the LMU Munich
- 2 years, 4 semesters, start in October (winter semester)
- All courses taught in English
- Course total: 120 credit points (ECTS)

More information is available on the program's website: < <http://www.mgap.geo.uni-muenchen.de> >

For the winter semester 2020-2021 (courses will start in November), the application period for applicants from

EU countries ends on June 30, 2020.

Applications have to be submitted via our online submission portal:

< <https://www.efv.verwaltung.uni-muenchen.de/-mageopal> > oliver.voigt@lmu.de

MolEcol SpecialIssue

Dear Colleagues,

We are looking for contributors to submit a paper to a special issue planned for Molecular Ecology on the topic of "The use of whole-genome sequences in molecular ecology". This special issue aims to bring together empirical studies, targeted reviews, methodological advances and perspectives on the potential and pitfalls related to the application of whole-genome sequence data to consequential questions in molecular ecology.

If you are interested in potentially contributing a paper to this proposed special issue, please send a short email reply to any one of the guest editors briefly outlining your expression of interest and describing the topic you are considering. Please reply prior to June 1, 2020, and note the anticipated schedule outlined below.

Cheers,

Guest Editors:

Andrew Foote <andrew.foote@ntnu.no> Evelyn Jensen <evelyn.jensen@yale.edu> Rebecca Taylor <rebeccataylor@trentu.ca> David Coltman <dcoltman@ualberta.ca>

Anticipated Schedule: Invitation Issued: May 1, 2020
Authors Confirm Commitment: June 1, 2020
First Submission Due Date: November 30, 2020
Manuscript Final Due Date: June 28, 2021
Issue Compilation Date: August 30, 2021
Issue Publication Date: November 1, 2021
"rebeccataylor@trentu.ca" <rebeccataylor@trentu.ca>

Teaching about Mimicry

Hi everyone,

For decades I have run a practical at the start of my relatively introductory Evolutionary Biology module where students play games as predatory birds attacking butterflies. They end up getting to grips with frequency dependent selection through Batesian mimicry.

It will not survive social distancing, so I have been looking for a simple simulation or on-line game which covers this, so far without much success. Does anyone know of anything suitable?

More generally, I guess this is one example of a much bigger issue we are all going to be tackling this summer anyone for an on-line compilation of such resources for teaching Evolutionary Biology?

Best wishes,

Mike Ritchie

Mike Ritchie Centre for Biological Diversity, School of Biology,

University of St Andrews, Fife. Scotland KY16 9TH
UK I do not expect people to answer e-mails outside of office hours

Michael Ritchie <mgr@st-andrews.ac.uk>

Teaching Mimicry answers

Hi

I posted a query recently about finding a mimicry game for teaching on-line and mentioned general resources now that we are all planning for remote teaching.

Very many thanks for all the helpful responses and comments, and nice to hear from so many of you! Many people asked to see what came in. Below I will paste in a simple list of links, many of which look really helpful.

Excellent EvolDir-ing, everyone.

All the best, Mike

Mimicry and other resources
Mimicry games:
Great Heliconius game: <http://heliconius.org/-evolving.butterflies/> (See also <https://royalsocietypublishing.org/doi/10.1098/rspb.2020.0014>)
Other one, a bit less friendly: <https://ccl.northwestern.edu/netlogo/models/Mimicry>
Camouflage practical <https://alexis-catherine.github.io/-publication/natural-selection-and-camouflage/> (NetLogo also has one: <https://ccl.northwestern.edu/-netlogo/models/BugHuntCamouflage>)
Peppered moth game: <https://askabiologist.asu.edu/peppered-moths-game/play.html>
General resources
The always popular Populus: <https://cbs.umn.edu/populus/overview>
Drift & Gene Flow <https://cartwrig.ht/apps/genie/> (Cock van Oosterhout has a great ppt to lead students through this) See also <https://cartwrig.ht/-apps/redlynx/> <https://demonstrations.wolfram.com/-ReplicatorMutatorDynamicsWithThreeStrategies/>
NetLogo: <http://ccl.northwestern.edu/netlogo/-models/index.cgi>
Population Genetics: https://www.radford.edu/~rsheehy/Gen_flash/popgen/
Evolution in general <https://evolution.berkeley.edu/-evolibrary/home.php>
Mitochondrial Eve: <https://projects.ncsu.edu/cals/gn/ex/mit-eve.html>
Y chromosomes: <https://projects.ncsu.edu/cals/gn/ex/y-chrom.html>
A professional online package from Michael Kasumovic: <https://arludo.com/> a compilation of resources: <https://planted.botany.org/index.php?P=Home>
Finally, Donald Forsdyke has some great on-line videos explaining evolutionary principles (occasionally in a fake Scottish accent): <http://post.queensu.ca/~forsdyke/videlectures.htm>
Mike Ritchie Centre for Biological Diversity, School of Biology,

University of St Andrews, Fife. Scotland KY16 9TH
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Michael Ritchie <mgr@st-andrews.ac.uk>

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BangorU MolecularEcology

The Molecular Ecology & Fisheries Genetics Laboratory (MEFGL) at Bangor University is seeking qualified candidates to develop fellowship applications under the Marie Skłodowska-Curie Individual Fellowship action. Importantly, the Brexit arrangements support full funding for the UK under the 2020 submission to this scheme.

Fellowship Details: Marie Curie Individual Fellowships are prestigious and competitive awards that are given to promising early career researchers that hold a doctoral degree or at least four years' full-time research experience by the time of the call deadline (9 Sept 2020); there are opportunities for EU nationals and from global applicants. These fellowships provide funds for 12-36 months and are an exciting opportunity to develop an independent and advancing research portfolio that will be mutually beneficial to the host institute and the Fellow. To apply, a research proposal is typically written jointly with your chosen host group(s) and organisation(s). Bangor University has a dedicated research office to guide proposal development.

The application deadline is 09/09/2020, but we encourage those interested in developing an application to get in contact with a member of our groups by 24/05/2020 to allow sufficient time to assess fit to call, suitability and then develop a competitive application.

For more information on the MSCA Individual Fellowship, see: https://ec.europa.eu/research-mariecurieactions/actions/individual-fellowships_en

About the MEFGL: we are a collaborative group of investigators interested in diverse questions in fields ranging from microbial and disease ecology to fisheries genetics, biodiversity monitoring, local adaptation, and speciation. A common theme across MEFGL groups is that we are interested in tackling pressing questions utilizing approaches at the forefront of molecular ecology and evolutionary genetics/genomics. For more information on specific research areas and interests, please refer to staff members content pages (<http://mefgl.bangor.ac.uk/staff/>), publications and see: http://mefgl.bangor.ac.uk/research_interests.php. To Apply: If you are interested in developing a collaborative mobility MCSI Fellowship application, please contact relevant group members: <http://mefgl.bangor.ac.uk/staff/>, and provide a brief motivation statement and CV for more information.

Contacts: <http://mefgl.bangor.ac.uk/staff/a.comeault@bangor.ac.uk>

Beijing BeetleMetagenomics

Beijing.IOZ Chinese Academy of Sciences.BeetleMetagenomic

Postdoctoral position, Beetle Metagenomic, Institute of Zoology, Chinese Academy of Sciences, Beijing, China

One full-time PIFI postdoctoral position for two years (with a possible extension) is available at Prof. Bai's lab from Institute of Zoology, Chinese Academy of Sciences, located in Beijing, P.R. China.

Topic Coleoptera is the most biodiversity in organic sphere. Based on metagenomics by high-throughput sequencing, the large-scale biodiversity assessment of beetles from different sites from China will be explored, which can reveal the species catalogue, species richness, distribution status, community structure and so on. The relationship of genetic diversity, species diversity and ecological diversity were inferred too.

The work conditions are 1. Two year contract with a possible extension; 2. The appointment ideally starts this June but negotiable; 3. An annual salary to postdoctoral researchers to cover living expenses and health insurance in China. Each selected awardee will receive a pre-tax stipend of ~250,000 RMB (~35,000 USD) per year plus benefits. In addition, the fellowship provides an economy- class round-trip international travel; 4. Be under the age of 40.

Qualified candidates are requested to send a CV with a brief motivation to baim@ioz.ac.cn with a title [Postdoc Application - fullname].

About the Institute Institute of Zoology (IOZ), Chinese Academy of Sciences (CAS), is a government-funded research institution in zoological sciences. It has a long history of over 80 years. The predecessor of IOZ was Fan Memorial Institute of Biology founded in 1928. Many distinguished scientists including thirteen CAS Academicians started their research career in IOZ. Some of them are founders of various sub-disciplines of zoology in China, such as Professor Bing Zhi, first director of IOZ and one of the main founders of modern biology in China. Several sub-disciplines in zoological sciences in China were derived from IOZ, such as entomology, animal ecology, and experimental embryology. IOZ also has a long history of service to the country with many significant contributions, such as successful control of China's chronic agricultural pest-locust, control and

management of other pest insects and rodents, establishment of nature reserves in China, conservation of giant panda, crested ibis and other endangered wildlife, reproduction and contraception, and fish nuclear transfer. Zoological Museum of IOZ has over 8 million animal specimens. Several field stations and research bases also play important role in IOZ research programs.

About the PI Dr. Bai has been engaged in the systematics and evolution of insects, e.g. scarabs and ice crawlers. On the basis of inheriting the traditional taxonomy, he has opened up a new research direction of the new taxonomy driven by new technologies such as quantification, Big Data and Artificial Intelligence. The main academic achievements are as follows. (1) He systematically revised the Chinese Scarabaeoidea and Grylloblattodea, built a database on Chinese insect type specimens, and published a new insect order, 4 new families, and more than 200 new genera. (2) In the three key aspects of taxonomic research (character cognition, character comparison, character evolution), new technology innovation-driven research has been carried out, including the development of new instruments and new software in digital and three-dimensional technologies, the integration of quantitative geometric morphometrics and erection on the new research paradigm. The establishment of a new insect order, Alienoptera, and the systematic status of some important extinction groups were revealed. The origin of dung feeding behavior was investigated. An Intelligent Identification System of World Beetles (BICS, <http://beetle.ioz.ac.cn/>) was created.

Contact Ming BAI Ph.D. Full Professor Principal Investigator of the Group of Morphology and Evolution of Beetles Address: Box 92, Institute of Zoology, Chinese Academy of Sciences No. 1, Beichen West Road, Chaoyang District, Beijing, P.R. China Email: baim@ioz.ac.cn [CN] http://sourcedb.ioz.cas.cn/-zw/zjrc/201102/t20110224_3075281.html [EN] http://sourcedb.ioz.cas.cn/yw/scs/pi/201102/-t20110224_3075281.html [BICS] Beetle Intelligent Classification System: <http://beetle.ioz.ac.cn/> Reprints (PDF): https://www.researchgate.net/profile/-Ming-Bai2?ev=hdr_xprf "Prof. Dr. BAI Ming" <baim@ioz.ac.cn>

Bishop Museum Hawaii Biodiversity Informatics

The Bernice Pauahi Bishop Museum, the premier museum of Natural History and Culture of the Pacific is accepting applications for the *Joshua Copus Memorial Postdoctoral Fellowship.*

The Malacology collection at Bishop Museum is seeking highly qualified applicants for an NSF-funded postdoctoral position in Biodiversity Informatics and Computational Biology. The selected applicant will join a team of researchers and collection managers from six national museums to catalog, digitize, aggregate, and mobilize specimen data and resources for Pacific Island land snails. The primary responsibility of the postdoctoral fellowship position will be to lead the development and implementation of an online portal (e.g. Symbiota) for museum data aggregation and assist in taxonomic and nomenclatural evaluations of Pacific Island land snails under the supervision of PI Dr. Norine W. Yeung and collaborators. The position will require the understanding of international biodiversity informatics standards (particularly DarwinCore), and the coordination and communication with national and international biodiversity informatics initiatives, including Global Biodiversity Information Facility (GBIF), Catalog of Life, World Register of Marine Species, and others as appropriate.

For details and to submit application materials visit <https://www.bishopmuseum.org/careers/> Informal inquiries can be emailed to Dr. Norine Yeung at nyeu@hawaii.edu

Kenneth A. Hayes

Director of Pacific Center for Molecular Biodiversity

Bishop Museum

T: 808.847.8217

On View Now < https://www.bishopmuseum.org/exhibits/#_blank >

Follow us on Facebook < https://www.facebook.com/BishopMuseum/#_blank >, *Instagram < <https://www.instagram.com/bishopmuseum> >*, & Twitter < https://twitter.com/bishopmuseum#_blank >

*Bishop Museum inspires our community and visitors through the exploration, celebration**, and perpetuation of the extraordinary history, culture, and environ-

ment of Hawai**É»**i and the Pacific.*

Ken Hayes <hayes.ken@gmail.com>

CharlesU Prague GenomicsGenomeDuplication

*** ERC-funded postdoctoral position in the evolutionary genomics of whole genome duplication

*Start (negotiable): autumn/winter 2020 *Duration: 2 years (with possibility for an extension) *Place: Department of Botany, Charles University, Prague, Czech Republic, EU

We seek a highly motivated, independent early career researcher interested in developing a research program within the context of an ERC-funded project focused on the evolutionary consequences of whole genome duplication (for details see below). The successful candidate will join the team of Ecological Genomics lead by Filip Kolář (<https://botany.natur.cuni.cz/ecolgen>). This project will involve close collaboration with other labs focused on ecological and evolutionary genomics of polyploidy, Levi Yant (University of Nottingham, UK) and Christian Parisod (University of Bern, Switzerland).

**Requirements - innovative thinking, enthusiasm for evolutionary biology - keen interest in leading an independent research program and collaborating both within the group and internationally - a strong background in structural, statistical, and/or population genetics/genomics - PhD in evolutionary biology, genetics, bioinformatics, or related fields

**We offer - competitive monthly salary of 2,000 EUR (note that average gross salary in the Czech Republic was ~1,350 EUR monthly in 2019 and living expenses are generally lower in CZ than in western Europe) - work in a young, dynamic and international environment, situated in an inspiring city centre - co-supervision of a PhD student in the same project - involvement in international collaboration including stays in collaborating labs

**Optional - further possibilities for strengthening academic career - take part in teaching relevant courses - supervision of master project(s) in the Bioinformatics or Evolutionary Biology program - participate in fieldwork in Europe or North America - opportunity to develop independent research follow-up project - support for seeking additional self-funded projects in national (e.g.

Junior Researcher projects within The Czech Science Foundation) and international funding schemes (e.g. Marie Curie, EMBO fellowship)

***Project details Whole genome duplication (WGD, polyploidization) is a dramatic genome-wide mutation whose ubiquity across eukaryotes suggests an adaptive benefit, although the underlying mechanism remains unknown. The project will build on our research in *Arabidopsis arenosa* that demonstrated that WGD can increase the capacity of its natural populations to accumulate adaptive variation, but the candidate will extend well-beyond this system to additional species. General conclusions will be drawn taking advantage from replicated ploidy-variable plant species naturally facing multiple environmental challenges, which are partly already sampled and sequenced. Alongside the head - start with available preliminary data, the candidate is expected to be fully involved in the overall project design and lead the analytical part of the project. For overall info on the Starting ERC project see <https://botany.natur.cuni.cz/ecolgen/node/48> . **Pool of potential research topics/areas: - challenging theory on polyploid adaptation towards environmental challenge with novel empirical data (genomic, experimental), possibly with further theory development - design, maintenance and analysis of ecological genomic / quantitative genetic experiments focused on polyploid adaptation - analysis of structural changes in a genome following in natural and experimentally induced WGD - analysis of genomic landscape of introgression between ploidy levels and consequences for adaptation and speciation

Please send your CV, contact details for two referees and a half-page motivation letter as a single pdf file to Filip Kolář (filip.kolar@natur.cuni.cz). Review of the applications will begin on May 25th 2020 and will continue until the position has been filled.

Filip Kolar Department of Botany Faculty of Science, Charles University Benatska 2, CZ - 128 01, Prague, Czech Republic *<https://botany.natur.cuni.cz/ecolgen/> Filip Kolar <filip.kolar@gmail.com>

ClemsonU PlantEvolutionaryEcology

Clemson Department of Biological Sciences Clemson, South Carolina Koski Lab

Position Details:

The Koski Lab in the Department of Biological Sciences at Clemson University seeks a postdoctoral researcher to study local adaptation in floral thermoregulatory mechanisms on an altitudinal gradient. The project involves a combination of lab-based ecological genetic studies (10mo/year at Clemson) and fieldwork in the San Juan Mountains in Colorado (2mo/year). The postdoc will examine mechanisms of differential floral thermoregulation and the impacts of floral temperature on pollen and ovule viability and plant-pollinator interactions. The postdoc will be encouraged to contribute to ongoing projects in the lab and develop new directions in the realm of plant evolutionary ecology and pollination biology. The postdoc will additionally contribute to mentoring undergraduates in the lab in both research and educational outreach efforts. Support is for up to three years pending satisfactory performance after year 1. The Koski Lab and Clemson University are committed to building a culturally diverse community, and encourage applications from members of underrepresented groups in STEM.

Clemson University in upstate South Carolina on the shores of Lake Hartwell and surrounded by the Clemson Experimental Forest. It is close in proximity to the Blue Ridge mountains, as well as larger urban areas. The university hosts excellent facilities to conduct the advertised research. We have access to Clemson's Greenhouse Complex, Herbarium, Multi-User Analytical Lab and Metabolomics Core, Palmetto Computing Cluster, Light Imaging Facility, Genomics and Bioinformatics Facility, and Electron Microscopy Facility.

Qualifications:

Applicants should have a PhD in ecology, evolution, genetics, botany, or a related field; peer-reviewed publications; experience with botanical fieldwork and plant care; experience in research mentoring; and demonstrated skills in experimental design, data management, and data analysis. Basic molecular skills and proficiency with R are preferable.

Strong candidates will demonstrate the ability to work

as part of a team of diverse individuals, and strong written and oral communication skills.

Application Instructions:

Applicants must submit the following: (1) cover letter, (2) a curriculum vitae, (3) a description of relevant research experience and motivation/interest in the current position (1 page maximum), and (4) contact information (including telephone numbers and e-mail addresses) for two to three professional references. Please apply at <http://apply.interfolio.com/76288> Review of applications will begin June 22 2020 and continue until the position is filled.

For more information contact Matt Koski: mkoski@clemsen.edu

Matthew Koski Assistant Professor Clemson University Biological Sciences <https://koskimatt.wixsite.com/-matthewkoski> mkoski@clemsen.edu

Göttingen TreeGenomics

The Department of Forest Genetics and Forest Tree Breeding at the Georg-August-University of Göttingen is offering a position for a

Research Scientist (Postdoc) - Salary is E13 TV-L (100%)

The position is limited to 36 months. The earliest start-date will be 01.06.2020.

The successful candidate will work in the Federal Ministry of Education and Research funded project: 'Bioeconomy in the North: TreeGeneClimate: Sustainable wood and biomass production: Novel property traits, resilience to climate change, pest and diseases'. We will closely cooperate with the Forest Pathology Research group at the Faculty of Forest Sciences and Ecology.

Your tasks - Exome sequencing in *Picea abies* using target enrichment probes - Genome-wide association analyses (GWAS) for the identification of genes for wood properties, decay resistance, growth, and resistance against *Heterobasidion* sp. - Genomic selection for phenotype prediction - Bioinformatic and genetic analyses - Publication of results in peer-reviewed journals - Assistance with the organization and coordination of the project

Your profile - PhD or Master's degree in biology, agricultural sciences, forest sciences or related disciplines - High motivation and enthusiasm - Sound knowledge and

understanding of molecular breeding methods - Experience and profound knowledge in statistics, quantitative genetics and data analysis - Excellent English language skills - Very good publication record (dependent on the career stage) - Very good written and oral communication skills - Ability to work in a team

The University of Göttingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply in fields in which they are underrepresented. The university has committed itself to being a family-friendly institution and supports their employees in balancing work and family life. The mission of the University is to employ a greater number of severely disabled persons. Applications from severely disabled persons with equivalent qualifications will be given preference. Applications should be sent to:

Georg-August-Universität Göttingen, Abt. für Forstgenetik und Forstpflanzenzüchtung, Bessengeweg 2, 37077 Göttingen, forstgen@gwdg.de.

Contact: Prof. Dr. Oliver Gailing, Phone: 0551 39 33536, E-Mail: ogailin@gwdg

"Gailing, Oliver" <ogailin@gwdg.de>

GUFrankfurt PlantEvolutionaryEcology

The Goethe University Frankfurt, positioned among the top international research universities, offers a wide variety of academic programmes, a diverse group of research institutes, and a focus on interdisciplinary approaches to solving complex problems. Today, the Goethe University is the only university in Germany that enjoys significant public funding alongside administrative autonomy and the ability to create a private endowment. Situated in Germany's most cosmopolitan and international city, the university attracts a diverse body of students and researchers from around the world and is with about 46.000 students and 4.600 employees the biggest university in Hessen.

At the Goethe University Frankfurt, Institute of Ecology, Evolution and Diversity, the new working group of Plant Ecology (led by Prof. Dr. J.F. Niek Scheepens) offers a position for a

Research Assistant (postdoc) (m/f/d) (E13 TV-G-U)

The position will be available for 3 years. The starting

date is 01.09.2020. The position is full-time. The salary grade is based on the job characteristics of the collective agreement (TV-G-U) applicable to Goethe University. The restriction of the term of the employment contract is based on the Wissenschaftszeitvertragsgesetz in connection with the Hessisches Hochschulgesetz.

Our working group The current biodiversity crisis manifests itself in loss of landscape, species, and genetic diversity. The overarching goal of our research is to understand the distribution, function and dynamics of intraspecific phenotypic and genetic variation in plants within the context of global change. We specifically investigate rapid adaptation of plant populations to changes in climate and land use. We love to do experiments - e.g. classical common gardens, reciprocal transplantations and evolution experiments - and we combine concepts and methods from classical plant ecology, evolutionary biology, quantitative genetics, and population genetics and genomics. Our working group has access to modern labs and greenhouses and to an experimental field site and offers technical and administrative support in research and teaching.

Qualifications We are looking for an enthusiastic researcher with strong interest in the field of plant evolutionary ecology who is keen to develop an own research profile and simultaneously enjoys collaborating with others. The job includes a teaching duty in Bachelor, Master and teacher programmes. Interest in applying for external funding is a plus.

Requirements are a completed academic degree (Master or equivalent) and a PhD in biology, environmental science or a related discipline with a focus on evolutionary ecology, experimental ecology or a related field of research as well as a strong publication record in international peer-reviewed journals. The successful candidate has very good knowledge of experimental design and statistics and is very well acquainted with R. Very good English and communication skills as well as pronounced teamwork and organizational skills are expected; German language skills are a big advantage for teaching.

Please send your application with CV, a list of publications, contact details of two or three references, and a maximum 3-page synopsis of the planned research focus, by 14.06.2020 exclusively in electronic form in a single PDF file to: Prof. Dr. J.F. Niek Scheepens (anken@bio.uni-frankfurt.de). Questions about the advertisement can be sent to the same email address. The University promotes equal employment opportunities between men and women and supports the employment of disabled persons. Qualified women or persons with physical disabilities are therefore strongly encouraged to

apply and will be given preference in case of appropriate qualifications and aptitudes.

– Plant Evolutionary Ecology Institute of Evolution and Ecology University of Tübingen Tübingen - Germany <http://www.uni-tuebingen.de/PlantEvoEco> <http://grene-net.org> <http://gfoe.org/en/node/169> “niek.scheepens@biologie.uni-tuebingen.de”

InstZool Beijing BeetleMetagenomics

Beijing.IOZ Chinese Academy of Sciences.BeetleMetagenomic

Postdoctoral position, Beetle Metagenomic, Institute of Zoology, Chinese Academy of Sciences, Beijing, China

One full-time PIFI postdoctoral position for two years (with a possible

extension) is available at Prof. Bai's lab from Institute of Zoology,

Chinese Academy of Sciences, located in Beijing, P.R. China.

Topic Coleoptera is the most biodiversity in organic sphere. Based on metagenomics by high-throughput sequencing, the large-scale biodiversity assessment of beetles from different sites from China will be explored, which can reveal the species catalogue, species richness, distribution status, community structure and so on. The relationship of genetic diversity, species diversity and ecological diversity were inferred too.

The work conditions are 1. Two year contract with a possible extension; 2. The appointment ideally starts this June but negotiable; 3. An annual salary to postdoctoral researchers to cover living expenses and health insurance in China. Each selected awardee will receive a pre-tax stipend of \$B!o(B200,000 per year. In addition, the fellowship provides an economy-class round-trip international travel; 4. Be under the age of 40.

Qualified candidates are requested to send a CV with a brief motivation to baim@ioz.ac.cn with a title [Postdoc Application - fullname].

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Many distinguished scientists including thirteen CAS Academicians started their research career in IOZ. Some of them are founders of various sub-disciplines of zoology in China, such as Professor Bing Zhi, first director of IOZ and one of the main founders of modern biology in China. Several sub-disciplines in zoological sciences in China were derived from IOZ, such as entomology, animal ecology, and experimental embryology. IOZ also has a long history of service to the country with many significant contributions, such as successful control of China's chronic agricultural pest-locust, control and management of other pest insects and rodents, establishment of nature reserves in China, conservation of giant panda, crested ibis and other endangered wildlife, reproduction and contraception, and fish nuclear transfer. Zoological Museum of IOZ has over 8 million animal specimens. Several field stations and research bases also play important role in IOZ research programs.

About the PI Dr. Bai has been engaged in the systematics and evolution of insects, e.g. scarabs and ice crawlers. On the basis of inheriting the traditional taxonomy, he has opened up a new research direction of the new taxonomy driven by new technologies such as quantification, Big Data and Artificial Intelligence. The main academic achievements are as follows. (1) He systematically revised the Chinese Scarabaeoidea and Grylloblattodea, built a database on Chinese insect type specimens, and published a new insect order, 4 new families, and more than 200 new genera. (2) In the three key aspects of taxonomic research (character cognition, character comparison, character evolution), new technology innovation-driven research has been carried out, including the development of new instruments and new software in digital and three-dimensional technologies, the integration of quantitative geometric morphometrics and erection on the new research paradigm. The establishment of a new insect order, Alienoptera, and the systematic status of some important extinction groups were revealed. The origin of dung feeding behavior was investigated. An Intelligent Identification System of World Beetles (BICS, <http://beetle.ioz.ac.cn/>) was created.

Contact Ming BAI Ph.D. Full Professor Principal Investigator of the Group of Morphology and Evolution of Beetles Address: Box 92, Institute of Zoology, Chinese Academy of Sciences No. 1, Beichen West Road, Chaoyang District, Beijing, P.R. China Email: baim@ioz.ac.cn [CN] http://sourcedb.ioz.cas.cn/-zw/zjrc/201102/t20110224_3075281.html [EN] http://sourcedb.ioz.cas.cn/yw/scs/pi/201102/-t20110224_3075281.html [BICS] Beetle Intelligent Classification System: <http://beetle.ioz.ac.cn/> Reprints (PDF): <https://www.researchgate.net/profile/->

[Ming_Bai?ev=hdr_xprf](mailto:baim@ioz.ac.cn) “Prof. Dr. BAI Ming” <baim@ioz.ac.cn>

JiangxiAgU China HoneyBeeGenomics

Title: Honeybee biology Post-doctoral Researcher

Position Overview: Honeybee Research Institute is recruiting an early career researcher. The candidate with insect genetic background is strongly encouraged to apply. The candidate with his/her own proposal is preferred.

Requirement:

1. The candidate must have PhD degree or submitted PhD thesis upon the application.
2. A minimal 1 peer reviewed publication in a leading Journal of the field is preferred.
3. The candidate need to communicate with English fluently both orally and in written form.

Funding: The salary and research grant are available for 2 years and the extension for 1 year is possible depending on the performance. The annual salary is 180,000 Yuan (before tax), plus social benefit.

The successful candidate will be based in Honeybee Research Institute, Jiangxi Agricultural University (<http://english.jxau.edu.cn/>), and join a group of enthusiastic young scientists focused on bee biology. The institute respects all forms of diversity and personality. The University provide family friendly community including within campus apartment, free kindergarten and elementary school entrance. The position is available immediately until filled. The candidate with more than 5 years research experience after PhD is not encouraged to apply.

The applicant needs to send a CV to Dr. Huang (qiang-huang@live.com).

For more information please contact Dr. Huang (qiang-huang@live.com)

Qiang Huang Associate Professor Honeybee Research Institute, Jiangxi Agricultural University Zhimin Ave. 1101, Nanchang 330045, China

Qiang Huang <qiang-huang@LIVE.COM>

KTH Sweden DogEvolution

We are looking for a talented postdoc to investigate the role of gene regulatory networks in evolution of dogs from their wolf ancestors. The project is led by Pelin Sahlén, expert in the gene regulation and epigenomics, inventor of Capture Hi-C method, and Peter Savolainen, world leading expert in dog evolution. We have collected several tissue samples (including five different brain tissues) from three European grey wolf, and collection of tissue samples from ancient and modern breed dogs are ongoing. We will first use CUT&RUN and RNA-seq technologies to map enhancers and transcription profiles in these tissues. We will then use Capture Hi-C to generate high resolution promoter-enhancer interaction maps and investigate the dynamic of genomic interactions between wolves and dogs. We will integrate the regulatory networks with genomic, transcriptomic and epigenomic datasets to discover and validate the functional role of enhancers in dog evolution. The successful candidate will also perform functional validations using various assays, including CRISPR activation. This project will pioneer the utilisation of epigenomic and enhancer datasets in the field of molecular evolution for understanding the genetic mechanisms behind selection under rapid evolution.

The successful candidate will work at the SciLifeLab, Solna. Science for Life Laboratory (SciLifeLab, www.scilifelab.se/) is a national center for large-scale life science research with an advanced technological infrastructure. At SciLifeLab, multidisciplinary research is carried out based on DNA sequencing, gene expression analysis, proteomics, bioinformatics, biostatistics and system biology. Examples of thematic research areas that are currently being processed within SciLifeLab are clinical genomics/proteomics, cancer genome and the genomics of complex diseases as well as ecological and environmental genomics.

Qualifications Requirements A doctoral degree or an equivalent foreign degree in molecular biology or related field
Experience in advanced molecular biology techniques
Desired skills Experience in epigenetic assays
 Experience in gene activation/repression assays using CRISPR activation/interference
 Some programming experience in R or Python
Application Apply to this scholarship by e-mail to egrehn@kth.se. You are the main responsible to ensure that your application is complete

according to the ad. Your complete application must be received at KTH no later than 2020-06-15. Mark your application with reference number C-2020-0803. The application must include the following documents:

* Curriculum vitae * Cover letter * Contact information for two references
 Please observe that you apply for a scholarship, not an employment. About the position/positions
 Period: 2 years
 Extent: Full-time
 Amount of scholarship: According to agreement.
 Location: SciLifeLab, Solna

Best, Pelin

Pelin Sahlén Associate Professor

KTH Royal Institute of Technology
 Science for Life Laboratory
 School of Engineering Sciences in Chemistry, Biotechnology and Health
 Tomtebodavägen 23A
 SE-171 65 Stockholm, Sweden
 Skype for Business: pelinak@ug.kth.se

pelinak@kth.se

LaRochelleU AmphibianEvolution

A postdoctoral position is offered to work on the effects of agricultural practices on development, physiology and behaviour of amphibians. The postdoc will be supervised François Brischoux at the CEBC-CNRS (La Rochelle Université), and will interact closely with Frédéric Angelier (CEBC-CNRS). The project is part of a three-years long ANSES-funded research program that aims at improving general understanding of the exposure levels and sublethal effects of agrochemicals on wildlife with birds and amphibians as research models.

The postdoc will analyse (data already collected) the presence and concentrations of contaminants in several breeding sites of amphibians in agricultural versus forested areas, as well as in nearby rivers, in order to assess exposure levels of developing eggs and tadpoles in the wild. In addition, She/he is expected to develop lab and/ or field studies that aim to assess the effects of agricultural practices (including agrochemical use) on the development, the physiology and/or the behaviour of wild amphibians (mainly *Bufo spinosus*, but other species are also available at our study sites) during development (embryos/tadpoles) or later life-history stages. Ambition and capacity to address independent questions are welcome. The postdoc will also be encouraged to join laboratory and field studies with other collaborators of this project. Available facilities at the CEBC include

indoor thermally controlled rooms, and outdoor enclosures. The CEBC has developed a recognized expertise to measure a suite of pertinent physiological markers (hormones, telomeres, metabolism) and has developed collaborations to measure complementary markers (e.g., oxidative stress, microbiota); most of which should be available for the proposed position.

The successful candidate will be recruited by CEBC-CNRS for a 14 months long period starting from mid-November 2020. She/he will be supervised by CNRS Researcher François Brischoux. The post-doctoral fellow is expected to work in an interdisciplinary and lively research environment and will contribute to a national collaborative program.

Requirements

Candidates should meet the following requirements (1) have a PhD in ecotoxicology, ecophysiology or a related field; (2) a successful publication record and (3) be creative and independent. Candidates are encouraged to come with their own ideas provided they are feasible during the time frame of the project.

Terms and salary

The position is available for a period of 14 months starting preferably in November 2020. Gross salary is ca. euro 2,600 per month. The initial appointment is for 14 months with potential renewal contingent on additional funding.

How to proceed

Applications should be sent through the “Portail Emploi CNRS” webpage (<https://emploi.cnrs.fr/>, reference for the application: UMR7372-FRABRI-001, short url: <https://bit.ly/2y2SeAr>). Applications should include a curriculum vitae including a full list of publications, a cover (motivational) letter with a brief description of skills and research interests, and contact details and recommendation letters from 1 to 3 referees. Review of applications will begin as soon as candidates are applying and continue until the position is filled. For more details on the offer and/or application process you can contact François Brischoux (francois.brischoux@cebc.cnrs.fr).

BRISCHOUX

<Francois.BRISCHOUX@cebc.cnrs.fr>

Francois

Madrid Experimental Evolution

POSTDOCTORAL RESEARCHER - EVOLUTIONARY REPEATABILITY IN MICROBES

The role: we are seeking to appoint a highly-motivated Postdoctoral Researcher to investigate how the interplay between genetic constraints, phenotypic plasticity and environmental fluctuations drives the repeatability of evolution. The successful candidate will construct a variety of mutant libraries (from single genes to multi-strain consortia), which s/he will then subject to high-throughput fitness assays and evolve-and-resequence experiments.

Profile: the ideal candidate should be highly-motivated to increase our molecular understanding of evolutionary processes. Preference will be given to those with a strong background in molecular genetics or synthetic biology in bacteria, but candidates with backgrounds in plant-microbe interactions or experimental evolution are also welcome. Expertise in modular gene assembly (e.g. Gibson, golden gate) or high-throughput techniques (e.g., TnSeq, multiplexed mutagenesis) is desirable. Good English communication skills, both written and oral, are essential.

Details: we anticipate the position having a substantial degree of independence. The successful candidate will contribute to experimental design, data analysis and manuscript preparation. There will be ample opportunity for career development, including the possibility to co-supervise PhD, MSc and undergraduate students, apply for funding, teaching and present her/his work on international conferences. The position offers a highly competitive salary with all the benefits of the Spanish National Social Security System, comprising generous sick/maternity/paternity leaves and health, unemployment and retirement insurances. The post is available from September 2020 for 2 years in the first instance, renewable for additional years.

Environment: the successful candidate will join a young, international team led by Dr Couce at the Centre for Plant Biotechnology and Genomics (CBGP), a mixed research centre supported by the Technical University of Madrid (UPM) and the National Institute for Agricultural and Food Research and Technology (INIA). The centre is funded through the Severo Ochoa Excellence program, an award reserved only to the top research institutions across all disciplines in the country. The

everyday working language in the laboratory is English, and most administrative tasks, training and seminars arranged by the centre are conducted in English. Being the third-largest metropolitan area in the EU, Madrid is a vibrant, multicultural hub with a high quality of life and a thriving cultural scene.

How to apply: Interested candidates please send a single PDF file with a motivation letter and a CV including publication list to Dr Alejandro Couce (a.couce@upm.es). Candidates short-listed for interview will be additionally requested two recommendation letters. Please include the word \$B!H(BEvolRepeatMicrob\$B!I(B in the subject line.

– Dr Alejandro Couce Severo Ochoa & CAM Talento Fellow Centre for Plant Biotechnology and Genomics Technical University of Madrid, Spain

a.couce@upm.es

MWLR NewZealand FungiEvolution

We are looking for an enthusiastic and self-motivated researcher with a strong interest in mycology and or fungal ecology

About The Opportunity

The purpose of this role is to lead and undertake research as part of a Marsden Fund project aimed at gaining a deeper understanding of the evolutionary history and dispersal ecology of New Zealand s trufflelike fungi

Specifically the role will require the successful candidate to plan and undertake fieldwork collect and analyse field-based evidence of animal-fungi interactions measure and analyse adaptive traits scent spectral reflectance in trufflelike fungi and perform spatial trait-mapping of trufflelike fungi

This position is fixed-term three years and may be based at our Auckland or Lincoln sites

About You

You will possess a PhD in ecology or a similar field a strong interest in mycology and or fungal ecology and a research background relevant to one or more of the following topics ecological interactions coevolution fungi adaptation and dispersal sensory ecology animal behaviour

You will be enthusiastic and willing to learn new techniques and have experience organising and leading field-

work in remote places

The ideal candidate will have excellent communication skills and a solid publishing record relative to opportunity

Why Manaaki Whenua

Our land our future this is the essence of why Manaaki Whenua Landcare Research exists

At Manaaki Whenua we undertake research that focuses on preserving New Zealand s rich biodiversity improving biosecurity and protecting the health of the land fresh water and soil resources we need for a prosperous future

We recognise the importance of partnerships the special role of Māori and the need to ensure that all New Zealanders have the knowledge understanding and tools to truly live in harmony with our precious environment

We are recognised nationally and internationally for the quality of our research and work with a wide range of organisations within New Zealand and globally

Manaaki Whenua embraces diversity and is committed to an inclusive and respectful workplace where everyone is valued for their unique contribution

What we offer

As an employee of Manaaki Whenua Landcare Research you will work with passionate and talented people in a caring and family friendly environment enjoy good staff benefits and the opportunity for personal growth and career development

How to apply

Enquiries about the position may be directed to Jamie Wood <woodj@landcareresearch.co.nz>

For further details about Manaaki Whenua-Landcare Research visit our website www.landcareresearch.co.nz

Applications close on Thursday 28 May 2020 at 5pm NZT <https://careers.sciencenewzealand.org/-jobdetails/ajid/NGk29/Post-Doctoral-Researcher-Ecology-,38246.html> Industry Non-profit Organization Management Research Government Administration

Employment Type-Full-time

Woodj@landcareresearch.co.nz

North Carolina Bioinformatics Microbial Evolution

Postdoc: Bioinformatics - microbial genomics and evolution

A postdoctoral position is available in the lab of Dr. Louis-Marie Bobay in the department of Biology at the University of North Carolina Greensboro. The lab focuses on microbial evolution and genomics using bioinformatic approaches. Our research topics currently include: 1) the evolution of recombination in bacteria and archaea 2) the processes of speciation in microbial populations and 3) the evolution of gene diversity in prokaryotes. To find out more details about our research, you can visit: <https://louismariebobay.wixsite.com/bobaylab> The hired postdoc will work on an NIH-funded project which aims to characterize the impact of homologous recombination on microbial evolution. Other components of the project include the characterization of adaptive versus neutral processes on the evolution of microbes and the evolution of pan genomes. The project is exclusively computational. Thus, the candidate must be proficient in programming, preferably in Python. Some of the desired skills and areas of expertise include bioinformatics, evolution, population genomics, microbiology, machine learning, and metagenomics.

Salary and benefits will be paid from a five-year R01 NIH grant recently obtained by Dr. Bobay (lead PI) and Dr. Dan Schrider (co-PI) from UNC Chapel Hill. The position will be funded for two years (renewable upon performance).

To apply, email Louis-Marie Bobay at ljbobay@uncg.edu. Please include a CV, a short research statement and the name and email address of at least two referees.

Greensboro is a dynamic city of ~300,000 inhabitant (750,000 metro area) located near the Appalachians and the coast and near the Research Triangle. To find out more information about Greensboro, North Carolina you can visit: <https://realestate.usnews.com/places/-north-carolina/greensboro> Louis-Marie Bobay

– Louis-Marie Bobay, PhD Assistant Professor Department of Biology - EBER 102-117 Univ. of North Carolina at Greensboro Greensboro, NC 27403 USA Phone: (336) 256-2590 Website: <https://louismariebobay.wixsite.com/bobaylab> Louis-Marie Bobay <ljbobay@uncg.edu>

Norway Arctic Genomics

The Molecular Ecology Laboratory of the NIBIO Svanhovd Research Station in northern Norway is seeking postdoctoral researchers that would be interested in joint development of applications for Marie Skłodowska-Curie Actions Individual Fellowships. MSCA-IF grants are available for individual researchers having a PhD degree or four years of equivalent experience, and the deadline of this year's call is September 9, 2020. For more information, see https://ec.europa.eu/research/mariecurieactions/-actions/individual-fellowships_en).

The NIBIO Svanhovd Research Station is a hub for ecological and genetics-based research and monitoring of arctic and subarctic ecosystems (<https://svanhovd-molecol.no/>). We are seeking highly motivated biologists with expertise in molecular ecology, landscape or evolutionary genomics, or metabarcoding and eDNA methods interested in collaboratively developing an incoming MSCA-IF grant application with us, preferably in one of the projects outlined below. To ensure that we have enough time to prepare the application(s), we would be thankful to receive a letter of interest, stating your interest and experience, and a CV by June 15, 2020, sent by e-mail to cornelya.klutsch@nibio.no and snorre.hagen@nibio.no. The nature of the envisioned projects requires prior experience in genetic/genomic laboratory work (e.g., preparation of high-throughput sequencing (HTS) libraries) and bioinformatic processing of HTS data. However, projects can include also ecological fieldwork, depending on the interests of potential candidates.

The Svanhovd Research Station is located in the village of Svanvik beside the Pasvik river, in the middle of the wedge of Norwegian land that separates Russia and Finland in the north. The region represents a transition zone where the eastern Siberian taiga meets the western Boreal forest, and where northern mountain birch forests transition into arctic tundra. Numerous characteristic species of plants, mammals, birds, and insects are found at this intersection of different ecosystems. With a modern molecular-genetic lab on-site, NIBIO Svanhovd presents an ideal location for a molecular geneticist with outdoor tendencies.

Our research station is involved in a broad range of basic and applied eco-evolutionary questions and transna-

tional monitoring of wildlife and fish species. These range from the application of genetic and genomic tools for population and conservation genetics to the use of metabarcoding and eDNA approaches for studying soil and freshwater biota as well as animal diets.

Potential postdoctoral projects include, but are not limited to:

1. Understanding re-colonization mechanisms in large carnivores:

NIBIO Svanhovd has a long tradition of non-invasive genetic monitoring of brown bear populations in Norway, Finland, and Russia. We are now expanding our research activities to genomic approaches studying re-colonization processes in populations of large carnivores. Recolonization can result in rapid shifts in the distribution and density of populations, resulting in changes in selection pressures acting on functional traits connected to dispersal, exploratory behavior, reproduction, and immunity. Building on a large existing in-house collection of scat and hair samples, we will apply different functional genomic approaches to identify gene regions under selection. This project includes also the opportunity to collaborate with our international partners in Fennoscandia and Russia. Alternatively, metabarcoding and microbiome analyses to study spatial and seasonal dietary changes in large carnivores, parasite loads, and the microbiome are possible based on existing collections.

2. Freshwater fish genomics:

Arctic and subarctic freshwater ecosystems are exposed to multiple stressors (e.g., climate change, arrival of invasive species from more southern regions, eutrophication, pollution). Yet, many species, interactions, and systems remain understudied and monitored in these ecosystems. Several lines of research are possible, ranging from dietary analyses based on metabarcoding and microbiome analyses of existing collections to investigating the impact of invasive species, like pink salmon, on native fish populations or more population genomics research of specific fish species (for example, brown trout, grayling, etc.).

Please contact Cornelya Klutsch (cornelya.klutsch@nibio.no) or Snorre Hagen (snorre.hagen@nibio.no) for any questions.

Kind regards,

Cornelya

Cornelya Klutsch, PhD Researcher Norwegian Institute of Bioeconomy Research Department of Ecosystems in the Barents Region Svanhovd Research Station NO-9925 Svanvik, Finnmark Email: cornelya.klutsch@nibio.no

Phone: +47 47902 85 906

Cornelya Klutsch <cornelya.klutsch@nibio.no>

Paris Marine Plankton Metagenomics

POSTDOCTORAL RESEARCH POSITION IN METAGENOMICS

TOPIC: Unravelling the Marine Planktonic Genomic Dark Matter

One full-time postdoctoral position for 1 year is available at the Muséum National d'Histoire Naturelle (MNHN) and Sorbonne Université (<http://www.sorbonne-universite.fr/>), located in Paris, France.

The post-doctoral fellow will work in the framework of the European project *Blue-Cloud* (<https://www.blue-cloud.org/>), which aims at improving the knowledge of our oceans and seas and bringing them closer to citizens. The post-doc will be part of the *Plankton Genomics* demonstrator (<https://www.blue-cloud.org/-demonstrators/plankton-genomics>).

Despite its importance for human well being, marine plankton remains poorly characterized and understood, in particular because of its high diversity in terms of species, functions, but also behaviours, and more globally their role(s) in the ecosystems. Recent metagenomic studies have revealed that marine plankton is far more diverse than previously thought, with hundreds of thousands of genetically distinct taxa and more than 150 million genes documented, however more than half of the planktonic omic sequences has still unknown taxonomy and/or function. The post-doc will unravel the meaning of this planktonic omic 'dark matter' in order to:

- 1) characterize the extent and the distribution of planktonic omic dark matter at a global scale and describe the environmental contexts and ecological preferences;
- 2) infer gene functions based on sequence similarity and co-expression patterns across a wide range of marine environments and biogeographies.

A specific focus on eukaryotic communities will be done for cross-reference purpose with imaging data.

Within the "Institut de Systématique, Evolution et Biodiversité" at the MNHN (<http://isyeb.mnhn.fr/en>), the post-doc fellow will be hosted in the team *Atelier de Bioinformatique*, and she/he will work in di-

rect collaboration with the *Genoscope* (Laboratoire d'Analyse Génomique des Eucaryotes, Evry, France) and the LOV (*Laboratoire d'Océanographie de Villefranche*, Villefranche-sur-mer, France). He/she will benefit from the active network from the european *Blue-Cloud* project and from the other ongoing projects from the labs (i.e. FORMAL project & consortium, From Observing to Modelling ocean Life; Oceanomics project & Tara Oceans consortium). The post-doc fellow will interact with experts in bioinformatics, data assimilation (omics, imaging), biostatistics and numerical modelling, but also in evolution, ecology and marine biology.

QUALIFICATIONS - PhD in Bioinformatics (or Biology with strong skills in Bioinformatics).

The candidates are expected to have an experience in programming, statistics and omic studies. Interests in ecology, evolution and/or oceanography is considered as a plus.

SALARY - about 2100 euro per month after taxes (more depending on experience); includes extensive healthcare and benefits. Position is full-time and funded for 1 year, with opportunities for extensions.

APPLICATION PROCEDURE:

The application should include a (1) CV detailing experience and list of publications & communications, (2) the name and contact details of two academic referees.

The *application should be emailed* to lucie.bittner@upmc.fr and eric.pelletier@genoscope.fr *before the 1st of June 2020*.

Interviews will be organized remotely starting mid-June and the *position is available immediately*.

Applicants are encouraged to contact us as soon as possible.

For informal enquires and more details, email lucie.bittner@upmc.fr and/or eric.pelletier@genoscope.fr

Selected publications

Carradec, Q., Pelletier, E., Silva, C.D., Alberti, A., Seeleuthner, Y., Blanc-Mathieu, R., Lima-Mendez, G., Rocha, F., Tirichine, L., Labadie, K., Kirilovsky, A., Bertrand, A., Engelen, S., Madoui, M.-A., Méheust, R., Poulain, J., Romac, S., Richter, D.J., Yoshikawa, G., Dimier, C., Kandels-Lewis, S., Picheral, M., Searson, S., Jaillon, O., Aury, J.-M., Karsenti, E., Sullivan, M.B., Sunagawa, S., Bork, P., Not, F., Hingamp, P., Raes, J., Guidi, L., Ogata, H., Vargas, C., Iudicone, D., Bowler, C., Wincker, P., 2018. A global ocean atlas of eukaryotic genes. *Nature Communications* 9, 373. <https://doi.org/10.1038/s41467-017-02342-1> Faure, E., Not, F., Benoiston, A.-S., Labadie, K., Bittner, L., Ayata, S.-D., 2019.

Mixotrophic protists display contrasted biogeographies in the global ocean. *The ISME Journal* 13, 1072-1083. <https://doi.org/10.1038/s41396-018-0340-5>

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PennState EcolEvolutionaryGenomics

I am hiring 1-2 postdoctoral researchers to work on ecological & evolutionary genomics projects. We are working on studies of local adaptation, co-evolution, invasion, and domestication. Projects are briefly described on my lab website. Positions here: https://psu.wd1.myworkdayjobs.com/-PSU_Academic/job/University-Park-Campus/-Postdoctoral-Scholar_REQ_0000000871-1 Jesse Lasky

Department of Biology Pennsylvania State University
laskylab.org < <http://www.laskylab.org> >

“Jesse R. Lasky” <jrl35@psu.edu>

Shenzhen 2 GenomicsHerbs

Genomics of Chinese herbal medicine, Shenzhen, China
The Center of Synthetic Biology at Agricultural Genomics Institute of Chinese Academy of Agricultural Sciences (CAAS) at Shenzhen is hiring 2 postdocs starting as soon as possible.

The total income per year is around \$46,000.

The position is limited to 24 months with the possibility of extension based on satisfactory performance for another 12 months.

Your tasks:

The postdocs will work closely with the PI, collaborators, and lab personnel to utilize multi-omics data and

bioinformatic tools to investigate the molecular mechanism of effective constituents of Chinese herbal medicine. The position also involves preparing manuscripts, data management and dissemination, and mentoring graduate and undergraduate students. The ideal candidate will demonstrate the ability to identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions. In addition, the postdocs will participate in a variety of projects and cooperate with national and international partners.

Preferred Qualifications: PhD degree was required by the appointment start date (must-to-have); Demonstrated expertise in programming languages, such as unix shell scripts, R or Python; Demonstrated expertise in population genetics, such as GWAS, detection of selection etc.; Demonstrated expertise in analysis of genomic, transcriptomic or metabolomic datasets.

To Apply: Please send your CV (including a list of three potential referees) and cover letter to wangli03@caas.cn.

All letters will be treated as confidential. This recruitment will remain open until filled.

If you have any questions, please contact PI Dr. Li Wang, Phone: +86 13560761317, E-Mail: wangli03@caas.cn

Chinese Academy of Agricultural Sciences (CAAS) is an Equal Opportunity Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or any other protected status.

Agricultural Genomics Institute (AGIS) is located at the hinterland of Dapeng New District in Shenzhen, which is surrounded by mountains, close to the subtropical sea and regarded as the paradise of outdoor activities. AGIS is a scientific research government-supported organization in fields of agricultural genomics, molecular breeding, food safety, agriculture and food metagenome etc. Founded in 2014, AGIS has been developing at a rocket speed. AGIS aims to become a first-class international research institute. For the complete information, please see <http://agis.caas.cn/en/index.htm> <wangli03@caas.cn>

UAlberta HostParasiteInteractions

POSTDOCTORAL POSITION in: Ecology and Evolution of Host-Parasite Interactions University of Alberta

A post-doctoral position is available starting January 2021 to study the ecology of fear in host-parasite interactions. Hosts avoid exposure to infection by avoiding infective stages, associated cues, infected individuals, or alter their habitat use to avoid encountering parasites. These non-consumptive effects (NCE) are known as the “ecology of fear”. Potential projects include, but are not limited to investigating the: 1) state-dependent nature of NCE, 2) trait-mediated NCE, 3) NCE of parasites on host metabolism, and 3) evolutionary consequences of NCE. Successful applicants will investigate these questions using a fruit fly-mite system, applying concepts and techniques from behavioral ecology, physiological ecology, and/or experimental evolution. For more information: <https://grad.biology.ualberta.ca/luong/> QUALIFICATIONS:

PhD in ecology, evolutionary biology, parasitology, or related fields

strong English written and oral communication skills

experience in small animal respirometry preferred

ability to work as a part of a collaborative team

previous experience supervising undergraduate and/or graduate students

track record of first author, peer-reviewed publications

To Apply: Please send a cover letter, curriculum vitae, and contact information for three academic references to Dr. Lien Luong (lluong@ualberta.ca).

Closing date: The position will remain open until filled.

We thank all applicants for their interest; however, only those individuals selected for an interview will be contacted.

Lien T. Luong, PhD Associate Professor Department of Biological Sciences CW 405, Biological Sciences Bldg. University of Alberta Edmonton, AB T6G 2E9 Canada Office: (780) 492-1818 <https://hocking.biology.ualberta.ca/labs/luong/> Lien Luong <lluong@ualberta.ca>

UCalifornia Berkeley EvolutionaryGenetics

The Department of Plant and Microbial Biology at the University of California, Berkeley seeks applications for a Postdoctoral Scholar in the Blackman Lab, in the area of Evolutionary and Ecological Genetics, at 100% time,

with an anticipated start in summer or fall 2020.

Applying tools from evolutionary genomics, molecular genetics, and field ecology in sunflowers (*Helianthus*) and monkeyflowers (*Mimulus*), research in the Blackman Lab addresses the following questions: How do plants cope with daily and seasonal environmental fluctuations? How and why do these responses evolve along environmental gradients? How are multi-trait adaptations assembled over evolutionary time?

Responsibilities: The postdoc will work closely with the PI, collaborators, and lab personnel to design and lead research in the lab and field on the genetics and ecology of natural variation in floral development in sunflower. The position also involves preparing grant proposals and manuscripts, data management and dissemination, and mentoring graduate and undergraduate students. The ideal candidate will demonstrate the ability to integrate across biological disciplines, identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions.

The Position: The aims of the position will be tailored to the expertise of the successful applicant while serving as a complement to the Blackman Lab's broad interests in the genetic basis of adaptation and domestication, the ecology and evolution of plant development, as well as the mechanisms of organism-environment interaction. Current NSF-funded work in the Blackman Lab is focused on following the history and function of sunflower domestication alleles with ancient DNA and gene expression studies as well as the genetics of natural variation in solar tracking and floret maturation. Additional lab and field work in wild sunflowers and monkeyflowers centers on the genetic changes and ecological pressures contributing to clinal variation in developmental plasticity, with an emphasis on responses to seasonal cues.

Basic Qualifications (By application date): Candidates must have completed all degree requirements except the dissertation or be enrolled in an accredited PhD, or equivalent international degree program

Additional Qualifications (By start date): PhD (or equivalent international degree) required by the appointment start date The candidate may have no more than four years of post-degree research experience

Preferred Qualifications: (By start date): Demonstrated expertise in evolutionary and developmental genetics Demonstrated expertise in analysis of genomic or transcriptomic datasets, programming for bioinformatics, biostatistics, image analysis, machine learning, plant physiological ecology, QTL mapping/GWAS, or gene expression studies

Appointment: This position reports to Professor Benjamin Blackman. The initial appointment will be at 100% time for one year with the possibility of extension based on satisfactory performance and availability of funding.

Salary and Benefits: Salary will be commensurate with qualifications and experience and based on UC Berkeley Postdoctoral salary scale. Generous benefits are included <https://vspa.berkeley.edu/postdocs> To Apply: Visit: <https://aprecruit.berkeley.edu/JPF02561> Specific questions regarding the recruitment can be directed to Professor Blackman, bblackman@berkeley.edu

This recruitment will remain open until filled.

All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e. dossier service or career center) to the UC Berkeley Statement of Confidentiality (<http://apo.berkeley.edu/evalltr.html>) prior to submitting their letters.

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

The University of California, Berkeley has an excellent benefits package as well as a number of policies and programs in place to support employees as they balance work and family.

Benjamin Blackman Department of Plant and Microbial Biology University of California, Berkeley 361 Koshland Hall

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UEdinburgh

Cross-SpeciesRNACommunication

Postdoctoral Research Associate in the Computational Analysis of Cross-Species RNA Communication at the University of Edinburgh, UK

We are looking for a postdoctoral researcher to apply computational analyses to the study of cross-species communication mediated by small RNAs. The project involves comparative analysis of small RNA-producing loci in closely related gastrointestinal nematode parasites and analysis of changes in small RNA populations in response to variable environmental conditions (nutrient availability/co-infections).

This is a demanding but exciting opportunity for an ambitious, driven individual to develop expertise in small RNA biology, evolutionary biology, and cross-species communication in a host-parasite context.

A PhD (or near completion) in evolutionary biology, computational biology, genomics, RNA biology, parasitology, ecology or related field is required. The ideal candidate will have previous experience in transposable elements and/or small RNA biology and experience in using/developing imaginative or innovative approaches to solving bioinformatic problems and/or evolutionary biology problems.

This project is funded by the Leverhulme Trust and involves a cross-disciplinary team of collaborators/advisors including Amy Buck (small RNA biochemistry), Amy Pedersen (ecology of host-parasite interactions in the wild), Darren Obbard (population genetics and small RNAs), Cei Abreu-Goodger (small RNA analyses and targets) and Mark Blaxter (nematode genomics).

This is a full time post, available until 30th June 2022.

Salary: 33,797 to 40,322 per annum

Closing date: 18th June 2020 at 5pm

To apply: https://www.vacancies.ed.ac.uk/pls/-corehrrecruit/erq.jobspec_version.4.jobspec?p_id=-052161 Please email Dr Amy Buck (a.buck@ed.ac.uk) and/or Dr Amy Pedersen (amy.pedersen@ed.ac.uk) if you have any questions about the position.

Dr. Amy B. Pedersen Reader

Institute of Evolutionary Biology & Centre for Immunity, Infection and Evolution (CIIE) School of Biological Sciences University of Edinburgh Kings Buildings Ashworth Laboratories, Charlotte Auerbach Road Edinburgh EH9 3FL, UK

amy.pedersen@ed.ac.uk +44(0) 131 650 8674

<http://www.biology.ed.ac.uk/research/groups/-apedersen/> The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

WILSON Amy B Pedersen <Amy.Pedersen@ed.ac.uk>

UGöttingen 2 TreeGenomics

The Department of Forest Genetics and Forest Tree Breeding at the Georg-August-University of Göttingen is offering a position starting as soon as possible for a

Research Associate (Postdoc) (all genders welcome) - Salary is E13 TV-L (100%)

The position is limited to 36 months with the option of renewal for another 36 months.

Your tasks

You are expected to develop an independent cutting-edge research program in the field of population genomics of trees. In addition, you will participate in a variety of projects and cooperations with national and international partners. Finally, your participation in undergraduate and graduate teaching according to ?? 31 NHG and service at the Department of Forest Genetics and Forest Tree Breeding is expected.

Your profile Prerequisites are a PhD degree and a proven track record of in the field of population genetics, molecular biology, bioinformatics or similar research fields. High motivation to participate in and to develop new projects and cooperations are essential for the position. Experience in teaching both in English and German are desirable. Well-founded knowledge of the German language is not a prerequisite, but a solid command of the German language should be acquired in a timely manner. International experience and an excellent research track record are desirable. The candidate has the opportunity to gain a post lecturer qualification (Habilitation) which enables the supervision of PhD students at German Universities.

We offer * A well-equipped molecular lab (MassARRAY genotyping platform, capillary sequencers) and access to genome and transcriptome sequencing facilities. * Participation in ongoing population genomic projects * Cooperation with a highly motivated team of populations geneticists and molecular biologist * Technical support for lab and field experiments * Opportunity to develop an independent research program

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

Please send your application with the usual documents (curriculum vitae and scientific background, certificates, references from a university teacher) (in electronic form preferably in a single PDF-file) by e-mail within three weeks after publication of the job description.

Georg-August-Universität Göttingen, Abt. für Forstgenetik und Forstpflanzenzüchtung, Bismarckweg 2, 37077 Göttingen, forstgen@gwdg.de.

If you have any questions, please contact: Prof. Dr. Oliver Gailing, Phone: ++49 551 39 33536, E-Mail: ogailin@gwdg

Please note: With submission of your application, you accept the processing of your applicant data in terms of data-protection law. Further information on the legal basis and data usage is provided in the Information General Data Protection Regulation (GDPR)

The Department of Forest Genetics and Forest Tree Breeding at the Georg-August-University of Göttingen is offering a position starting as soon as possible for a

Research Associate (Postdoc) - Salary is E13 TV-L (100%)

The position is limited to 36 months. The successful candidate will work in the Federal Ministry of Food and Agriculture funded project: "Analysis of genetic, epigenetic and phenotypic variation in Douglas-fir natural populations and in German plantations".

Your tasks - Next Generation methylome and genome analysis - Identification of genetic and epigenetic variation (SNPs und SMVs) associated with growth and qual-

ity traits - Association genetic analyses in Douglas-fir provenance trials Characterization of gene-environment interactions Organization of sample collection - Publication of results in peer-reviewed journals - Assistance with the organization and coordination of the project

Your profile - PhD or Master's degree in biology, agricultural sciences, forest sciences or related disciplines - Sound knowledge and understanding of molecular and genetic methods - Experience and profound knowledge in statistics and data analysis - Excellent English language skills - Very good written and oral communication skills

High motivation and enthusiasm as well as teamwork skills are desirable.

The University of Göttingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply in fields in which they

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UHelsinki 2 SalmonEvolution

A postdoctoral position is available at the University of Helsinki, Finland working in Prof. Craig Primmer's research group (<http://www.helsinki.fi/evolution-conservation-and-genomics>) as a part of an ERC-funded project aiming to investigate evolutionary and ecological factors behind a large effect locus controlling salmon age at maturity (Barson et al. 2015), with the current focus being on common garden and semi-natural experiments (e.g. Debes et al. 2020).

The postdoc will be responsible for continuing experiments on Atlantic salmon studying reaction norms of fitness-related traits in common garden and semi-natural conditions, as well as analyzing 3 years of available data. This work is complemented by molecular, ecological, evolutionary and quantitative genetic research being conducted within the same project.

An appointee to the position shall hold a doctoral degree and have the ability to conduct independent scholarly work. Suitable applicants will have a strong background

in the design and implementation of common garden experiments as well as in statistical analysis of evolutionary ecological data, as demonstrated by publications on relevant topics. Experience in evolutionary or quantitative genetics and/or experience with aquatic animal husbandry and experimentation is an advantage. The ability to work as a part of a larger research team addressing related questions is also important.

The position is initially available until 8/2022, possibly with a 1 one year extension option. The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance with the overall starting salary amounting to c. 3052-3580 EUR per month, depending on the previous relevant research experience of the candidate.

Formal applications should include as a single pdf file: - a CV including a list of publications and with names and contact details of at least two referees - a max. 2 page letter of motivation

To apply, please submit your application using the University of Helsinki electronic recruitment system via the following link <https://www.helsinki.fi/en/open-positions/postdoctoral-researcher-in-salmon-evolutionary-ecology> (via "Apply for the position").

The deadline for applications is 10 June 2020, with the preferred starting date being August / September 2020. Informal inquiries can be directed to Professor Craig Primmer ([craig.primmer\(at\)helsinki.fi](mailto:craig.primmer(at)helsinki.fi)).

Finland is a member of the EU, has high quality free schooling (also in English), very affordable childcare, generous family benefits and healthcare, and was recently ranked as the best country in the world for expat families and in the world's top ten most livable cities. The University of Helsinki is a top 100 ranked university in most ranking lists, and is currently investing heavily in life science research (see <https://www.helsinki.fi/en/helsinki-institute-of-life-science>). Primmer's research group currently consists of around 20 people, including 6 post docs, 6 PhD students and 6 research assistants with 11 different nationalities.

Relevant articles:

Barson et al. (2015) Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. *Nature* 528:405-408.

Debes et al. (2019). Large single-locus effects for maturation timing are mediated via condition variation in Atlantic salmon. *BioRxiv*, 1-15. doi: 10.1101/780437 <https://www.biorxiv.org/content/10.1101/780437v3>

Craig Primmer, Academy Professor PO Box 56 Organismal & Evolutionary Biology Research Program | Biotechnology Institute 00014, University of Helsinki, FINLAND Visiting: Room 3404, Biocenter 1C Mobile +358 503116374 craig.primmer@helsinki.fi Twitter @FishConGen <http://www.helsinki.fi/evolution-conservation-and-genomics> —

A postdoctoral position is available at the University of Helsinki, Finland to work in Prof. Craig Primmer's research group (<http://www.helsinki.fi/evolution-conservation-and-genomics>). The position is a part of a research program aimed at understanding the molecular mechanisms of a large effect locus controlling age at maturity in Atlantic salmon (see Barson et al. 2015; Kurko et al 2020; Verta et al. 2019). Salmon age at maturity is a key fitness-related trait, where 40% of maturation age variation is linked to the genotype at the *vgll3* locus.

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UJyvaskyla StressGenomics

Postdoctoral Researcher in stress genomics at the Department of Biological and Environmental Science, University of Jyväskylä, Finland. Starting 1 September 2020 or as soon as possible thereafter, contract length maximum of two and half years.

We are seeking an innovative postdoctoral researcher to join our group <https://www.jyu.fi/science/en/bioenv-research/biosciences/stress-genomics> to study genomic basis of stress tolerance with specific focus on transposable elements (TEs). In our group we investigate how chromosomal inversions, TEs and alternative splicing of the genes affect species' ability to respond to various environmental stressors. We are focusing on the interaction between these mechanisms at the genomic and phenotypic level using long-read PacBio genome sequencing, specific stress tolerance experiments and northern *Drosophila* species as a model.

The postdoctoral researcher will join Dr. Maaria Kankare's research group at the Department of Biological and Environmental Science. S/he will also spend 2 months in the laboratory of Dr. Josefa González at

the Universitat Pompeu Fabra in Barcelona, Spain (in autumn 2020 or spring 2021) to carry out collaborative bioinformatic analyses in TEs. Our group has strong international collaboration and the selected candidate can also be part of the European Drosophila population Genomics Consortium (droseu.net) that brings together 61 research labs across 27 countries.

To be eligible, the candidate needs to have a doctoral (PhD) degree in evolutionary biology, (evolutionary) bioinformatics or in closely related biological field, as well as good communication and writing skills in English. Experience in bioinformatic analyses of different types of genomic data sets is required. Importantly, the candidate should have a strong interest in evolutionary genomics and especially in the role of transposable elements. Experience with molecular biology laboratory methods and/or statistics is an advantage.

The annual salary range will be approximately 38,000 EUR (gross income, including holiday bonus), depending on the qualifications and experience of the candidate.

For further details, please contact: Dr. Maaria Kankare, maaria.kankare@jyu.fi

Application form and extra information in https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&jc=12&id=-00009305&lang=fi s.maaria.kankare@jyu.fi

UKansas IRACDA EvolutionaryQuantitativeGenetics

The Macdonald and Unckless labs at the University of Kansas invite applications to work on aspects of Drosophila quantitative and evolutionary genetics as an IRACDA postdoc. The IRACDA program provides trainees with both rigorous research and real college teaching experience and is ideal for trainees interested in positions where teaching is a focus.

The Macdonald lab (<https://molecularbiosciences.ku.edu/stuart-j-macdonald>) studies the quantitative genetics of complex traits including xenobiotic and heavy metal tolerance as well as the regulation of gene expression in these and other contexts. The Unckless lab (<http://uncklesslab.com>) studies the evolutionary genetics of innate immunity and genetic conflict. Both labs use a combination of computational, genomic, wet lab and classical genetic approaches. IRACDA postdocs could work

in either lab exclusively or propose to work on a project on quantitative genetics of immune defense which would span the two labs. Because this project is externally funded, there is some latitude in project choice. If interested, please contact Stuart Macdonald (sjmac@ku.edu) or Rob Unckless (unckless@ku.edu) or both to discuss possibilities.

The Institutional Research and Academic Career Development Award (IRACDA) program is an NIH-funded training program. To be eligible, applicants must be US citizens or permanent residents, and within 2 years of receiving their PhD at the time of appointment. For more information on the IRACDA program, please visit: <https://iracda.ku.edu/apply> . “unckless@ku.edu” <unckless@ku.edu>

UKansas PlantMicrobiomeEvolution

A postdoctoral researcher position is available in the Wagner Lab at the University of Kansas (<http://wagnerlab.faculty.ku.edu>) to investigate how a shared abiotic stress affects the evolution of plant-microbe interactions. The overarching goals of this NSF-funded project are to identify soil metagenome features associated with historical exposure to drought; to identify mechanisms of rapid adaptation to drought for both host-associated and free-living soil microbial communities; and to assay the consequences of soil microbiome drought adaptation for host plant physiology and performance. This is an international collaboration with researchers from the group led by Dr. Gabriel Castrillo (University of Nottingham, UK).

The postdoctoral researcher will be responsible for leading experiments, analyzing data, and writing manuscripts to accomplish the goals of the grant. Specific responsibilities will include sequencing soil metagenomes/metatranscriptomes; executing greenhouse experiments; collecting plant phenotype data; and testing for gene expression changes in plants and microbes. The postdoc will also have opportunities to develop additional, independent lines of research within the scope of the grant.

The successful candidate will have a publication record in at least one of the following areas: plant-microbe interactions, functional genomics, microbial ecology, evolutionary genetics, plant ecological physiology, molecular ecology, or related field(s). Desirable skills include plant cultivation, a strong statistical foundation, bioinformat-

ics, experience with standard molecular biology methods (nucleic acid purification, PCR, etc.), and experience with other experimental methods related to plant or microbial physiology.

Women, first-generation academics, scientists of color, and members of under-represented groups are strongly encouraged to apply, even if you don't have all of the skills mentioned above. Mentorship and training are included in this position, and the Wagner lab is committed to recruiting, retaining, and supporting talented researchers from diverse backgrounds.

KU is located in Lawrence, Kansas a vibrant college town with easy access to both Kansas City and the beautiful Flint Hills region, the largest remaining tract of old-growth tallgrass prairie in North America. This position is funded for 3 years (contingent on satisfactory performance) and includes benefits, a competitive salary, and professional development opportunities. The start date is somewhat flexible but ideally August, 2020.

Applicants should submit a cover letter describing why this position is a good match for their research interests, experience, and goals; a CV; and the contact information for three professional references. Please submit these materials as a single PDF in an e-mail to maggie.r.wagner@ku.edu using the subject line "Postdoc application - <your last name>". Review of applications will begin June 5th and will continue until a suitable applicant is found. Informal inquiries before application are welcome.

Maggie R. Wagner, Ph.D. Assistant Professor, Department of Ecology and Evolutionary Biology Assistant Scientist, Kansas Biological Survey University of Kansas maggie.r.wagner@ku.edu

"Wagner, Maggie" <maggie.r.wagner@ku.edu>

tid fruit fly pests. This specific project is funded by the Plant Protection Act (USDA-APHIS) and expands on our previous work (e.g. Dupuis et al. 2019 *Evol App* 12:1641-1660) using population genomics to develop diagnostic tools for the Mexican fruit fly. This project will leverage large population genomic datasets (thousands of individuals) to create/improve diagnostic marker sets for identification/delimitation of sterile insect technique (SIT) strains, genetic characterization of SIT mass rearing colonies, and geographic source determination (pathway analysis).

The applicant will be expected to work independently and supervise technical staff and students, as well as work as part of a larger research team. Required qualifications include strong interpersonal skills and experience in population genomics (data analysis, statistics, curating large datasets), wet-lab molecular biology (RADseq/GBS), and bioinformatic analysis of high-throughput sequence data (linux/unix, scripting, etc.). Minimum PhD in genetics, biology, entomology, or similar is required.

Position is full-time and funded for 1 year with opportunity for renewal contingent on continued external funding. Salary is ~\$48,000/year plus benefits. If interested, please submit a cover letter, CV, and contact info for three references to julian.dupuis@uky.edu.

– Julian R. Dupuis, Ph.D. Assistant Professor Department of Entomology University of Kentucky Lexington, KY 40546 (859) 562-2544 julianrdupuis.com

"Dupuis, Julian R." <Julian.Dupuis@uky.edu>

UKentucky InsectPopulationGenomics

Postdoc position in insect population genomics

I am seeking an enthusiastic, self-motivated postdoctoral researcher to join my research group at the University of Kentucky (www.julianrdupuis.com) with an anticipated (but flexible) start in fall 2020. This position would join a collaborative research group working on the development of molecular diagnostic tools for species identification and pathway analysis in invasive tephri-

UOulu QuantGenetics ForestBreeding

Apply here! https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&lang=en&id=-00009150&jc=1 Postdoctoral Researcher in Quantitative Genetics: Genomic Predictions in Forest Tree Breeding

The University of Oulu is an international scientific community, with approximately 15 000 students and 3 000 employees. The strengths of the University are wide multidisciplinary study and research interests, modern research and study environment and extensive cooperation with international educational and research institutes.

The Faculty of Science at the University of Oulu is announcing an open postdoctoral position, which will be located at the Research Unit of Mathematical Sciences (<http://www.oulu.fi/mathematics/>) which has an internationally strong position at the forefront of research in its focus areas. The Research Unit is a partner in one Finnish Centre of Excellence in Inverse Modelling and Imaging (<https://www.helsinki.fi/en/researchgroups/centre-of-excellence-of-inverse-modelling-and-imaging>). The appointee will also work in close collaboration with the Research Unit of Ecology and Genetics and Natural Resource Institute of Finland (LUKE).

This position is aimed at strengthening the participating research units as well as the HiDyn program funded by the Academy of Finland PROFI5. Data Insight for High-Dimensional Dynamics (HiDyn) is a program devoted to multidisciplinary data science and artificial intelligence. It will offer mathematical and methodological expertise to understand high-dimensional dynamic systems.

The postdoctoral position is for 18 months and is aimed to start on August 2020 or as soon as possible thereafter.

Description of the position

The research project “quantitative genetics: genomic predictions in forest tree breeding” aims to combine expertise in quantitative genetic methodology and forest genomics and breeding. The research will concentrate on developing and applying new methodologies of data science and artificial intelligence to tackle research problems related to genomic predictions in forest tree breeding.

The new Postdoc researcher is expected to write and publish scientific articles in international peer-reviewed journals documenting the achievements of the work. Some participation in teaching is required.

The work will be supervised by the collaborative research group (Tanja Pyhäjärvi, Katri Kärkkäinen, and Mikko Sillanpää).

Requirements

A Ph.D. (or equivalent) in Computational or Applied Mathematics, Statistics, Quantitative Genetics, Forest Genetics or a related field is required. Some postdoctoral experience is of advantage, but the applicant should have attained a Ph.D. no more than 10 years before the end of the application period.

The candidate is expected to have computational orientation and knowledge in at least one of the related fields of the project. This includes quantitative genetics methods, GWAS, Bayesian statistics, longitudinal analysis and linear mixed models. Knowledge of forest tree breeding are considered as an advantage, but are not necessary.

Special emphasis will be given to research expertise within the subject field, demonstrated by an international publication record. Work abroad and other international experience will be regarded as an asset.

Salary

The salary of a Postdoc will be based on levels 5 - 6, of the requirement level chart for teaching and research personnel in the salary system of Finnish universities. In addition to the basic salary, the appointee will be paid a salary component based on personal work performance with a maximum of 50% of the basic salary. The full salary is approximately 3,400 - 4,300 euros per month.

How to apply

Applications must be accompanied by the following English-language documents:

- Brief curriculum vitae (Max. size limit of the attachment: 5 Mbytes and 4 pages) - List of publications where it is clearly indicated which publications are peer reviewed - Brief motivation letter summarizing applicant's professional experience and expertise and describing why applicant is interested in about this position. Also, information on personal research interests and career plans are valuable to provide here (max 2 pages).
- Full name and e-mail addresses for at least two persons who are willing to give reference letters (if separately asked).

Applications, together with all relevant enclosures, should be submitted using the electronic application form by 22th of May 2020.

Contact

Professor Mikko Sillanpää, mikko.sillanpaa (at) oulu.fi, puh. 040-6734474

About the City of Oulu

The City of Oulu is Northern Finland's largest and oldest city, with



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UPennsylvania ComputationalPopGenomics

Postdoctoral position in Population and Computational Genomics

Position summary

The Gao lab at the University of Pennsylvania is recruiting two postdocs in population and computational genomics. Ziyue Gao is a new tenure-track assistant professor in the Department of Genetics at Perelman School of Medicine, University of Pennsylvania.

Our lab uses computational approaches to address questions in human genetics in an evolutionary context, such as the mechanisms and consequences of mutation rate variation, the impacts of natural selection on the human genome and phenotypes, and the genetic basis and evolution of human disease and polygenic traits. One major research direction is investigating how and when genetic mutations arise and accumulate over the lifetime of an individual in the germline and in somatic tissues. Another direction is to understand the genetic architecture and evolution of complex traits, including common diseases.

Both postdocs will work on these problems by analyzing genomic data, primarily of modern and ancient human populations. We are also open to candidates with their own research projects in the broad area of human population and evolutionary genetics. In addition, there will be opportunities to work on other projects involving population genomic analysis and collaborating with other labs in the department.

Both positions have flexible start dates and may begin as early as Oct 1, 2020. The appointment is initially for

one year with the opportunity to be renewed for up to three more years, depending on performance, funding, and the postdoc's personal preference. We particularly encourage applications from candidates who have recently completed, or will soon complete, their PhD.

Qualifications

Required:

- PhD in genetics, evolutionary biology, computational biology, bioinformatics, statistics, computer science or a related quantitative field;
- robust mathematical and statistical skills, with a track record of applying them to genomic or other biological data;
- comprehensive experience in working with linux/unix-based environment and command lines;
- proficiency in one or more programming languages (e.g., R, Python, Perl, C/C++);
- good scientific communication skills in writing and in oral presentations.

Nice to have:

- strong motivation and ability to work independently;
- formal training in population genetics or statistics (e.g., demonstrated in transcripts);
- experience with population genetic analyses;
- familiarity with whole-genome sequencing data generation, processing and analysis;
- enthusiasm to mentor graduate students;
- broad interests in biomedical science outside genetics.

To apply

Interested applicants please contact Ziyue at ziyue-gao[at]pennmedicine[dot]upenn[dot]edu with a brief summary of your background and research interests as well as CV including a complete publication list (preprints on bioRxiv or other public repositories can be included). Please also be prepared to have three recommenders send letters of reference on your behalf.

ziyuegao@gmail.com

Uppsala DarwinsFinchesAndAtlanticHerring

Postdoctoral opportunity in Evolutionary Genomics/Bioinformatics - Atlantic herring and Darwin's finches

We are looking for a highly motivated post-doctoral fellow in Evolutionary Genomics/Bioinformatics for a two-year position at the Department of Medical Biochemistry and Microbiology, Uppsala University in Prof. Leif Andersson's research group (http://www.imbim.uu.se/Research/+Genomics/-Andersson_Leif/?languageId=1).

Major ongoing projects where strong bioinformatics expertise is needed include (PMID for recent publications that illustrate ongoing research): Evolution and genetics of ecological adaptation in Atlantic herring (PNAS: PMID: 31451650; Genome Research: PMID: 31649060); The evolution of Darwin's finches and their beaks (Science: PMID:29170277; Nature Ecology and Evolution: PMID:32367030).

Duties: Take part in bioinformatic analysis of whole genome sequence data (short reads as well as long read data, RNAseq, DNA methylation and ATAC-seq data; population genetics analysis including detection of signals of selection based on whole genome sequence data from thousands of individuals; take part in improving assemblies as well as in generating high quality functional annotations of our genomes of interest.

Qualifications: A PhD in bioinformatics or a related area earned not later than 5 years ago (time spent on parental leave can be deducted). Experience in handling large scale next-generation sequence data is an absolute requirement. Competence in computational biology, population genetics and/or genome assembly is a merit. Since the project requires interacting with other team members and other research groups, an ability to interact with others is an asset.

Further information and applications: Prof. Leif Andersson, Department of Medical Biochemistry and Microbiology, Uppsala University, email: leif.andersson@imbim.uu.se Please include CV, a letter describing your research interest and skills, and the names and contact information (address, email address, and phone number) of at least two reference persons.

Deadline: You are welcome to submit your application no later than May 31, 2020 by email: leif.andersson@imbim.uu.se. The position is available as soon as the current conditions permit.

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

Vienna PolygenicAdaptation

Polygenic adaptation: a postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (<https://www.vetmeduni.ac.at/en/population-genetics/>). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

Vienna has an outstanding community of evolutionary biologists (<https://www.univie.ac.at/evolvienna/>) and a unique cluster of scientists with a keen interest to understand polygenic adaptation (e.g.: N. Barghi, N. Barton, R. Bürger, J. Hermisson, R. Kofler, M. Nordborg and H. Sachdeva).

Adaptation to new environments is frequently driven by traits with a polygenic basis. Nevertheless, the characterization of the adaptive architecture, in particular in natural populations, is challenging. The contribution of individual loci to the phenotypic changes associated with adaptation to new environmental conditions is so small that their identification and functional characterization is frequently not possible.

The successful candidate will join a team of scientists taking advantage of experimental evolution to study the adaptive architecture of temperature adaptation - a highly polygenic trait. Manipulating the genetic composition of a series of founder populations provides an unmatched opportunity to study polygenic adaptation in *Drosophila*. We are using a combination of genomic analyses with high throughput molecular phenotyping

(RNA-Seq, metabolomics, proteomics) and targeted high-level phenotypes (e.g. behavior) to study these experimental populations. The goal is to understand polygenic adaptation in the context of the underlying functional variation and use this information to predict adaptive responses in the laboratory and natural populations.

We are looking for a candidate with a background in quantitative genetics and experience in handling large data sets. A solid background in population genetics and statistics will be further assets. The successful applicant will be supported by technicians for the collection of phenotypic data and the maintenance of experimental populations.

Upon outstanding performance, a group leader position can be offered to establish her/his independent research at the institute.

The position is available for at least two years starting August 2019, but the exact starting date is negotiable. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by 15.6.2020 to ensure full consideration.

Background on our experimental system:

Jaksic, A. M.* et al.* Neuronal function and dopamine signaling evolve at high temperature in *Drosophila*. *Molecular Biology and Evolution*, doi:10.1093/molbev/msaa116 (2020).

Barghi, N., Hermisson, J. & Schlötterer, C. Polygenic adaptation: a unifying framework to understand positive selection. *Nature Reviews. Genetics*, in press (2020).

Barghi, N.* et al.* Genetic redundancy fuels polygenic adaptation in *Drosophila*. *PLoS Biology* *17*, e3000128, doi:10.1371/journal.pbio.3000128 (2019).

Hsu, S. K.* et al.* Rapid sex-specific adaptation to high temperature in *Drosophila*. *eLife* *9*, doi:10.7554/eLife.53237 (2020).

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Yale Human Population Genomics

Postdoctoral Associate Positions at Yale University Human Evolutionary Genomics

Principal Investigator: Serena Tucci

Position Description

The Tucci laboratory (<https://serenatucci.wordpress.com>) at Yale University invites applications for Postdoctoral Research Associate positions. Our research addresses fundamental questions in Human Evolutionary Genomics by using field work, laboratory work, and cutting-edge computational approaches to disentangle the evolutionary forces that have shaped patterns of genetic variation in human populations.

Responsibilities:

A successful candidate will develop and use statistical frameworks to analyze large-scale genomic data sets to reconstruct the evolutionary history of modern and ancient human populations (as well as human and non-human primates) and to gain insights into genetic adaptations.

Expected responsibilities include conducting research, attending weekly lab meetings, participating to scientific journal clubs, preparing research findings for publication and presenting reports at professional meetings. Opportunities exist for mentoring graduate and undergraduate students.

Qualifications

- PhD in Evolutionary Biology, Computational Biology, Population Genetics, Statistics, Biostatistics, Computer Science, Biological Anthropology, or disciplines with strong quantitative backgrounds
- Strong programming and bioinformatics skills (R, Python Perl, or C/C++, Bash scripting, cluster computing, etc)
- Research experience in population genetics analyses and working with large sequencing data sets.
- Strong background in statistical inference
- Independent, motivated, creative, and collegial
- Strong writing skills.

Salary and duration

The initial appointment is for one year, renewable an-

nually up to three more years, pending satisfactory performance and continued funding. Salary is commensurate with qualifications and experience. Flexible start date in Fall 2020.

Applications must be submitted online at: tucci.serena@gmail.com and will be reviewed until the positions are filled.

Applications should include:

- A curriculum vitae
 - A list of publications (for each publication please add a brief description of your contribution).
 - A brief statement of research interests and goals
 - Names and contact information for three references.
- Informal inquiries are welcome. Please contact Principal Investigator Serena Tucci at tucci.serena@gmail.com
- Serena Tucci <tucci.serena@gmail.com>

Workshops Courses

Online Adaptation Genomics Sep14-18 63	Online RNAseq InR Jun15-19 Deadline 67
ONLINE Comparative Genomics Sep21-25 64	Online Seascape Genomics Oct12-16 67
Online Deep Learning Sep28-Oct1 64	Online Whole Genome Sequencing Oct19-22 67
Online Introduction To NGS Sep7-11 65	Summer Inst Stat Genetics Online Jul13-31 68
Online Intro To Phylogenomics Oct1-9 65	
Online R Evolutionary Data Jun23-24 66	

Online Adaptation Genomics Sep14-18

Dear all,

the registrations are now open for the Physalia course on Adaptation Genomics, which will take place ONLINE from the 14th to the 18th of September: (<https://www.physalia-courses.org/courses-workshops/-courseadaptationgenomics/>)

Instructors: Dr. Anna Tigano (University of New Hampshire) and Dr Claire Merot (University Laval).

This course provides an introduction to the study of the genomic basis of adaptation using population genomics approaches applied to the analysis of both sequence

and structural genetic variation. The instructors will guide the participants from the handling of raw genomic data and data exploration (e.g., summary statistics and population structure) up to more advanced methods, including genotype-environment associations based on both sequence and structural variants. Through hands-on exercises, the course will teach basic bioinformatics skills and how to manipulate, visualize and interpret genomic data and patterns.

Learning Outcomes

- 1) Handling genomic data from raw reads to genetic variants
- 2) Calculating basic population genetic statistics
- 3) Visualizing genetic population structure
- 4) Searching for signatures of selection in the genome
- 5) Accounting for putative structural variants

6) Understanding the potential and the limitations of different methods to study the genomic basis of adaptation

Programme: (<https://www.physalia-courses.org/courses-workshops/courseadaptationgenomics/-curriculumadaptationgenomics/>)

Our other online courses: (<https://www.physalia-courses.org/courses-workshops/>)

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org/> =0A=0ATwitter: @physacourses mobile: +49 17645230846

info@physalia-courses.org

ONLINE ComparativeGenomics Sep21-25

Dear all,

the 3rd edition of the Physalia course on Comparative Genomics will be held ONLINE from the 21nd to the 25th of September: <https://www.physalia-courses.org/courses-workshops/course34/> Instructors: Prof. Ingo Ebersberger (Goethe University Frankfurt, Germany) and Dr. Fritz J. Sedlazeck (Human Genome Sequencing Center at Baylor College of Medicine, USA).

This course will introduce biologists and bioinformaticians into the field of comparative genomics. We will cover a broad range of software and analysis workflows that extend over the spectrum from assembling and annotating small eukaryotic genomes, via the identification of single nucleotide variants (SNVs) and structural variants (SVs) within the population, to the assessment of their likely functional impact of the detected variants in an evolutionary context.

Learning outcomes:

- 1) Identification of SNPs and SVs using de novo genome assembly and read mapping strategies
- 2) Assessment of strengths and weaknesses of the different DNA sequencing technologies, Illumina, Pacific Bioscience, Oxford Nanopore, for the detection of variations
- 3) Strengths and pitfalls of de novo assembly and map-

ping approaches for comparative genomics

4) Hands on experience of state of the art methods to compare multiple genomes

5) Annotation of variations and comparative genomics analysis

6) Familiarity with biological sequence analysis in an evolutionary context

Programme: (<https://www.physalia-courses.org/courses-workshops/course34/curriculum-34/>)

Other upcoming Physalia courses will be also held online: <https://www.physalia-courses.org/courses-workshops/> Should you have any questions, please feel free to contact us at info@physalia-courses.org

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

Online DeepLearning Sep28-Oct1

Dear all,

registrations are now open for the Physalia course on “INTRODUCTION TO DEEP LEARNING FOR BIOLOGISTS”, which will be held online from the 28th of September to the 1st of October.

Course website:(<https://www.physalia-courses.org/courses-workshops/course67/>)

The course is aimed at advanced students, researchers and professionals interested in learning what deep learning is and how to develop a deep learning model for applications in biology. It will include information useful for both absolute beginners and more advanced users willing to delve into some aspects of the implementation of deep learning. We will start by introducing general concepts of deep learning presenting a functioning model and then we will progressively describe the main building blocks of a deep learning model and how the internal machinery works. Attendees are expected to have a background in biology and the research problems involving prediction, inference, pattern discovery; previous exposure to predictive experiments would be beneficial. There will be a mix of lectures and hands-on practical

exercises using mainly Python, Jupyter Notebooks and the Linux command line. Some basic understanding of Python programming and the Linux environment will be advantageous, but is not required.

Learning outcomes

At the end of the course the student will have an understanding of:

- the basic theoretical background of deep learning, both in terms of basic building blocks and of commonly used, state-of-the-art architectures
- differences between classification, regression, segmentation, and how to frame a real-world problem in terms of these classes
- the main steps involved in building a deep learning model for prediction problems in biology, comprising how to evaluate prediction accuracy and how to compare and choose different models
- how to use real-world data for statistical learning, comprising data preparation and data augmentation

Programme: (<https://www.physalia-courses.org/courses-workshops/course67/curriculum67/>)

Our other online courses: (<https://www.physalia-courses.org/courses-workshops/>)

All the best,

Carlo

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brian@helix.mcmaster.ca

Online Introduction To NGS Sep7-11

Course: INTRODUCTION TO NGS data analysis

When: 7-11 September 2020

Where: Due to the COVID-19 outbreak, this course will be held online

Website: <https://www.physalia-courses.org/courses-workshops/course68/> Instructors: Daniel A. Pass, PhD (Cardiff University, UK) and Christoph Hanh, PhD (University of Graz, Austria)

This course will introduce participants into the field

of Next Generation Sequencing biology, understanding both the concepts and handling of the data. We will cover a broad range of software and analyses from quality assessment of sequencing runs, through assembling and annotating small genomes, RNAseq and differential gene expression, and phylogenomics with NGS data. Primarily focussed with Illumina data, we will also look at the different requirements and opportunities when utilising long read data (Nanopore/PacBio). This course will be accompanied with sessions on the use of the Linux command line, and docker which is the preferred platform for most bioinformatic analyses, as well as software containers, through Docker or Singularity, with particular focus on best practices for reproducibility.

Programme: (<https://www.physalia-courses.org/courses-workshops/course68/curriculum68/>)

Should you have any questions, please feel free to contact us at: info@physalia-courses.org

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> "info@physalia-courses.org" <info@physalia-courses.org>

Online IntroToPhylogenomics Oct1-9

Dear colleagues,

Registration is open for Transmitting Science ONLINE course: INTRODUCTION TO PHYLOGENOMICS 'V 2nd edition.

Dates: October 1st-9th, 2020.

Instructors: Jeremy M Brown (Louisiana State University, USA) and Robert Thomson (University of Hawaii, USA).

Course Overview

This workshop will introduce participants to the theory and tools for phylogenetic inference in the era of genome sequencing. Course material will focus on statistical methods for phylogeny estimation, software implementing these methods, applications of these methods to large molecular datasets, and discuss trade-offs and

tools for improving the accuracy of phylogenomic analyses. In hands-on practical sessions, participants will gain experience working with bioinformatic and statistical tools for analyzing large datasets.

The course is intended to facilitate ongoing or planned phylogenomics projects by students, so they are encouraged to notify instructors in advance about the topics of greatest relevance to their own work.

Example software: RevBayes, IQTree, SVDQuartets, ASTRAL, TreeScaper

More information and registration: <https://www.transmittingscience.com/courses/evolution/introduction-to-phylogenomics/> or writing to courses@transmittingscience.com

Payment is not required at the registration.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD Scientific Director
Transmitting Science www.transmittingscience.org

Soledad De Esteban Trivigno
<soledad.esteban@transmittingscience.org>

Online R EvolutionaryData Jun23-24

ONLINE COURSE 'V R for ecologists and evolutionary biologists (IRFB04) - Using datasets from biology with a strong focus on evolutionary data, this course will build required R skills and statistical understanding to be able to analyse datasets most common to this field

This course will be delivered live from the 23rd - 24th June.

<https://www.prstatistics.com/course/introduction-to-r-for-ecologists-and-evolutionary-biologists-irfb04/>

TIME ZONE 'V Western European Time 'V however all sessions will be recorded and made available allowing attendees from different time zones to follow a day behind with an additional 1/2 days support after the official course finish date (please email oliverhooker@prstatistics.com for full details or to discuss how we can accommodate you).

using bitesize 2 day courses

"1" June 4th - 5th Introduction to statistics using R and Rstudio <https://www.psstatistics.com/course/introduction-to-statistics-using-r-and-rstudio-irrs01/>

"2" June 18th - 19th Introduction data visualization using GG plot 2 (R and R studio) <https://www.psstatistics.com/course/introduction-to-data-visualization-using-gg-plot-2-r-and-rstudio-dvvg01/>

"3" July 9th - 10th Introduction data wrangling using R and Rstudio <https://www.psstatistics.com/course/introduction-data-wrangling-using-r-and-r-studi-dwrs01/> "4" July 23rd - 24th Introduction to generalised linear models using R and Rstudio <https://www.psstatistics.com/course/introduction-to-generalised-linear-models-using-r-and-rstudio-iglm01/> "5" August 6th - 7th Introduction to mixed models using R and Rstudio <https://www.psstatistics.com/course/introduction-to-mixed-models-using-r-and-rstudio-immr02/>

Stable Isotope Mixing Models using SIBER, SIAR, MixSIAR (SIMM06) <https://www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm06/>

Reproducible Data Science using RMarkdown, Git, R packages, Docker, Make & Drake, and other tools (RDRP01) <https://www.psstatistics.com/course/reproducible-data-science-and-r-package-design-rdrp01/>

Applied Bayesian modelling for ecologists and epidemiologists (ABME06) <https://www.prstatistics.com/course/applied-bayesian-modelling-for-ecologists-and-epidemiologists-abme06/>

Species Distribution Modeling using R (SDMR02) <https://www.prstatistics.com/course/species-distribution-modeling-using-r-sdmr02/>

Fundamentals of populations genetics using R (FOPG01) This course will be delivered live <https://www.prstatistics.com/course/fundamentals-of-populations-genetics-using-r-fopg01/> - Oliver Hooker PhD. PR statistics

2020 publications; Parallelism in eco-morphology and gene expression despite variable evolutionary and genomic backgrounds in a Holarctic fish. PLOS GENETICS (2020). IN PRESS

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Oliver Hooker <oliverhooker@prstatistics.com>

Other upcoming courses

5 part R series designed to build skills in certian areas

Online RNAseqInR Jun15-19 Deadline

Dear all,

we have the last 4 places left on the Physalia course on “ RNAseq data analysis with R/Bioconductor ” which will be held ONLINE from the 15th to the 19th of June: <https://www.physalia-courses.org/courses-workshops/course19/> This course was designed for those students interested in working with RNAseq data in R and Bioconductor and with no previous programming experience. The course assumes basic familiarity with genomics, but does not assume prior statistical training.

Learning outcomes

By the end of this course students will be able to perform:

- 1) exploratory data analysis;
- 2) principal components analysis;
- 3) clustering, differential expression
- 4) gene set analysis.

Programme: (<https://www.physalia-courses.org/courses-workshops/course19/curriculum-19/>)

Our other online courses: (<https://www.physalia-courses.org/courses-workshops/>)

All the best,

Carlo

info@physalia-courses.org

Online SeascapeGenomics Oct12-16

Dear all,

registrations are now open for the Physalia course on “Seascape Genomics”, which will take place ONLINE from the 12th to the 16th of October.

Instructors:

Dr. Laura Benestan (CEFE-CNRS, FR) and Oliver Selmoni (EPFL, CH).

Course website: (<https://www.physalia-courses.org/courses-workshops/course70/>)

In this course, students will learn the basics of this approach and train using state of the art methods. Firstly, students will learn how to extract environmental data from publicly available databases and how to use it to characterize the seascape structure and conditions. For instance, students will learn how to use remote sensing data to describe sea water temperature oscillations or sea water movements. Next, the course will bring its focus on genomic analyses: students will learn how to evaluate genetic structures in the marine environment and how to calculate and display connectivity between populations. The combination of environmental and genomic data will also lead to the study of local adaptation. Students will learn different methods to discover genetic/genomic signatures potentially involved in adaptation against specific environmental constraints. The course will also cover the critical task of the interpretation and validation of the results, particularly in an applied conservation and management context. Finally, the workshop will consider the crucial aspects and good habits to account for designing a seascape genomics experiment (e.g. sampling design) from a relevant scientific question.

Should you have any questions, please feel free to contact us at: (info@physalia-courses.org)

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
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 <info@physalia-courses.org>

Online WholeGenomeSequencing Oct19-22

ONLINE course “Population genomic inference from low-coverage whole-genome sequencing data”

When: 19-22 October 2020

Instructors: Dr. Nina Overgaard Therkildsen (Cornell University, US) and Dr. Matteo Fumagalli (Imperial College London, UK)

Course website: (<https://www.physalia-courses.org/courses-workshops/course64/>)

In this course, we will explore workflows and the underlying rationale behind producing, processing, and analyzing low-coverage sequencing data for population genomic inference. Given that most species have insufficient reference data to allow reliable genotype imputation, we will focus on genotype likelihood-based methodology that can be applied to any system. We will primarily cover methods and algorithms implemented in the ANGSD software package and associated programs, providing best-practice guidelines and discussion of how participants can make maximal use of low-coverage whole genome re-sequencing data for their studies.

The course is aimed at researchers who might have previous experience with next generation sequencing (NGS) data (e.g. exome/RAD/pooled sequencing) and wish to explore the potential for using low-coverage whole-genome sequencing for their studies.

All hands-on exercises will be run in a Linux environment on remote servers. Statistical analyses and data visualization will be run in R.

Should you have any questions, please feel free to contact us: (<mailto:info@physalia-courses.org>)

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org/> [@physacourses](https://twitter.com/physacourses) mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

SummerInstStatGenetics Online Jul13-31

The Summer Institute in Statistical Genetics (SISG) will move online July 13-31 in 2020 for its 25th anniversary year. It will offer 18 short courses across a wide range of topics in statistics and genetics. Full details are at www.biostat.washington.edu/suminst/sisg The goal of SISG is to strengthen the statistical and genetic proficiency and career preparation of scholars from all backgrounds, especially those from groups historically underrepresented in STEM such as racial and ethnic minority groups, low income, first generation college students, veterans, and differently abled and 2SLGBTQ groups.

Registration fees have been halved for 2020. Registration scholarships are available for US graduate students who wish to take courses not available at their home institutions and/or would have difficulty in paying the registration costs. Registration and scholarship applications are now being accepted at www.biostat.washington.edu/suminst/sisg Bruce Weir bsweir@uw.edu

Bruce S Weir <bsweir@uw.edu>

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 EvoDir 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 EvoDir direct them to the email evodir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX 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 send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most 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^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.