EvolDir

December 1, 2019

Month in Review

Foreword

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

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

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

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Avignon France ForestGeneticRescue Jan28-29

New extended dates!

Conference: Genetics to the rescue, Managing forests sustainably in a changing world In Avignon, France, 28-29 January 2020.

The open conference days (28-29 January 2020) are built around four topical sessions: - Genomes and the environment - Local adaptation of climate change-related traits - Conserving and using genetic diversity - Evolutionary management of forests

Important dates: - Submit your abstracts and posters: closed - Early bird registration ends November 30, 2019 - Registration closes January 10, 2020

Reduced registration fees for students - financial help for registering possible

More info:https://colloque.inra.fr/confgentree2020 Twitter: #rescueforest

The week also consists of the partners' annual assembly (Jan 27), a joint stakeholder consultation co-organized by EUFORGEN (Jan 30), a genomics training session (Jan 30) and a Wikipedia editing session (Jan 31). The scientific conference will welcome a maximum of 250 participants while the training and the stakeholder sessions held back to back with the conference will welcome no more than 80 participants each.

The conference is organized by the H2020 project GenTree (http://www.gentree-h2020.eu/) (@GentreeProject) and is held at the beautiful University of Avignon, France

Contact: Bruno Fady <bruno.fady@inra.fr>, INRA Avignon, France

"bruno.fady@inra.fr" <bruno.fady@inra.fr>

Avignon France ForestGenetics Jan28-29

Last days to register and send your abstracts!

Conference: Genetics to the rescue, Managing forests sustainably in a changing world In Avignon, France, 28-29 January 2020.

The open conference days (28-29 January 2020) are built around four topical sessions: - Genomes and the environment - Local adaptation of climate change-related traits - Conserving and using genetic diversity - Evolutionary management of forests

Important dates: - Submit your abstracts and posters by October 31, 2019 - Early bird registration ends November 20, 2019 - Registration closes January 10, 2020

More info:https://colloque.inra.fr/confgentree2020 Twitter: #rescueforest

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Contact: Bruno Fady <bruno.fady@inra.fr>, INRA Avignon, France

Bruno Fady <bruno.fady@inra.fr>

Debrecen Hungary WildlifeConservation Jan10-12

III. ÃLVONAL Conference 10-12 January 2020 INTEGRATING SOCIAL BEHAVIOUR AND POPULATION DEMOGRAPHY FOR CONSERVATION OF WILD POPULAITON

The Conference will take place between 10th and 12th of January 2020 in Debrecen (Hungary). The Conference will start on Thursday 9th January with a slide-show and traditional Hungarian dinner, will include two days of scientific talks by top scientists, post-docs and students, and an optional bird watching trip with a social event on Sunday 12th January. The conference will focus on conservation aspects of behavioural and demographic studies. Speakers will cover a range of organisms and will use variety of research tools and methodologies. We invited elite scientists from Hungary and abroad to discuss recent advances in demography, behaviour and conservation biology.

We are honored to announce our invited speakers: Dr. Ãdám Lendvai (University of Debrecen) Prof. Robert Freckleton (University of Sheffield) Prof. Oliver Krüger (University of Bielefeld) Dr. Barbara Caspers (University of Bielefeld) Prof. Innes Cuthill (University of Bristol) Prof. Miroslav Salek (Czech University of Life Sciences Prague) Pavel Tomkovich (Lomonosov Moscow State University) Dr. Zhenwang Zhang (Beijing Normal University) Dr. Brett Sandercock (Norvegian Institute for NatureResearch).

The Conference will also offer opportunities to young scientists and students to present their work and discuss potential projects with senior scientists. The Conference will be hosted by the Debrecen Academy of Sciences.

Registration deadline: 10th December 2019 Registration available here: https://forms.gle/-PptQZbERvnEcUJQA9 Contact: elvonalconference@gmail.com

Looking forward seeing you there.

Fanni Takács, Karola Szemán, Dr Vojtech Kubelka, Prof Tamás Székely

Fanni Takács <fannitakacs.94@gmail.com>

Frankfurt ConservationGenetics Feb26-28

Dear friends and colleagues,

We are happy to announce that the

" 4th Annual Meeting in Conservation Genetics - from Genomes to Application"

will be held in Frankfurt am Main from 26.-28.02.2020 at the Senckenberg Research Institute and Natural History Museum and the registration is now open!

The conference series Annual Meetings in Conservation Genetics was launched in 2015 to help bridging the gap between modern genetic/genomic research and applied nature and species conservation. The conference serves as a platform both for experts as well as others interested in applying modern genetic and genomic tools for conservation. We will have different sessions on diverse topics such as eDNA, molecular wildlife forensics or landscape genetics, and workshops on topics such as policy, society & outreach.

The meeting is intended for scientists in the fields of conservation genetics, ecological genomics, and related fields, and researchers, students, conservationists and environmental managers interested in applying conservation genetics and genomics .

For further details and to register please visit: https://consgen20.de .

We hope to welcome you soon in Frankfurt!

Alina von Thaden , Stefan Prost , Carsten Nowak and the Organization Team

Senckenberg Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß ç 22 BGB) Senckenberganlage 25 60325 Frankfurt Mail: consgen20@senckenberg.de www.consgen20.de www.senckenberg.de/en/ Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Karsten Wesche; Präsidentin: Dr. h.c. Beate Heraeus; Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

consgen20 <consgen20@senckenberg.de>

Helsinki EvolutionInsectViruses Jul19-24

We would like to invite submissions to two symposia addressing the vast increase in insect virus discovery that has taken place in recent years. The symposia will be held during the International Congress of Entomology (ICE 2020), Helsinki, Finland, July 19-24, 2020.

The symposia will be held consecutively on Thursday July 23rd, 2020, and aim to bring together recent contributions to insect virus discovery, with a focus on evolutionary and/or ecological implications.

Symposium 1: Ecological implications of the recent huge increase in insect virus discovery (organised by Elisabeth Herniou and Jenny Cory): High throughput sequencing has accelerated virus discovery and notably in insects. Many new insect species are now associated with a diverse range of viruses, many of which were previously unknown and belong to undescribed viral families. Each new discovery adds new potential interactions in the ecological network of any focal hosts at multiple trophic levels. This calls for rethinking our understanding of host-pathogen interactions in a broader ecological and evolutionary context at the cellular, organismal, community level.

Submissions through this link: https://submit.peerageofscience.org/conference/ICE_2020/109474 Symposium 2: The evolution of insect-virus associations (organised by Dino McMahon and Vera Ros): Our ability to characterize and understand the biology of insect-virus associations has risen dramatically in recent years following the advent of accessible omics approaches. This progress is timely given the vital and growing importance of insects to global ecosystems and wildlife and human health. Our symposium welcomes new research that is mechanistic as well as ecological in scope, focusing on the diversity, evolution and origin of insect viruses, their spread within and between species and the evolution of virulence in the context of dynamic host virus defenses and changing environments.

Submissions through this link: https://submit.peerageofscience.org/conference/ICE_2020/109513 Deadline for submission of abstracts for these two symposia: December 15, 2020.

More information about the conference: https://ice2020helsinki.fi/ Dr. ir. Vera I.D. Ros Assistant Professor

Laboratory of Virology | Plant Sciences Group | Wageningen University | Droevendaalsesteeg 1 | 6708 PB Wageningen, The Netherlands | +31-317-484461 | vera.ros@wur.nl | www.vir.wur.nl "Ros, Vera" <vera.ros@wur.nl>

Marseilles 24thEvolBiol Sep22-25 EarlyRegistration

Dear all : the Early registration dead line , for the next Evolutionary Biology Meeting at Marseilles , is January 31 2020. The congress will take place from September 22nd to 25th

more info aeeb.fr

best regards

Pierre

< https://twitter.com/pontarotti >

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

NewYork PopGen Jan17 DeadlineNov25

The 2020 New York Area Population Genomics meeting!

NYAPG 2020 January 17, 2020 19 University Place, Room 102 New York University

Keynote speakers: Elodie Ghedin (NYU) and Sarah Kocher (Princeton)

The program will include short talks selected from abstracts. We will provide coffee breaks and lunch, and this year we are introducing a poster session to provide more opportunities for early-career researchers.

Visit www.nypg20.org to register (free but required) and to submit abstracts.

*** THE ABSTRACT DEADLINE IS MONDAY, NOV 25 ***

We hope to see you in January!

Program Committee Elizabeth Alter (York College, CUNY) Christopher Brown (University of Pennsylvania) Barbara Engelhardt (Princeton University) Eimear Kenny (Mount Sinai) Matthew Rockman (New York University) Guy Sella (Columbia University) Adam Siepel (Cold Spring Harbor Laboratory) Li Zhao (Rockefeller University)

Local Organizing Committee (NYU) Jane Carlton David Gresham Yevgeniy Plavskin Michael Purugganan Matthew Rockman

Matthew Rockman <mrockman@nyu.edu>

NHM London YoungSystematists Nov22

Last chance to register as a non-presenting attendee for this energetic day of exciting, enthusiastic evolutionary biology! Check out the draft programme, attached. Register by midday Monday and we can host you for tea, coffee, lunch and wine. Fill in your details here:

https://ysf2019_systematics-association.eventbrite.co.uk/ If you're willing to help out on the day, we are also looking for a few more people to be part of the team for logistics and judging presentations.

21stYOUNG SYSTEMATISTS??? FORUM

Friday 22nd November 2019, 9:30 am

Venue: Flett Lecture Theatre,

Natural History Museum, London, UK

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

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

Registration isFREE.

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

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

Abstracts must be submitted by e-mail in English and in Word format no later than Friday 25 October 2019. The body text should not exceed 150 words in length. Title, authors, and their professional affiliations/addresses should be included with the abstracts.If the presentation is co-authored, the actual speaker (oral) or presenter (poster) must be clearly indicated in BOLD text. The file should be in editable format (.doc or .odt, not pdf) and titled Surname_First-name_YSF2019.doc, for example Doe_Jane_YSF2019.doc.

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

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

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

QuebecCity SMBE-2020-Call-for-Abstracts Jun28-Jul2

Dear SMBE members,

We invite you to submit an abstract for the 2020 annual conference of the Society for Molecular Biology and Evolution (SMBE 2020) athttp://smbe2020.org/-abstracts/abstract-submission/ . SMBE 2020 is taking place in Québec City, Canada, from 28 June - 2 July 2020.

The deadline for abstract submission is Monday 20 January 2020, 23:59 (GMT).

Several awards are available and can be applied for during abstract submission. They require SMBE membership at the time of application (3 years costs $10 for students and $30 for others).

Membership can be applied for at https://-www.smbe.org/smbe/MEMBERSHIP.aspx Carer awards can also be applied for at registration or by email.

Awards include:

1)The Walter M.Fitch Award for current graduate and recent postdoctoral researchers; Extended abstracts are not required, just the conference abstract and a CV. Unsuccessful Fitch Award applicants will automatically be considered for Young Investigator and Registration-only awards.

2)The Young Investigator Award substantially funds the cost of attending, is for any graduate student or postdoc, requires a conference abstract and a CV, and will automatically also be considered for Registration -only awards.

3)The Undergraduate Travel & Mentoring Award (including Masters students under a 3+2 system) requires title, abstract, a short explanation (250 words) of why you want to attend this meeting, including a mention of whether you fall into a group traditionally underrepresented at SMBE such as enrolling in university later in life or being the first in your family to attend university. A short letter of support (250 words) should also be sent from your academic supervisor to Sarah Schaack and Mary O'Connell (SMBE.contact@gmail.com) confirming that you are undergraduate or a Masters student under 3+2, and that the research to be presented is your own.

4) Carer Travel Awards can be applied for during registration, or by email to smbe2020@mci-group.com if an earlier response is needed. Up to $2000 may be awarded for members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as to facilitate member's attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while you're at the meeting, or extra help paying for on-site daycare.

If interested in sponsorship of the meeting, please contact SMBE2020@mci-group.com.

For any queries over abstracts or registration, please contact SMBE2020@mci-group.com.

We look forward to welcoming you in Québec City.

Dr Lulu Stader Executive Administrator, Society for Molecular Biology and Evolution smbe.contact@gmail.com

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

Roros Norway EvoDemo7 Apr15-19

Dear all,

The deadlines for the Evolutionary Demography Society's 7th Annual Meeting in Røros, Norway, have been extended.

Abstract submission: Thursday 12th of December 2019
Early bird registration: Sunday 15th of December 2019

Register at https://evodemo7.weebly.com/ We hope that gives everyone just enough time to make any final preparations to attend. We look forward to seeing all of you there!

Best regards, EvoDemo7 organizing committee 15-19 April 2020

If you have any questions, please email evodemo7@bio.ntnu.no

"Stefan J.G. Vriend" <stefan.vriend@ntnu.no>

SMBE2020 CallForAbstracts TravelAwardApplications

Dear SMBE members,

We invite you to submit an abstract for the 2020 annual conference of the Society for Molecular Biology and Evolution (SMBE 2020) athttp://smbe2020.org/-abstracts/abstract-submission/ . SMBE 2020 is taking place in Québec City, Canada, from 28 June - 2 July 2020.

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We look forward to welcoming you in Québec City.

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

SMBE CallForProposalsToHost2023 DeadlineNov30

Subject: Call for Proposals to Host SMBE 2023 - Deadline 30 November 2019

Dear SMBE Members:

Want to meet like-minded colleagues from all over the world?

Wish you could have an international conference in your field closer to home?

SMBE is looking for a local host for its 2023 international meeting. Informal expressions of interest should be from a prospective local organizing committee of scientists headed by an SMBE member, and should reach SMBE President-Elect Marta Wayne by 30 November 2019. Full proposals will need to be submitted using the SMBE template by 30 April 2020. Please email your proposal to Smbe.contact@gmail.com.

For details of meeting organization, please see the SMBE Conference Guidelines (https://www.smbe.org/smbe/-MEETINGS/ConferenceGuidelines.aspxand specifically Appendix 2 which outlines the format of proposals).

The primary role of the local organizing committee will be to plan the scientific programme. All other aspects of the organization will be done in association with SMBE representatives and a professional conference organizer appointed by SMBE.

SMBE rotates its meetings geographically to encourage international participation. For 2023, we are particularly requesting proposals from North America. The next three years' meetings will be in Quebec, Canada (2020), Auckland, NZ (2021) and Ferrera, Italy (2022).

Please note that SMBE is not interested in proposals from professional conference organizers.

Looking forward to hearing from you.

Sincerely,

Marta Wayne President-Elect, SMBE Smbe.contact@gmail.com

Dr Lulu Stader

Executive Administrator, Society for Molecular Biology and Evolution

smbe.contact@gmail.com

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

Subject:Conference:ULeicester UK PopulationGeneticsGroup Jan5-8

Dear Colleagues,

Registration for the 53rd running of the Population Genetics Group (PopGroup) meeting is open and talk slots are filling up fast

The meeting will be held at University of Leicester (UK), 5-8th Jan 2020.

We are delighted to announce that our plenary speakers this year will be: Katrina Lythgoe, Stuart West, Melissa A. Wilson and Anne Yoder.

In addition Oliver Pybus will deliver the Genetics Society's Mary Lyon Medal lecture.

There will be a welcome reception on the evening of Sunday 5th January, followed by 2.5 days of talks, running from 9am on Monday 6th until lunchtime on Wednesday 8th January 2020.

As usual there are no symposia and talks will be allocated on a first-come first-served basis.

Full details, including links to registration and abstract submission, can be found at: http://-www.populationgeneticsgroup.org.uk/ The organising committee - Rob Hammond, Richard Badge, Max John and Ed Hollox - look forward to seeing you in Leicester in early 2020

Twitter: @popgroup #pgg53

Popgroup53 <popgroup53@leicester.ac.uk>

Switzerland SpeciesRanges Jul19-23

Conference on ?Constraints on species? ranges and niche evolution?, from 19 to 23 July 2020 in Ascona, Switzerland.

The aim of the conference is to synthesize perspectives on the causes of range limits and constraints on the evolution of the ecological niche. Our goal is to bring together researchers with ecophysiological, genomic, quantitative genetic, and community ecology perspectives to share ideas and find ways to generate new insights by combining these complementary approaches to study ecological niches.

There will be a maximum of 80 participants. We aim for close interaction among participants during scientific presentations and informal conversations in a beautiful setting at Monte Verit? in southern Switzerland. The scientific program will consist of posters, short talks, keynote talks, and breakout sessions. For more information about the program, focus topics, keynote speakers, venue and registration please go to the homepage https://duw.unibas.ch/de/csf-2020/ We recommend registering until March 2020. Young researchers (PhD students) may apply for financial support to franziska.grob@unibas.ch by January 31, 2020 (for specific information see https://duw.unibas.ch/de/csf-2020/).

We hope to see you in Switzerland in July 2020. Feel welcome to contact us if you have any questions regarding the conference.

The organizers,

Yvonne Willi, Univ. Basel Torsten Kristensen, Univ. Aalborg Josh Van Buskirk, Univ. Z?rich Jake Alexander, ETH Z?rich

Emails to Franziska Grob, Univ. Basel: franziska.grob@unibas.ch

Yvonne Willi <yvonne.willi@unibas.ch>

UCambridge EvolutionaryGeneticsGenomics Mar17

Dear Colleagues,

The annual Evolutionary Genetics and Genomics Symposium (EGGS) will take place on Tuesday 17th March 2020 at the University of Cambridge. This Genetics Society meeting attracts participants from across Europe and is a friendly and informal way to meet researchers in the field and listen to interesting talks. We aim to bring together participants from a range of backgrounds, with a particular focus on genomics and evolutionary biology. EGGS 2020 will feature keynotes from:

Mattias Jacobsson Professor at Department of Organismal Biology, Human Evolution, Uppsala universitet

Claudia Bank Principal Investigator, Gulbenkian Institute

Mark Blaxter Professor & Programme Lead for the Tree of Life Programme, Wellcome Sanger Institute Talk title: Sequence everything: first fruits from the Tree of Life

Registration is now open and costs just 5. Please register at https://onlinesales.admin.cam.ac.uk/-conferences-and-events/department-of-genetics/-evolutionary-genetics-and-genomics-symposium/-evolutionary-genetics-and-genomics-symposium-2020 Abstract submission is also open and the deadline is 20/1/2020. If you are interested in presenting a talk, please submit a title and upload your abstracts (250 words) in Word or PDF formats as attachments during registration. Registrations can be cancelled with a full refund until the registration deadline on 10th March 2020.

With best wishes,

The organising committee.

“Dr A. Ramesh” <ar885@cam.ac.uk>

ULeicester UK PopulationGeneticsGroup Jan5-8

There is just one day left to register for the 53rd running of the Population Genetics Group: https://www.populationgeneticsgroup.org.uk/ A very limited number of talk slots are still available and posters are most welcome.

The meeting will be held at University of Leicester (UK), 5-8th Jan 2020.

We are delighted to announce that our plenary speakers this year will be: Katrina Lythgoe, Stuart West, Melissa A. Wilson and Anne Yoder. In addition Oliver Pybus will deliver the Genetics Society’s Mary Lyon Medal lecture.

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Full details, including links to registration and abstract submission, can be found at: https://www.populationgeneticsgroup.org.uk/ The organising committee - Rob Hammond, Richard Badge, Max John and Ed Hollox - look forward to seeing you in Leicester in early 2020.

Twitter: @popgroup #pgg53

"rh225@leicester.ac.uk" <rh225@leicester.ac.uk>

GradStudentPositions

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Antwerpen CichlidAdaptation 11
AuburnU EvoDevo 12
BangorU DrosophilaPopGen 13
CaseWesternReserveU RecombinationInDrosophila 13
ChicagoBotanicGardens PlantBiologyConservation 14
Clemson OralMicrobeEvolution 14
Cornell EvolutionaryConservationGenomics 15
CRAG Barcelona AncientDNA 15
CzechAcademySci EvolutionPlantDefences 16
DurhamU KelpBiodiversity 17
Eawag UBern FishMigrationEvol 18
Edinburgh InsectHermaphroditism 19
ErlangenNurnbergU PlantBioinformatics 20
ETH Zurich BacterialAdaptation 20
Europe MEME MasterProgramme 21
GhentU ComputationalBiologyInPlants 21
GhentU SeaweedAdaptation 22
JohnMooresU Liverpool NematodeGenomics 23
KielU EvolutionaryMicrobiology 24
KULeuven EvolutionMicrobiomeDaphnia 24
LundSweden PlantInsectInteractions 25
McMasterU SexDeterminationInAmphibians 26
MichiganStateU FishEvoDevoGeno 27
MichiganStateU WeedEvolution 28
MississippiStateU ButterflyEvo 28
MPI Ploen Evolution tRNASets 29
NorthernArizonaU EvolutionaryGenomics 29
Norwich UK 2 Bioinformatics 30
OklahomaStateU AmphibianDiseaseResistance 30
OklahomaStateU HerbariumInformatics 31
OxfordU PlanarianEvolution 32
PennsylvaniaStateU GallWaspEvolution 33
Ploen MathematicalBiology 33
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StAndrewsU CrowBehaviour 35
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TexasAMU InvertPopulationGenomics 36
TexasAMU MarineMicrobiomeDiversity 36
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UAlmeria Spain EcoEvolutionaryBioinformatics 38
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VIB Gent PlantComputationalTools 63
WageningenU CovertVirusInfectionsInInsects 64
WesternWashingtonU EvolutionaryBiology 64
WestvirginiaU PlantEvolution 65

AdamMickiewiczU InsectAdaptation

MSc Project in insect community biology

We offer opportunities to gain experience with field experiments in evolutionary ecology, entomology, and data analysis in the project "Insect adaptation to individual trees in a forest as a function of isolation from neighboring trees: field experiments on oaks". We are testing predictors of insect communities on individual trees, and perform reciprocal transplant experiments. Practical work includes sampling insects and leaves from mature oak trees, rearing moths and leaf miners, sorting and measuring insects. The fieldwork takes place in Puszcza Zielonka, a forest near Poznan, Poland. You would be supported by a great team of researchers including experts in entomology, ecology and evolution, and population genetics. Scholarships are available for students registered at Polish universities https://www.ncn.gov.pl/baza-ofert/?akcja=wyswietl&id=181616. For more information, please contact Freerk Molleman (fremol@amu.edu.pl).

Freerk Molleman, Urszula Walczak, Iwona Melosik, Andreas Prinzing (Rennes, France), Edward Baraniak, Toomas Tammaru (Tartu, Estonia).

https://www.researchgate.net/profile/Freerk_Molleman

+ 48 618 29 5801 Adam Mickiewicz University in Poznan, Poland Faculty of Biology Department of Systematic Zoology room 1.52 Ul. Uniwersytetu Poznañskiego 9, 61-614 Poznañ

Freerk Molleman <fremol@amu.edu.pl>

Antwerpen CichlidAdaptation

Deadline approaching

Fully funded PhD position in cichlid fish Evolutionary Genomics available in the Svardal lab at the University of Antwerp

Application deadline: 29 November 2019

The hundreds of closely related but ecologically diverse species of Lake Malawi cichlid fish provide an exceptional model to study the genomic mechanisms involved in rapid adaptation and diversification. In the Svardal lab we are interested in both the fundamental evolutionary processes involved in the formation of new species and the molecular basis of adaptive phenotypes.

Several projects are available that will allow you to combine aquarium experiments and state-of-the-art genomic approaches to study explosive speciation and/or recent adaptation to heavy fishing pressure in Malawi cichlids.

Depending on your interest, the project can have more of a bio-informatic or more of an experimental focus, but in any case strong quantitative skills and motivation to delve into computational data analysis are desired.

For more information and to apply, visit

https://www.uantwerpen.be/en/jobs/vacancies/ap/2019bapdocproex301/ Best wishes, Hannes Svardal

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

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

Hannes Svardal <Hannes.Svardal@uantwerpen.be>

AuburnU EvoDevo

The Range lab in the Department of Biological Sciences at Auburn University is recruiting graduate students interested in evolutionary and developmental biology (www.therangelab.com). Research in the lab focuses on understanding how an interconnected network of three different Wnt signaling pathways (Wnt/Beta-catenin, Wnt/JNK, and Wnt/Ca2+) coordinate the exact positions of the gene regulatory networks that establish the primary germ layers along the anterior-posterior axis during early embryogenesis. We use sea urchin and hemichordate (acorn worm) embryos as the primary model systems. Remarkably, functional and expression studies in many metazoans (vertebrates, urochordates, hemichordates, echinoderms and cnidarians) suggest that many aspects of this Wnt signaling network governing AP axis specification is an ancient mechanism that existed in the common ancestor of bilaterians and cnidarians. We also work closely with the Counterman lab at nearby Mississippi State University to study how Wnt signaling is involved in butterfly wing pattern development. In collaboration, we have begun to characterize the Wnt network of signaling governing pigmentary and structurally based color patterns.

The position is for a talented PhD student beginning in the Fall of 2020. The student will have the choice to work on any number of projects in the lab that focus on the roles of Wnt signaling during early AP axis specification and patterning in sea urchin and hemichordate embryos. The student will also have opportunities to contribute to our collaboration with the Counterman lab. The position offers training in a combination of molecular manipulations, high-throughput genome-wide assays and bioinformatics, gene regulatory network analysis as well as classical embryology.

Auburn University is situated in the quintessential college town of Auburn, Alabama and is located close to several major cities (e.g. Atlanta [1.25 hrs] and Birmingham [2 hrs]), the beaches along the Gulf of Mexico and Atlantic Ocean, and the Appalachian Mountains. You can learn more about the Department of Biological Sciences at Auburn University at http://www.auburn.edu/cosam/departments/biology/ . Interested applicants should contact Dr. Ryan Range at range@auburn.edu. With your inquiry, please include a CV and a brief description of your research interests and experience. GRE scores are not required by the Department of Biological Sciences at Auburn. Applications for Fall 2020 are accepted until February 1st, 2020. In-person interviews at Auburn are available. There will be a graduate student recruitment hosted by the Department of Biological Sciences from January 21st - 23rd for interested students if they contact Dr. Range before December 31st, 2019.

Recent publications related to the position:

Integration of canonical and non-canonical Wnt signaling pathways patterns the neuroectoderm along the anterior-posterior axis of sea urchin embryos. Range RC, Angerer RC, Angerer LM. PLoS Biol. 2013;11(1):e1001467. doi: 10.1371/journal.pbio.1001467. PMID: 23335859

Specification and positioning of the anterior neuroectoderm in deuterostome embryos. Range R. Genesis. 2014 Mar;52(3):222-34. doi: 10.1002/dvg.22759. Review. PMID: 24549984

An anterior signaling center patterns and sizes the anterior neuroectoderm of the sea urchin embryo. Range RC, Wei Z. Development. 2016 May 1;143(9):1523-33. doi: 10.1242/dev.128165. PMID: 26952978

Khadka, A, Martinez-Bartolomé, M, Snyder, S, and Range, RC . A novel gene's role in an ancient mechanism: secreted Frizzled-related protein 1 is a critical component in the Wnt signaling network governing anterior-posterior neuroectoderm patterning in sea urchin embryos. EvoDevo. 2017. DOI:10.1186/s13227-017-0089-3.

Range RC. Canonical and non-canonical Wnt signaling pathways define the expression domains of Frizzled 5/8 and Frizzled1/2/7 along the early anterior-posterior axis in sea urchin embryos. Developmental Biology. 2018. pii: S0012-1606(18)30238-0. DOI: 10.1016/j.ydbio.2018.10.003.

Ryan Range <range@auburn.edu>

BangorU DrosophilaPopGen

Bangor University Drosophila Pop Gen & Biomechanics To apply visit: http://www.envision-dtp.org/2019/aerodynamic-invasions-does-the- biomechanics-of-flight-affect-dispersal-and-genetic-diversity-in-invasive-species/. NERC funded PhD Project:

Aerodynamic invasions: Does the biomechanics of flight affect dispersal and genetic diversity in invasive species?

Supervisors: Aaron Comeault (Bangor University), Kristen Crandell (Bangor University), Alex Papadopulos (Bangor University), and Si Creer (Bangor University)

Project Description

What are the factors that facilitate successful biological invasions? This question has been a central focus in invasion ecology and genetics for over a half-century, and has important ramifications for the effective management of invasive species. The ultimate goal of this project is to generate novel insight into the dynamics of biological invasions. The successful candidate will work at the interface of biomechanics and genomics to test timely questions in invasive species biology: What are the functional links between dispersal traits and genetic diversity in invasive species? How do dispersal traits differ between invasive and non-invasive species? And how does dispersal affect the spread of invasive species into novel habitats? To answer the questions described above, the student will collect phenotypic and genomic data from wild species of invasive and native Drosophilid fruit flies. The successful candidate will work at the interface between biomechanics and population genomics to perform integrative tests of the functional links between flight morphology, dispersal ability, and genetic diversity. Results will inform invasive species management by establishing direct links between morphology, dispersal, and genetic diversity. A resulting goal is to generate simple predictive tools for invasive propensity and management practices for ongoing invasions.

Training Outcomes

The studentship comes with the opportunity to develop marketable skills in big data science by learning and applying cutting-edge methods in the fields of biomechanics and population genomics. The successful candidate will also have the opportunity to conduct fieldwork, and travel extensively across the UK to sample different species of invasive and native Drosophila. Hosted in the Molecular Ecology and Fisheries Genetics Laboratory group (MEFGL), the student will be exposed to a diverse and vibrant research environment, conducting research fields ranging from molecular ecology and conservation genetics to evolution and speciation. Because of the interdisciplinary nature of this project, the successful candidate will have the opportunity to explore and develop their independent research interests in diverse areas of expertise.

Zaprionus indianus Drosophila hydei Drosophila suzukii

Figure 1. Three distantly related and independent examples of invasive Drosophilid species.

For informal enquiries, please contact Aaron Comeault (a.comeault@bangor.ac.uk) and Kristen Crandell (k.crandell@bangor.ac.uk)

For further details, and to apply, visit: http://www.envision-dtp.org/2019/aerodynamic-invasions-does-the- biomechanics-of-flight-affect-dispersal-and-genetic-diversity-in-invasive-species/. This studentship is in competition for funding with other studentships. The projects with the best applicants will be successful.

Kristen Crandell, PhD Lecturer & Leverhulme Early Career Fellow Bangor University p: 44 1248.382566 e:k.crandell@bangor.ac.uk w:http://www.kriscrandell.com Kristen Crandell <k.crandell@bangor.ac.uk>

CaseWesternReserveU RecombinationInDrosophila

A Ph.D. graduate student position is available in the lab of Dr. Nicole Crown in the Department of Biology at Case Western Reserve University. The Crown lab uses chromosome structural variants in Drosophila to understand the molecular mechanisms of meiotic recombination. Our lab uses a combination of whole genome sequencing, molecular genetics, imaging, and traditional Drosophila genetics. We study molecular genetics through an evolutionary lens and are looking to expand in areas of evolutionary genomics. We are a good fit for students with an evolutionary background looking to learn wet bench genetics. Your specific project will be focused on how heterozygous inversions impact the recombination. Learn more about the Crown lab here: http://crownlab.science The Crown lab is dedicated to providing a positive and supportive learning environment while also carrying out rigorous science. We value all people as they are and actively maintain an inclusive environment. Applicants should share in that philosophy.

Candidates should hold a degree in biology and have undergraduate research experience. The GRE is required to apply to our program but scores are not considered during the admission process. Applications can be submitted at https://biology.case.edu/graduate/- . Before applying, please contact Nicole Crown at knc38@case.edu. Please introduce yourself and share your research interests.

Nicole Crown, Ph.D. Assistant Professor of Biology Case Western Reserve University 112 Millis Hall 2074 Adelbert Road Cleveland, OH 44106 (216) 368-2206 www.crownlab.science Nicole Crown <knc38@case.edu>

ChicagoBotanicGardens PlantBiologyConservation

PLANT BIOLOGY AND CONSERVATION

The Graduate Program in Plant Biology and Conservation is a partnership between Northwestern University (NU) and the Chicago Botanic Garden (CBG). PhD, MS thesis-based, and MS internship-based degrees are offered. All degree programs offer a unique opportunity to study ecology, evolution, and environmental issues at the interface of basic and applied plant science. Students apply to the program through Northwestern University and take their courses at both NU and CBG with faculty from both institutions. The Plant Conservation and Science Center at CBG is a wonderful resource for students, and the Chicago region provides a vibrant community at the forefront of research in conservation and sustainability.

To learn more, contact program director, Nyree Zerega (nzerega@chicagobotanic.org) or visit our website: http://www.plantbiology.northwestern.edu/ Application deadlines: PhD: December 1, 2019 MS (thesis-based): February 15, 2019 MS (internship-based): Applications will be reviewed beginning February 15 and review will continue through April 30, 2019. Admissions are on a rolling basis.

n-zerega@northwestern.edu

Clemson OralMicrobeEvolution

Clemson.OralMicrobeEvolution

Vincent Richards' lab in the Department of Biological Sciences at Clemson University is accepting applications for a PhD position.

The overarching research theme will focus on the oral microbiome and the relationship between the bacterial and fungal components of this community. Specific questions include how these taxa respond and adapt to this dynamic environment. Operating over numerous time scales, multiple host factors such as diet, health, disease, and host genotype can impact the oral environment and hence are strong evolutionary forces that can shape and select for changes within the community. We are particularly interested in the interplay and co-evolution of bacterial and fungal components of the community and how these processes are impacted by immunosuppression. Multiple omic approaches such as comparative genomics, metagenomics, and metatranscriptomics will be coupled with network analyses to address these questions.

Desirable skills include experience analyzing next-generation sequence data and proficiency with Linux/bash. However, these are not absolute requirements as the student will be trained in numerous omic and bioinformatic approaches. Importantly, the student should possess a great deal of enthusiasm, curiosity, and imagination.

The position will be available Fall 2020 and the salary will initially range between $22,000/year and $25,000/year plus benefits and tuition (commensurate with experience and qualifications). Increases are possible. Applicants should contact Vincent Richards directly at vpricha@clemson.edu. Please provide a cover letter (describing research interests, experience, and career goals) and a CV that includes links to any authored publications.

Clemson University is ranked 27th among top national public universities and 70th among all national universities by U.S. News & World Report and is located on Lake Hartwell near the Blue Ridge Mountains in beautiful Upstate South Carolina.

Vincent P. Richards, PhD Assistant Professor Department of Biological Sciences Clemson University Clemson, SC 29634 Email: vpricha@clemson.edu Lab website:

http://www.vprichards-lab.com Vincent Paul Richards <vpricha@clemson.edu>

Cornell EvolutionaryConservationGenomics

PhD in Evolutionary/Conservation Genomics

The Hare Lab in the Department of Natural Resources at Cornell University is recruiting a PhD student to study evolutionary biology and conservation genomics with the eastern oyster as a study system. Desired start is Summer/Fall 2020.

The Hare Lab studies ecological and evolutionary factors that affect population responses to environmental change over timescales relevant to conservation and management. Some of our research also entails the application of genetic markers to inform population biology and ecology. The eastern oyster has been a longstanding focus of the Hare Lab because of its fascinating biology, keystone ecosystem function, strong and growing aquaculture industry interest, and the need to improve restoration success. The recent assembly of a chromosome scale reference genome has enabled highly informative genomic approaches to our studies. Oyster projects in the Hare Lab currently include tests for local adaptation, measurement of selection in the lab and field, tests for domestication selection in breeding programs, measurement of introgression from aquaculture to wild oysters, genomics of stress tolerance at different life stages, and mapping of larval dispersal patterns. These studies involve field collections, field experiments, aquatic lab experiments, population genomic analyses and outreach with stakeholders.

The exact project will be developed together with the selected candidate, depending on their interests. We seek a student with a strong academic record including courses in evolution, genetics, and quantitative analysis (stats, modeling). Desirable skills include R, computer programming, and bioinformatics, as well as knowledge of invertebrate biology, marine biology, and/or conservation biology. Previous research experience is needed.

The Hare Lab currently has one PhD student, one MS student, a pedagogy-focused postdoc, a research postdoc being recruited, and multiple undergraduate research assistants. Funding is from diverse sources including the National Science Foundation, New York Sea Grant, Mid-Atlantic Fishery Management Council, and Cornell Atkinson Center for Sustainability. Our home in the Natural Resources graduate field ensures continual multidisciplinary interactions. The Natural Resources graduate field includes faculty from across campus who address the social and ecological dimensions of natural resources and the environment to improve environmental sustainability. Conservation genomics is a strength within Natural Resources (Hare and Therkildsen labs), and population genomics applied to nonmodel as well as experimental model systems is a strength across campus. That strength is represented and reinforced by the Cornell Center for Comparative and Population Genomics (http://3cpg.cornell.edu/).

Interested applicants should contact Matt Hare at mph75@cornell.edu as soon as possible and send (1) an updated CV, (2) a summary of your academic and research experiences, and (3) a short description of the research questions you are passionate about. The deadline for a formal application to the Cornell Graduate School for this opportunity is December 1, 2019 (instructions: https://dnr.cals.cornell.edu/-graduate/application-procedure/). Applicants from groups traditionally underrepresented in the sciences and academia are especially encouraged to apply. For more information on research in the Hare Lab go to https://blogs.cornell.edu/harelab/- . Matthew Hare, PhD Associate Professor Fellow, Cornell Atkinson Center for Sustainability Department of Natural Resources Cornell University Ithaca, NY 14853 mph75@cornell.edu (607)255-5685 https://-blogs.cornell.edu/harelab/ mph75@cornell.edu

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CRAG Barcelona AncientDNA

PhD position available on Paleaogenomics of dog population in Europe.

The Botigue lab for “Genomics of ancient crops and domestication” in the Centre for Research in Agricultural Genomics (CRAG) in Barcelona is offering a PhD position under the La Caixa Foundation INPhINIT Programme to work on the genomic analysis of archaeological dog remains from Europe spanning from the Neolithic up to the Roman Period with the goal to understand population dynamics within the continent and gene flow during that period.

DEADLINE 4 February 2020 (Incoming modality) 26 February 2020 (Retaining modality)

TITLE: Genomic analysis of archaeological dog remains from Europe.

PROJECT DESCRIPTION: The European continent has played a major role in dog domestication. A recent genomic analysis of Neolithic dogs from Germany (Botigue et al. 2017 Nature Communications), though revealing genetic continuity, showed complex admixture patterns, including gene flow from a population similar to modern Indian dogs. Additionally, studies examining the mitochondrial genome of ancient and modern dogs have detected a replacement in Europe that took place some time between the Neolithic and the Middle Age. In the present project we plan to unravel this complex demographic scenario of prehistoric European dogs by analysing the genome of more than 30 ancient dog samples from the Iberian Peninsula and Germany from a period of over 4,000 years spanning from the Neolithic up to the Roman Empire. Analysis of the whole genome and the mitochondrial genome will be performed to determine the main demographic events that shaped dog populations during that period. Population structure and admixture will be studied in ancient dogs in the context of modern dog variation.

As a result, we will provide for the first time insights into the genetic structure, variability and admixture of dog populations in Europe over a period of 4 millennia, prior the generation of breeds. Results will elucidate demographic events surrounding dog prehistory in Europe and their relationship with humans migrating through the continent.

JOB POSITION DESCRIPTION The dearth and the ambition of the current project are ideal for a PhD candidate. We are therefore looking for a highly motivated student seeking to pursue his doctoral studies and specialise in genomics and bioinformatics by analysing whole genome sequenced data, including that from archaeological samples. The student will receive extensive training in a broad range of skills, including theoretical population genetics and biostatistics, learning concepts such as population structure, admixture and adaptation, and recognize the footprints these processes leave in the genome. Additionally, the student will also learn how to model demographic inference, gaining knowledge about coalescent theory and computational simulations. In order to analyse genomic data, the student will learn how to use and develop bioinformatic tools. This project is an international collaboration with researchers from the United States and Germany, so stays abroad are granted, giving the student a chance to meet and work with peers and learn new skills from renowned population geneticists. Opportunities to assist international meetings and present the research done will also be granted throughout the PhD. The PhD will be performed in CRAG'S Plant and Animal Genomics programme. During the first year of their studies, students receive teaching on state-of-the art technologies offered by the Core Units and Scientific Services of CRAG, such as genomics and next generation sequencing, proteomics, metabolomics, and bioinformatics. The student will also be able to attend internal and external seminars at CRAG and improve her oratory skills by giving seminars regularly. By the end of the PhD, the student will have become a population geneticist specialised in the analysis of modern and ancient genomes with a strong computational background and a wide network of peers.

REQUIREMENTS The doctoral fellowship programme INPhINIT "la Caixa" is devoted to attracting talented Early-Stage Researchers of any nationality who wish to pursue doctoral studies in Spanish or Portuguese territory.

The doctoral INPhINIT fellowships offer a highly competitive salary and complementary opportunities for training on transferrable skills (through the collaboration of leading entities such as Vitae and Oxentia), temporary stays in industry, incentives upon completion of the thesis, among other elements that make these fellowships some of the most attractive and complete in Europe.

CONTACT For questions about the position and further information about the project, contact Laura Botigué, Email: laura.botigue@cragenomica.es

HOW TO APPLY Applications should be done using La Caixa INPhINIT online application system . Please follow the link below to obtain further information about the PhD position and how to access the online application system:

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CzechAcademySci EvolutionPlantDefences

Graduate position:Biology.Centre.CZ.Evolution.of.plant.defences

PhD Studentship in Insect-Plant Interactions Project title: Why is there such high diversity of chemical defences? The role of insect herbivory in promoting chemical diversity in willows

Description: We are looking for an enthusiastic candidate to join a project exploring plant-herbivore interactions and evolution of host-plant defences in willows.

The successful candidate will dissect the mechanisms promoting chemical diversity in plants. Using a series of complementary approaches, the successful candidate will show how chemical diversity in plants arises from the pressure by herbivores and their interaction specificity, forming large-scale patterns and broad evolutionary trends. The study combines field component examining the impact of herbivores on plants, manipulative greenhouse experiments, with laboratory-based analysis of plant phylogeny and secondary chemistry. Please see the links below for more details on the project background.

- a MSc degree (non-negotiable requirement for applying for this PhD programme) - a deep interest in the ecology of insects or plants - experience in both field work and lab work - excellent skills in biostatistics, plus experience in (a) phylogenetic analysis and bioinformatics, or (b) plant chemistry analysis - fluency in spoken and written English - an ability to work independently - a driving license (optional, but highly recommended)

The successful applicant will join the Ecology Department at the Institute of Entomology, Biology Center of the Czech Academy of Science and the Zoology Department of the University of South Bohemia. The PhD study will be supervised by Dr. Martin Volf in collaboration with Prof. Vojtech Novotny (head of the Ecology Department) and Dr. Simon T. Segar (Harper Adams University. The candidate will live in Ceske Budejovice (Czech Republic) where the studies will take place. The programme offers an opportunity to conduct the laboratory work in the Czech Republic and abroad, within a collaborative network of our colleagues from Europe and overseas. The field work involves sampling in the Czech Republic, Austria, and the United States. Our department is a diverse, international team (11 nationalities) studying ecology, evolution and biogeography, and a world-class centre for interaction network research with regular publications in leading journals.

The deadline for applications is December 25th 2019. The best candidates will be interviewed on January 3rd and 4th 2020. The successful applicant is expected to start on March 1st 2020 (later start date negotiable). The student will receive a scholarship fully covering living expenses in the Czech Republic for 3 years. Applicants from all countries are eligible. To apply please send a CV, contact details for three references, and a cover letter stating qualifications, previous work and motivation to Dr. Martin Volf (volf@entu.cas.cz) where you can also send any queries.

Links: Project background: https://www.entu.cas.cz/en/departments/department-of-ecology-and-conservation-biology/laboratory-of-evolutionary-ecology/ the Biology Center of the Czech Academy of Science: https://www.entu.cas.cz/en/ Zoology Department of the University of South Bohemia: http://zoo.prf.jcu.cz/?lang=en Martin Volf: https://www.entu.cas.cz/en/staff/profile/393-martinvolf/ Vojtech Novotny: https://scholar.google.cz/citations?user=0jlGnogAAAAJ&hl=en Simon T. Segar: https://www.harper-adams.ac.uk/general/staff/profile/201598/Simon-Segar/ Volf Martin <volf@entu.cas.cz>

DurhamU KelpBiodiversity

Competitive PhD studentships available in the Molecular Ecology Group at Durham University:

1) Eco-evolutionary processes affecting biodiversity in British kelp forest communities 'V supported by the Durham Doctoral Studentship. The student will use genomic methods to compare the host kelp species with three dependant herbivore species to better understand the mechanisms that determine community structure in coastal marine ecosystems. Project will be co-supervised by Rus Hoelzel in Durham and Oscar Gaggiotti in St. Andrews.

2) Next generation conservation genetics at sea: detecting and conserving adaptive potential 'V supported by NERC DTP IAPETUS (http://www.iapetus.ac.uk/aboutstudentships/). The student will test hypotheses about the mechanisms that generate distinct patterns of diversity at functional loci across marine environmental gradients using high resolution data and working with reference genomes. Project will be co-supervised by Rus Hoelzel in Durham and Per Berggren in Newcastle.

3) Predicting risk and planning mitigation against regional impact from climate change on populations of Arctic char (Salvelinus alpines) 'V supported by the Durham Arctic CDT (https://www.dur.ac.uk/arctic/). The key objective will be to use genetic, fatty acid and ecological analyses to compare high Arctic populations from Svalbard with lower latitude populations in the UK to better understand the adaptive differences and potential for adaptation or acclimation to a changing climate in the Arctic environment. Project will be co-supervised by Rus Hoelzel and Martyn Lucas in Biosciences and Erin McClymont in Geography in Durham.

For more information about specific projects (detailed summaries available) please contact Rus Hoelzel (a.r.hoelzel@dur.ac.uk). Applications will be due before 10 January 2020 and should include a c.v., transcripts from undergraduate and post-graduate studies, a cover letter mentioning the project of interest, and 2 letters of support (sent independently to Prof. Hoelzel). Full support would only be provided for UK nationals with the exception of project 1, which is open to all nationalities.

"HOELZEL, RUS A.R." <a.r.hoelzel@durham.ac.uk>

Eawag UBern FishMigrationEvol

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based and internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institute of Science and Technology). It is committed to the ecologically, economically and socially responsible management of water resources and aquatic ecosystems.

The Department of Fish Ecology and Evolution (FishEc) located in Kastanienbaum (Lucerne) has a vacancy for a PhD student in Evolutionary Ecology of Fish Migration Applicants should have or anticipate finishing an MSc or similar before the summer 2020 in a relevant field of biology, ecology, or environmental science and a strong interest in evolutionary ecology, life history variation, and animal/fish migration.

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

The current project aims to investigate diversity of partially migratory brown trout meta-populations around the largest lakes in Switzerland. Hundreds of brown trout populations around the twenty largest Swiss lakes perform partial migrations from their natal streams to the foraging ground in the lakes, before returning to their natal streams for reproduction. Populations differ in their timing of migration, e.g. in terms of years spent in stream before migration, years spent in the lake before first return migration and seasonal timing, and in their foraging ecology in the lake environment. This variation is expected to be partly plastic and ontogenetic and partly genetically determined.

Our study system allows testing for drivers of diversity within populations, between populations within a meta-population and between meta-populations. The PhD-student will analyse this diversity with a combination of age/growth-, dietary- and genetic analyses and will additionally conduct PIT tag studies to track migration patterns and survival of juvenile brown trout. The project is linked to an applied project on structure and management of partially migratory trout populations, which generates a number of synergies and allows for knowledge transfer from basic scientific questions to management. The PhD-student will focus on the scientific questions in the project.

The position is funded for four years and will be hosted by the River Fish Ecology group, led by Dr. Jakob Brodersen (http://www.eawag.ch/en/department/-fishec/main-focus/river-fish-ecology/) within the FishEc Department (http://www.eawag.ch/en/department/-fishec/) and the Section of Aquatic Ecology at University of Bern (http://www.aqua.iee.unibe.ch/). Excellent communication and writing skills in English and ability to work in a team are essential. Communication skills in German and/or French is a benefit, but not a requirement for the position.

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

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Edinburgh InsectHermaphroditism

Dear all,

I am looking for a talented and enthusiastic evolutionary/molecular biologist or entomologist for a 4-year PhD position in my lab http://lauraross.bio.ed.ac.uk at the Institute of Evolutionary Biology, University of Edinburgh. There are funding options for both UK and international students. If you are interested please contact me directly (laura.ross@ed.ac.uk) to discuss. Deadlines vary depending on funding source: 13th of December for non-UK, 9th of January for UK, but please contact me at least a week before the official deadline if interested!

The evolution of hermaphroditism in insects

Summary Organisms reproduce in diverse ways. Yet it is unclear why and how new reproductive strategies evolve. This project focuses on the only case of hermaphroditism in insects: In species of the scale insect Icerya, female-like hermaphrodites produce both sperm and eggs and self-fertilize.

Project background Understanding why there is such variability in the way organisms reproduce is one the most important unsolved puzzles in evolutionary biology. This project aims to tackle this question by focusing on the unique and puzzling reproductive strategy of the scale insect Icerya purchasi. This species is the only insect unequivocally described as hermaphroditic; female-like hermaphrodites can produce both sperm and eggs and self-fertilize. But how can a female produce sperm? A recent hypothesis suggests that the sperm present in hermaphrodites seem to have originated from the individuals father "infecting" his future offspring with sperm-producing cells. However although the data is suggestive, this hypothesis requires further scrutiny. It is also unclear why, while most offspring develop as hermaphrodites, a small number develop as males. Finally it seems that while hermaphroditism is exceedingly rare in insects, it might have evolved independently in several close relatives of Icerya. This PhD project will explore how and why this unusual reproductive system evolved by using comparative methods across species as well as experimental and genomic analyses in the laboratory. Together this work will help us to better understand what evolutionary forces shape the ways animals reproduce.

Research questions The projects sets out to test a number of key questions to better understand the evolution of the only insect hermaphrodite:

* What is the evolutionary and developmental origin of the sperm produced by female-like hermaphrodites? * Hermaphrodites can self-fertilize, so why and how do they occasionally produce male offspring? * How frequently did hermaphroditism evolved within the clade of insects and do any ecological factors predict the patterns we observe?

Methodology The project will use two main approaches: The first will focus on collecting insect specimens of different Icerya species, and then use molecular phylogenetic methods to determine their evolutionary relationships, and to study transitions between reproductive strategies employed by the different species. This part of the project is in collaboration with Prof. Penny Gullan, The Australian National University, Canberra. The second part of the project will focus on Icerya purchasi. We will use laboratory experiments and a combination of cytogenetic and genomic approaches to study different aspects of the reproduction of this species.

Training A comprehensive training programme will be provided comprising both specialist scientific training and generic transferable and professional skills. Specifically the student will undertake training in the use of molecular wet lab techniques, the analysis of sequencing data and the use of microscopy and cytogenetic approaches.

Requirements Candidates must be highly motivated with a keen interest in evolutionary biology and genetics and a strong motivation to pursue a scientific career. Previous experience working with insects and phylogenetic and genomic analyses would be advantageous.

References - Bachtrog, Doris, et al. "Sex determination: why so many ways of doing it?." PLoS biology 12.7 (2014): e1001899. - Gardner, Andy, and Laura Ross. "The evolution of hermaphroditism by an infectious male-derived cell lineage: an inclusive-fitness analysis." The American Naturalist 178.2 (2011): 191-201. - Unruh, C. M., and P. J. Gullan. "Molecular data reveal convergent reproductive strategies in iceryine scale insects (Hemiptera: Coccoidea: Monophlebidae), allowing the reinterpretation of morphology and a revised generic classification." Systematic Entomology 33.1 (2008): 8-50.

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

ROSS Laura <Laura.Ross@ed.ac.uk>

ErlangenNurnbergU PlantBioinformatics

PhD student position: Applied bioinformatics in crop plants

Research: The aim of our research is the discovery of genes, markers, and signalling molecules associated to plant traits for improving crop characteristics, quality and productivity. We use the latest molecular and bioinformatics technologies for the generation, analysis and integration of multi-omic data (genome, epigenome, transcriptome, proteome, metabolome and phenome) in order to disclose the genetic basis of plant complex traits. We mainly work with two plant models, potato and cassava, which are, respectively, the third and fifth most consumed crop plants in the world and the main sources of starch for more than 800 million of people in many developing countries. The candidate of this position will learn and develop bioinformatics workflows to process, analyze, integrate and model omics data of those crop plants to elucidate the molecular mechanisms responsible for traits of agronomic interest. More information about the Biocomputing Group can be found in our homepage: https://www.biochemie.nat.uni-erlangen.de/English/research/corralgarcia.html Requirements:

We are looking for a talented and highly motivated PhD student with strong interest in bioinformatics and plant physiology. A master'Âs degree in bioinformatics, molecular biology, integrated life sciences, biochemistry, or related is required. Proficiency in R, MATLAB, Python and the use of shell script are highly advantageous, but not required. Good English communication skills as well as team work abilities are expected.

Comments:

The position is initially for a fixed term of three years with the possibility of extension. The payment follows the German TV-L scale being the first year 50% of the group 13, and the following years 65% of the group 13. The position is available immediately. Reviewing of applications will begin instantly and the position will remain open until a suitable candidate is found. Please send your application as a composite pdf-file in English (letter of motivation stating your research interests, CV, name and addresses of at least two referees) via email not later than 16.12.2019 to: bio-bcsekretariat@fau.de

Dr. Jose M. Corral Biocomputing Group Division of Biochemistry Department of Biology - Erlangen-Nurnberg University Staudtstr. 5 91058 Erlangen Germany

Jose Maria Corral Garcia <josemariacorral@hotmail.com>

ETH Zurich BacterialAdaptation

PhD position in Experimental Evolution

The recently formed group of Dr. Macarena Toll-Riera is seeking a PhD student to study bacterial adaptation to environmental changes through the combination of experimental and high-throughput sequencing approaches. We are hosted at the Institute of Integrative Biology (ETH Zurich), in the Professorship of Evolutionary Biology.

Project background Environments are under constant change and one of the main strategies that organisms have to respond to these changes is through evolutionary adaptations. Although evolutionary adaptations have been studied for long time, the genetic bases underpinning them are still not fully understood.

Most research done to understand how organisms adapt to changes in their environments has been done using model organisms. In this project, instead, we propose to study this question using a bacterium isolated from Antarctica. To survive to the harsh conditions found in cold environments, this bacterium has a unique set of adaptations that makes it a very interesting model organism to study the molecular mechanisms that can facilitate, or limit, adaptation to novel environments.

Job description The candidate will investigate the role that enzyme promiscuity and large genome duplications have on facilitating adaptation to environmental changes. As a proxy to environmental change, she/he will use a large array of carbon sources and will perform laboratory evolution experiments to challenge bacteria to adapt to novel environments. She/he will couple laboratory evolution experiments to next generation sequencing to disentangle which are the genetic changes underlying adaptation.

We offer 4 years of funding and to be part of a small, but collaborative and dynamic group. We are hosted at the Institute of Integrative Biology, ETH Zurich. The candidate will benefit from a vibrant and interdisciplinary academic environment with excellent opportunities for education, training and collaboration. Aside from the high quality of life, Zurich provides easy access to outdoor activities.

Your profile The successful candidate should hold a master degree in a relevant area such as evolutionary biology, microbiology or genomics, have a genuine interest in evolutionary biology and have a good command of English. Wet-lab experience, ideally in microbiology, programming skills and experience analysing next-generation sequencing data are an asset.

The candidate should be highly motivated, enthusiastic, curious and able to work independently but also as a team member.

Interested? We look forward to receiving your application with the following documents: motivation letter, CV, academic records, and contact information for 2-3 potential references. Please send your application (one single PDF file) by email to Macarena Toll-Riera (macarena.toll@env.ethz.ch). We will start to revise applications on 20th of December, until position is filled.

Starting date: preferably February-March 2020.

Toll Riera Macarena <macarena.toll@env.ethz.ch>

Europe MEME MasterProgramme

MEME: Application Cohort 2020 open

MEME (Erasmus Mundus Master in Evolutionary Biology) is a two-year research oriented master program for talented and motivated students who are interested in understanding evolution in all its facets. It intends to provide an optimal preparation for subsequent doctoral studies and eventually a career in academic research.

The MEME program addresses the driving forces of evolution at all levels of organismal organization (from cells and individuals to populations and ecosystems), and allows students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the program is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

To offer a program of such broad scope, four European universities (University of Groningen, Netherlands; University of Montpellier, France; Ludwig Maximilians University of Munich, Germany; Uppsala University, Sweden), have joined forces with Harvard University (USA) and the University of Lausanne as associate partners. Together, this consortium has put together an attractive multidisciplinary program that meets the highest standards. All students have to study at (at least) two partner universities, and they will receive a double degree from two partner universities they have attended.

A limited number of EMJMD scholarships are available for the highest ranked students. Details on the program and the selection procedure can be found on www.evobio.eu . Starting date: 1 September 2020 Application deadline: 15 January 2020

Please alert your students to this great opportunity!

More information and how to apply - please see www.evobio.eu Questions about the contents of the program: Leo Beukeboom (l.w.beukeboom@rug.nl) Questions about the requirements and the application procedure: Femke Schouten (f.a.schouten@rug.nl)

“Schouten, F.A.” <f.a.schouten@rug.nl>

GhentU ComputationalBiologyInPlants

The Comparative Network Biology lab, led by Klaas Vandepoele, of the VIB Center for Plant Systems Biology is home to an enthusiastic, diverse and international group of researchers in the field of plant bioinformatics. Beyond our expertise in plant genomics, comparative genomics and scientific creativity, we are looking for a new team member: PhD student ’Computational Tools for Network Biology in Plants’

Job description

* Fully funded PhD position with the aim to obtain a doctorate at Ghent University. In this project, the candidate is expected to: * i. develop new computational methods to accurately build gene regulatory networks

in different plants (model species & crops) with varying levels of genome complexity * ii. develop and evaluate methods to translate networks between model and crop species using different experimental data sources * Reporting of results through publications in peer-reviewed international journals. * Attending and presenting your results at international scientific events. * Access to a diverse set of training programs at UGent / VIB (both scientific & soft skills)

Profile

* MSc in Bioinformatics, Computer Science, Engineering, or similar * Good programming (Python, JavaScript and/or PHP) and Linux skills are a must * Experience with tool/web-development (for example, JavaScript frameworks like React, Vue, of Angular) is a plus * You are enthusiastic about scientific research, computational biology, and want to learn more about advanced biological concepts * You have good communication and writing skills * You are proficient in English

How to apply? Submit your application online (https://vibvzw.jobsoid.com/j/23481/phd-student-computational-tools-for-network-biology-in-plants) and please include a letter of motivation, a detailed CV and contact info of 2 references (including e-mail addresses and phone numbers). Applications will be accepted until the position is filled.

Klaas Vandepoele - Professor Comparative Network Biology

VIB-UGent Center for Plant Systems Biology Ghent University Technologiepark-Zwijnaarde 71 - 9052 Ghent - Belgium Tel. +32(0)9 331 38 22 [http://www.psb.ugent.be/ | www.psb.ugent.be]

Genome editing, cutting-edge technology for a sustainable agriculture

Klaas Vandepoele <Klaas.Vandepoele@psb.vib-ugent.be>

GhentU SeaweedAdaptation

Ghent University PhD position on the mechanisms and consequences of low sex in seaweed populations.

Description The Phycology research group (Olivier De Clerck's lab) is looking for a highly motivated PhD student for a project focusing on the effect of life cycle variation on genome organization, evolution and adaptation. The focus of the project is on seaweed populations (Dictyota) that display varying degrees of sexual versus asexual reproduction. The relative degree of sexual or asexual reproduction, likely determined by differences in sea surface temperature, should reflect on population genetic parameters and on the efficacy of natural selection. Using a combination of laboratory experiments, genetic data of natural populations and transcriptomic data, this project will 1) determine the precise mechanisms of asexual reproduction in Dictyota dichotoma; and 2) evaluate the consequences of mating system variation between Atlantic (sexual) and Mediterranean (largely asexual) populations on the genetic structure of the populations, the efficacy of selection and the adaptive potential of the populations.

We offer a fully funded PhD position with the aim to obtain a doctorate at Ghent University (4 years). He/she will work in a stimulating environment and gain expertise in evolutionary ecology combining field as well as lab experiments. In addition, he/she will have access to cutting-edge technologies (e.g. whole genome resequencing), personal career assistance and high level training courses. The position is available as of January 2020. The actual starting data is flexible.

Profile of the candidate You have a demonstrable interest in the field of evolutionary biology and handling genetic data. You have the necessary social skills, flexibility and critical thinking to function in a multidisciplinary and international academic environment. Competency of English (reading, writing, and speaking) is required. You have an independent, problem-solving, organized and result-oriented attitude.

How to apply: Applications have to be sent in via email to Olivier.declerck@ugent.be at the latest on December 15. The following documents should be attached: * cover letter * motivation letter * copies of your MSc degree * contact details of at least 2 persons. * Please merge all documents into one PDF attachment.

Olivier De Clerck Biology Department Krijgslaan 281 S8 9000 Gent - Belgium

[tel. -32-9-2648500 / room. 40.08.130.046A] [tel. -32-9-2648500 / room. 40.08.130.046A]

JohnMooresU Liverpool NematodeGenomics

Genomic analysis of the parasitic nematode Phasmarhabditis hermaphrodita (and other wild Phasmarhabditis species) - a biological control agent of slugs

Project Description

Understanding the genetic determinants of key traits in parasitic organisms provides important tools for developing novel pest control products. Slugs are serious pests in agriculture and a persistent problem for home gardens. They are commonly controlled using pesticide pellets, but as these can have negative effects on non-target organisms, including pets and wildlife, a more sustainable and ecologically sound alternative was developed. This is the nematode Phasmarhabditis hermaphrodita, a facultative parasite of slugs and snails. P. hermaphrodita was formulated into a biological control agent (NemaslugÂ) by BASF Agricultural Specialties for use by farmers and gardeners and since 1994 has been used regularly in the U.K. and Europe, provide significant protection against slugs. However, there are reports that P. hermaphrodita cannot kill larger pestiferous slug species. In order to better understand key traits such as virulence, longevity, stress tolerance and dispersal to improve the NemaslugÂ product, the student will apply cutting-edge genomic technologies to sequence the genomes of P. hermaphrodita (NemaslugÂ) and other Phasmarhabditis species isolated from the wild. The student will undertake genomic analyses of these nematodes, including genome assembly and annotation and comparative genomic analysis with other nematodes.

i) Whole genome sequencing and annotation of Phasmarhabditis hermaphrodita

The genome of the strain of P. hermaphrodita currently used in the production of NemaslugÂ (called DMG0001) will be sequenced using a combination of long read (Pacific BioSciences) and short read (Illumina) sequencing technologies. Whole transcriptome RNA sequencing will also be done to aid gene annotation. The student will assemble and annotate the genome. In addition to this reference genome for P. hermaphrodita, 10 strains recently isolated from the wild and kept in culture at LJMU will be re-sequenced and mapped to the reference genome for population and evolutionary genomic analysis. Candidate genes involved in virulence, longevity and stress tolerance will be tested in lab experiments carried out in parallel.

ii) Whole genome sequencing of other Phasmarhabditis species (P. californica and P. neopapillosa) isolated from the wild

In addition to P. hermaphrodita, the student will sequence the genomes of other Phasmarhabditis species, allowing comparative analyses of the genetics of virulence and other traits. 5 P. neopapillosa and 3 P. californica wild isolates currently in culture in LJMU will be sequenced (genomes and transcriptomes), assembled and annotated as for P. hermaphrodita. A genome exploration system will be developed to allow browsing and further investigation.

Ultimately, this project will provide the tools to enable genomic/genetic improvement of P. hermaphrodita as a biological control agent, as well as investigating the potential of other Phasmarhabditis species to be developed as alternative products. The project will provide an excellent opportunity for the student to apply state-of-the-art genome bioinformatics tools and technologies to advance knowledge of and improve an important biological pest control tool.

Qualifications/ Skills Required:

The candidate requires a 2:1 degree or above in a relevant subject area. A relevant MSc qualification is desirable, but not essential.

The candidate must have experience in bioinformatics. The project will suit a candidate with a firm knowledge of genomics and computational biology. Practical wet-lab experience and the ability to work independently are desirable, as is a knowledge and understanding of parasitology, particularly nematology.

Full training will be provided to the candidate along with access to the broad knowledge and expertise held by the supervisory team.

Deadline:

The deadline for submission of applications is midnight of 22/11/2019

Funding Notes This studentship is funded by BASF. Only UK & EU citizens can apply for this studentship. Funding will consist of full tuition fees for three years and the award of a living stipend at UK Research Council rates. References Informal enquiries are welcome. Applicants should email a CV, covering letter detailing their suitability for the project and contact details of two referees to Dr Robbie Rae: r.g.rae@ljmu.ac.uk and Dr. Gareth Weedall: g.d.weedall@ljmu.ac.uk

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KielU EvolutionaryMicrobiology

The Genomic Microbiology Group of Prof. Tal Dagan in the Institute of Microbiology at Kiel University, Germany, invites applications for a:

PhD position in evolutionary microbiology

The position is offered within the collaborative research center (CRC1182) on the origin and function of metaorganisms Deadline for applications is 2nd January 2020.

Project description: Our project aims to identify bacterial traits underlying the main stages in the life-cycle of seed-borne bacteria. Our research is focused on one member of the wheat microbiota, Pantoea agglomerans, which is known as growth promoting and with anti-fungal activity. Planned experiments on bacterial colonization dynamics within the wheat root are established in our lab.

Requirements: Currently we are looking for an enthusiastic microbiologist with a Master (or equivalent) in Microbiology or molecular biology to join us. Required skills: molecular microbiology techniques, work with environmental samples, isolation of microbial strains, plasmid engineering and generation of knockout mutant strains, evolution experiments.

Research Group: The PhD candidate will work in the Genomic Microbiology group led by Prof. Tal Dagan (http://www.uni-kiel.de/genomik) that is focused on microbial genome evolution. The group is international and multidisciplinary with both computational and experimental working scientists. For enquiries regarding the position and research topic please contact Prof. Tal Dagan: tdagan@ifam.uni-kiel.de

For further details on the collaborative center see: http://www.metaorganism-research.com/ Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology and microbiology are prerequisites for entering the program. We are looking forward to your online application for a PhD fellowship in the beautiful landscape of Northern Germany.

Applicants should send their application as a single pdf-document to the office of the CRC 1182 (office@metaorganism-research.com). The application should include (i) a curriculum vitae with a list of publications, (ii) Master or doctoral certificate or proof of records (iii) a motivation statement (max. 2 pages), (iv) a list of maximal 3 preferred positions (from among the offered projects) plus a short explanation of the preferences (max. 1 page), and (v) contact addresses of two possible referees.

Please abstain from sending application portraits.

Prof. Dr. Tal Dagan

Genomic Microbiology Group Institute of Microbiology Christian-Albrechts-University Kiel ZMB, Am Botanischen Garten 11 24118 Kiel, Germany

Tel: +49 431 880 5712 Fax: +49 431 880 5747 e-mail: tdagan@ifam.uni-kiel.de web: www.uni-kiel.de/genomik Tal Dagan <tdagan@ifam.uni-kiel.de>

KULeuven EvolutionMicrobiomeDaphnia

CSC-KULeuven PhD topic

The China Scholarship Council (CSC) and KU Leuven have agreed to fund up to 50 PhD scholarship positions in Science and Technology to outstanding Chinese PhD applicants at KU Leuven. We invite applications for the following approved CSC-KULeuven PhD topic:

Rapid evolution of tolerance to pesticides under warming in an aquatic invertebrate and its gut microbiome

Pollutants and warming are among the two most important anthropogenic stressors, moreover many pollutants are more toxic at higher temperatures. We will study two interrelated research topics to improve risk assessment, and more general to advance the emerging field of multi-stressor ecology. First, using powerful experimental evolution trials we will select for increased tolerance to a pollutant, to warming, and to their combination. To obtain mechanistic insights this will be combined with targeted analyses of the expression levels of genes known to be important in tolerance against each stressor separately. Second, we will study whether the rapid evolution of tolerance is causally associated with shifts in the gut microbiome communities. We will address these innovative research topics at the interface of ecotoxicology, global change biology and microbiology using the water flea Daphnia magna, a keystone species in aquatic food webs and a model organism in ecotoxicology, evolutionary biology and ecological genomics.

More information on the topic can be found here < https://set.kuleuven.be/en/csc/rapid-evolution-of-tolerance-to-pesticides-under-warming-in-an-aquatic-invertebrate-and-its-gut-microbiome >.

Some recent relevant publications: - Macke E, Callens M, De Meester L, Decaestecker E (2018). Host-genotype dependent gut microbiota drives zooplankton tolerance to toxic cyanobacteria. Nature Communications 8:1608. - Stoks R, Govaert L, Pauwels K, Jansen B, & De Meester L (2016) Resurrecting complexity: the interplay of plasticity and rapid evolution in the multiple trait response to strong changes in predation pressure in the water flea Daphnia magna. Ecology Letters 19:180-190. - Zhang C, Jansen M, De Meester L & Stoks R (2019) Rapid evolution in response to warming does not affect the toxicity of a pollutant: Insights from experimental evolution in heated mesocosms. Evolutionary Applications 12:977-988.

Team This topic is embedded in a larger project led by Prof. Luc De Meester, Prof. Ellen Decaestecker and Prof. Robby Stoks on eco-evolutionary dynamics in aquatic invertebrates with a strong focus on the gut microbiome. You will be part of an international, enthusiastic and dynamic team with ample expertise in using Daphnia as model systems to address key questions at the intersection of ecology and evolution. Our team has excellent research facilities including climate rooms and well-equipped ecophysiology and microbiology laboratories.

University Leuven is a beautiful historical university city with a very high and pleasant standard of living (https://www.kuleuven.be/english/living). Leuven is a 15-minute train ride away from Brussels International Airport and a 20-minutes train ride from Brussels itself. Brussels is one of the best-connected cities in Western Europe; Amsterdam, Paris and London are all reachable within 2 hours by train. The university, founded in 1425, has a top research and teaching standard. The KU Leuven < https://www.kuleuven.be/english/ > features consistently in Europe's top-15 universities and has been elected by Reuters for the fourth year in a row as most innovative university in Europe.

Profile

* Highly motivated Chinese student with an excellent academic record

* Very good command of both spoken and written English.

* Strong interest in evolutionary ecology and microbiology, and a high ability for accurate lab work.

* Proven microbiological skills are an asset, but training can be provided.

Interested? For more information please contact Prof. dr. Robby Stoks, tel: +32 16 32 37 10, mail: robby.stoks@kuleuven.be.

You have to apply for this position to KU Leuven before 15 December 2019. General information about CSC-KULeuven scholarships is available here < https://set.kuleuven.be/en/csc >. Go to the specific topic to apply here < https://set.kuleuven.be/en/csc/rapid-evolution-of-tolerance-to-pesticides-under-warming-in-an-aquatic-invertebrate-and-its-gut-microbiome >. The starting date is 1 October 2020.

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LundSweden PlantInsectInteractions

PhD positions in the evolutionary ecology of plant-insect interactions

Two PhD positions are currently available in the Evolutionary Ecology of Plant-Insect Interactions research group (EEPII) at Lund University (https://www.biology.lu.se/research/research-groups/evolutionary-ecology-of-plant-insect-interactions).

Research within the EEPII strives to understand the evolutionary forces driving diversification and adaptation in species interactions among plants and plant-feeding insects. We combine genomic, evolutionary and ecological studies to ask and answer questions about the distribution, diversification and conservation of biodiversity within and among species, and in particular how these patterns and processes are affected by the interaction between plants and insects. Our research bridges the gap between zoology and botany by integrating studies of animal- and plant biodiversity.

Position 1: https://lu.varbi.com/en/what:job/jobID:302793/ Position 2: https://lu.varbi.com/en/what:job/jobID:302607/ Deadline for both positions is the 10. January 2020.

Both projects focus on the evolution of fragrance-based pollination systems, are focused on well-established empirical systems (Position 1: Arabis alpina + Lithophragma bolanderi, Position 2: Dalechampia), and will combine field and greenhouse work with macroevolutionary analyses. We strongly encourage interested candidates to apply for both positions. Please note that this requires two separate applications.

Informal inquiries are welcome to Dr. Magne Friberg (magne.friberg@biol.lu.se) and Dr. Ãystein Opedal (oystein.opedal@biol.lu.se).

"oystein.opedal@biol.lu.se" <oystein.opedal@biol.lu.se>

McMasterU SexDeterminationInAmphibians

The Evans lab in the Biology Department at McMaster University is looking for graduate students interested in studying sex determination in amphibians to start in the Fall of 2020.

We combine approaches in bioinformatics, gene editing, and field work to understand genetic mechanisms of sex determination in African clawed frogs (Xenopus), including what genes trigger sexual differentiation, why these genes evolve rapidly and vary among species, and how these genes influence evolution of sex chromosomes and sex-related genetic pathways. A major effort in the lab is to use gene editing to test function of putative genetic triggers for sex determination, and transgenesis to insert a known genetic trigger for sex determination from one species into the genome of other species that lack this genetic trigger. In this way, our work aims to better understand "how important things evolve".

For additional information on our research, please check out some of our recent papers: https://benevanslab.wordpress.com/publications/ Qualifications:

Applicants should hold a bachelor's degree in science, math, or computer science before mid-2020. Applicants with a M.Sc. degree are generally eligible for entrance into our Ph.D. program.

Funding:

Financial support is provided through a combination of teaching assistantships and existing research funds from the Evans lab. Canadian citizens and permanent residents are eligible to apply for provincial (Ontario Graduate Scholarships) and federal funds (Natural Science and Engineering Research Council of Canada), and encouraged to do so. Other opportunities are available as well for international students (e.g., Vanier Award)

Environment:

The Biology Department at McMaster University is a wonderful intellectual environment with strengths in Evolutionary Biology, Bioinformatics, and Computational Biology. We have an excellent graduate program in the Biology Department with ~100 students. The Evans lab holds joint lab meetings with the Golding lab, and we interact extensively with several other groups (Dworkin, Dushoff, Bolker, Poinar, Wilson). Geographically, we are situated within a network of vibrant urban centres (Hamilton, Toronto) and we have easy access by foot or bike to green spaces (Cootes Paradise, Dundas Valley Conservation Area, dozens of waterfalls) and a relatively easy commute to some of Canada's iconic wonders (Bruce Peninsula, Niagara Falls and the Niagara Escarpment).

The Evans lab is very strongly committed to equity, diversity, and inclusion in the workplace.

Interested candidates should please email Ben Evans (evansbenj@gmail.com). Please include "Graduate Work" in the subject line, a brief description of your research interests, a description of your experience (if any) with R, python, perl, or other computer languages, bioinformatics, and/or lab work, a curriculum vitae, and names and email addresses of 2-3 references.

– Ben Evans Biology Department McMaster University Life Sciences Building room 328 1280 Main Street West Hamilton, Ontario L8S4K1 Canada phone (office/lab) : 905-525-9140 x 26973 <905-525-9140;26973>/27261 fax: 905-522-6066 Lab Website: http://benevanslab.wordpress.com/ Ben Evans <evansbenj@gmail.com>

MichiganStateU FishEvoDevoGeno

PhD Positions in Fish Evolutionary Developmental Genomics

The Fish Evo Devo Geno Lab (PI: Ingo Braasch) at Michigan State University is recruiting highly motivated PhD students interested in working on the genomic basis of vertebrate evolution and development to start in Summer/Fall 2020.

The Braasch Lab focuses on genomic and developmental changes that contribute to major transitions during the course of vertebrate evolution and studies evolutionary novelties at the levels of genome structure, gene family evolution, and gene regulation. We combine sequencing and comparative analyses of fish genomes with analyses of molecular evolution and functional genetic and developmental approaches (CRISPR genome editing, transgenics, gene expression analyses, epigenomic profiling) in a variety of model species (zebrafish, spotted gar, medaka, killifish, and others).

Graduate projects fall within the following broader research areas of the group:

1. Genomic and morphological evolution of fishes: How do morphological differences among fish and other vertebrate lineages arise from diversification of gene repertoires? What is the role of gen(om)e duplications and gene losses in generating phenotypic diversity? How do changes in gene regulation contribute to evolutionary novelties and key innovations? We study a number of gene families that are of particular importance for the evolution of the vertebrate body plan, e. g. genes involved in development of the vertebrate-specific neural crest cells.

2. Conquest of land and 'fish-out-of-water': We are studying genomic changes and their functional consequences leading to the evolution of tetrapods from fishes and other 'fish-out-of-water' scenarios, including the evolutionary loss of genes at the water-to-land transition and the gene regulatory basis of hatching.

3. Evolutionary genomic analyses of zebrafish and other biomedical fish models: Combining genomic sequence comparisons, gene expression analyses and epigenomic profiling, we aim to improve connectivity of teleost biomedical fish models such as zebrafish, medaka, killifishes, etc. to human biology and disease. This work is support by funds from the NIH.

For additional information on our research, see also Braasch et al. 2016, Nature Genetics (doi:10.1038/ng.3526) and Braasch et al. 2015, JEZB (doi:10.1002/jez.b.22589).

The Fish Evo Devo Geno Lab is part of the Department of Integrative Biology (IBIO), the Ecology, Evolutionary, and Behavior Program (EEBB), the Genetics and Genome Sciecne Graduate Program at Michigan State University, and member of the NSF BEACON Center for the Study of Evolution in Action.

MSU IBIO has a strong research commitment to vertebrate biology with a highly collaborative community, the MSU Vertebrate Genomics & Evolution Group (MSU VerGE) that includes labs working on vertebrate and fish evolution, genomics, development, population genetics, neuroscience, behavior, ecology, and conservation, allowing for vibrant exchange among fields, methods and model systems.

Qualifications: Applicants should hold a bachelor's degree in biology, genetics, genomics, molecular biology, bioinformatics, developmental biology, zoology or related fields. Suitable candidates should be enthusiastic about working in an interdisciplinary manner and have a passion for fish/vertebrate biology and evolution. Previous research experience in a relevant area is desired, but not required.

Admission: Students will be admitted through the MSU IBIO Graduate Program (https://integrativebiology.natsci.msu.edu/graduate-program/) and the MSU Ecology, Evolutionary Biology, and Behavior Program (https://eebb.natsci.msu.edu/). Another possible route of admission is through the MSU Genetics and Genome Science Graduate Program within the MSU BioMolecular Science Gateway (https://biomolecular.natsci.msu.edu/applicants/how-to-apply/).

Application deadline for the MSU IBIO and the MSU Genetics and Genome Science Graduate Programs is December 1, 2019.

Funding: Financial support is provided through research and teaching assistantships and the PI's external funding. Competitive applicants will be eligible for university fellowships and supported in applying for graduate fellowships from NSF, NIH, and other agencies.

Interested candidates should email Ingo Braasch (braasch@msu.edu) in advance of the application deadlines on December 1. Please include the following in your email:

1. Brief description of your research interests and how they align with pursuing a PhD in vertebrate Evo-Devo

and genomics 2. Curriculum Vitae 3. Names and email contacts of 2-3 references

We are looking forward to your application!

Ingo Braasch

Assistant Professor Department of Integrative Biology College of Natural Science Michigan State University

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MichiganStateU WeedEvolution

Job Description: The Patterson lab at Michigan State University is looking for a PhD student interested in genome evolution and how novel variation can be generated during periods of intense abiotic stress over short generational timescales. Students will develop independent dissertation projects that explore how human selection can change weedy genomes in agroecosystems and what that might mean for the future of weed control. Applications received before January 1st, 2019 will be given full consideration.

Lab Description: Dr. Patterson's research program utilizes the most current techniques in genomics to understand the structure and plasticity of weedy genomes and how that plasticity influences the success of weedy species. We are especially interested in how genome rearrangements (i.e. transposable elements and copy number variation) form and are utilized as novel sources of genetic variation for weed adaptation to abiotic stresses. We also work on herbicides and how they affect plant physiology and how resistance evolves on rapid timescales in weedy species. We also work to generate genomic resources for the weed science community and to discover the molecular mechanisms of resistance.

Requirements: A B.S. in Botany, Genetics, Agronomy, Evolutionary Biology or related field.

How To Apply: Contact Dr. Eric Patterson by email: Patte543@msu.edu and be sure to check: https://www.canr.msu.edu/psm/ . Eric Patterson Assistant Professor Plant, Soil, and Microbial Sciences Patte543@msu.edu

"Patterson, Eric" <patte543@msu.edu>

MississippiStateU ButterflyEvo

Graduate student opportunities are available to study butterfly evolution and development at Mississippi State University.

Background: Butterfly wing color patterns serve as fantastic models to study the origin of adaptive novelty from evolutionary and developmental perspectives. We are seeking students for two NSF funded projects (awards 1736026 and 1755329) aimed to explore the genomic and developmental changes responsible for adaptive variation in pigment and structurally based wing color patterns. We are particularly recruiting students interested in studying (1) the developmental pathways involved in structural coloration, or (2) the molecular evolution of gene families and networks across Lepidoptera. These are part of larger collaborative projects with Ryan Range (Auburn University), Federico Hoffmann (Mississippi State University), Riccardo papa (University of Puerto Rico) and Arnaud Martin (George Washington University). Students will have opportunities to work directly with the collaborative team to develop their specific research projects, including opportunities to visit and work directly with collaborating labs.

Qualifications: We are looking for highly motivated students interested in exploring the genomic and developmental drivers of evolutionary novelty. Candidates should have a strong background in biology, and preferably basic skills in computational biology and/or molecular biology research methods. Candidates should also have good organization skills and work well in a collaborative team environment.

How to apply: The positions will be based in the Counterman lab at Mississippi State University. Please email a statement of interest and CV to Brian Counterman, bcounterman@biology.msstate.edu

Student applications received by December 15th will be given priority consideration for competitively awarded stipend enhancements and have chances to be invited to an on-campus visit in Spring 2020.

Graduate Program: Mississippi State University is home to a growing group of faculty that study the evolutionary genomics of biological variation. The Department of Biological Sciences hosts an excellent graduate program in biology, and a new interdisciplinary, cross-college graduate program in Computational Biology is currently being established with anticipated start in Fall 2020. MSU is located in Starkville, a quaint southern college town with a historic downtown district that celebrates the local music and cuisine. For more information on the Counterman lab please visit the lab website: (www.countermanlab.org). Opportunities are available for both MS and/or PhD students.

Brian A. Counterman Associate Professor Department of Biological Sciences Mississippi State University

bcounterman@biology.msstate.edu
www.countermanlab.org "BCounterman@biology.msstate.edu"
<BCounterman@biology.msstate.edu>

MPI Ploen Evolution tRNASets

PhD position: Exploring the evolutionary fate of emergent tRNA genes in bacteria

A fully funded, three-year PhD position is available in the Microbial Evolutionary Dynamics Group at the Max Planck Institute for Evolutionary Biology (Plön, Germany), starting May 2020.

Project background: Our group is interested in the evolution of bacterial transfer RNAs (tRNAs). In a recent experiment, we deleted a tRNA gene from the bacterium Pseudomonas fluorescens SBW25, resulting in a decrease in growth rate. This was rapidly and repeatedly compensated during an evolution experiment, through duplication of large chunks of the genome. Each of the duplications contains a new, emergent copy of a compensatory tRNA gene.

Project: The aim of this PhD project is to investigate the fate of the large scale duplications. The student will firstly use experimental evolution, whole genome sequencing and tRNA-seq to track the fate of the duplicated regions over time. Concurrently, they will use targeted genetic engineering and biological assays to unravel how each of the original and duplicated tRNA genes contribute to translation and fitness in their respective genomic backgrounds. The results of this project will contribute to a broader picture of how tRNA genes emerge and spread through bacterial chromosomes, and ultimately how different tRNA sets evolve.

The institute and area: The MPI in Plön is a vibrant and interesting place to work. With three departments and around 20 research groups, it is one of the hubs of evolutionary research in Germany. There are PhD candidates from a wide range of countries, and the working language is English. There are plenty of opportunities to interact with top researchers in the field. Student life is affordable; many current students rent their own apartments.

Application information: We are looking for a highly motivated student to join our lab. The ideal candidate would have an MSc in molecular biology, microbiology, or related field, plus some experience of scripting in R. Some background in mathematics would also be useful; we are part of the Department of Evolutionary Theory, and there are opportunities for collaboration with theorists.

To apply, please send an application letter, CV, and contact details of two referees to gallie@evolbio.mpg.de by the 20th December 2019. Further information can also be requested at this address.

Dr Jenna Gallie Research Group Leader for Microbial Evolutionary Dynamics

Jenna Gallie <gallie@evolbio.mpg.de>

NorthernArizonaU EvolutionaryGenomics

The Tollis Lab at Northern Arizona University (NAU; https://tollislab.org) is seeking a highly motivated and enthusiastic PhD student to study vertebrate evolutionary genomics.

Research in the lab encompasses phylogenomics, comparative genomics, transposable element evolution, and the evolution of cancer suppression. The basic unifying premise of our research is to combine molecular and computational methods to uncover the mechanisms underlying the evolution of phenotypes and genome structure, as well as outstanding questions in phylogenetics. The taxonomic focus of these questions vary widely, but current projects include: molecular evolutionary rates and the phylogenomics of squamate reptiles; rates of transposition in rapidly evolving versus slowly evolving clades; population genomics of elephants, bats and other vertebrates; and differential gene expression of DNA damage response in various vertebrate species. The successful Ph.D. student will have considerable flexibility in crafting a thesis with Dr. Tollis that incorporates all of these topics and more.

The successful student will be admitted to the

Ph.D. program in Informatics with a Health and Bioinformatics Emphasis in the School of Informatics, Computing and Cyber Systems at NAU (https://nau.edu/school-of-informatics-computing-and-cyber-systems/phd-informatics-and-computing/). Health and Biological data are being generated at a rapid pace. Both data types fall into the category of big data science that requires considerable computational skill and infrastructure if we are to gain new insights into human health, disease, and biodiversity. The scientists in the Health and Bioinformatics research group at NAU have met this challenge by incorporating molecular biology, genomics, bioinformatics, health informatics, epidemiology, statistics, and computer science. Our expertise spans metagenomics, pathogen detection, infectious disease, phylogenetics, comparative genomics, population genetics, molecular evolution, secondary data analysis, epidemiological modeling, and cancer. We collaborate with community partners and research institutions throughout the world as well as here at NAU and in Flagstaff, and are funded by agencies such as the National Institutes of Health, the United States Department of Agriculture, the Department of Defense, Arizona Game & Fish Department, and the Arizona Department of Health Services.

A student stipend will be provided through a combination of research and teaching assistantships.

Flagstaff, AZ has been rated one of the happiest cities in America, with four seasons, year-round recreation, terrific college vibe, and a laid-back attitude. We are close to the Phoenix metropolitan area, but even closer to Sedona and the Grand Canyon, and are surrounded by mountainous national forest.

Interested students should e-mail Marc Tollis (marc.tollis@nau.edu) with the following:

1. A cover letter describing the student's educational background, research interests and experience, interest in the lab, and career plans with a Ph.D. 2. A curriculum vitae including contact information and references. 3. A writing sample that could include a co-authored published manuscript, preprint, undergraduate thesis.

Marc Tollis, Ph.D. Assistant Professor School of Informatics, Computing and Cyber Systems College of Engineering, Informatics, and Applied Sciences Northern Arizona University Room 117 | 1295 S Knoles Drive | Flagstaff, AZ | 86011 Phone: (928) 523-3406 https://tollislab.org/ Marc Tollis <Marc.Tollis@nau.edu>

Norwich UK 2 Bioinformatics

Dear Evoldir,

I wanted to advertise two PhD positions (BBSRC DTP programme) in Norwich, UK, at the Quadram/Earlham Institute. Both are bioinformatical and both are strongly relating to evolutionary questions, in combination with microbiology/metagenomics. The first is about strain level metagenomics and using population genetic tools in (mostly) gut microbiome data: https://biodtp.norwichresearchpark.ac.uk/projects/computational-metagenomics-in-personalized-medicine-defining-high-resolution-microbial-genotypes/ The second PhD is about environmental (soil) microbes and how they produce greenhouse gases, by reconstructing genomes from metagenomes (tool development): https://biodtp.norwichresearchpark.ac.uk/projects/reconstructing-microbial-genomes-from-environmental-samples-and-their-impact-on-greenhouse-gases/ I would appreciate if you could forward these to interested students that want to undertake a PhD in computational biology.

Have a nice day,

Falk Hildebrand PI Quadram / Earlham Institute Norwich Research Park www.falk.science

Falk Hildebrand <falk.hildebrand@googlemail.com>

OklahomaStateU AmphibianDiseaseResistance

Graduate Student Positions in Amphibian Disease Ecology/Evolution

The Waldman lab in the Department of Integrative Biology at Oklahoma State University studies amphibian ecology, evolution, behavior, and conservation biology. We take a multi-faceted approach to increasing our knowledge of how frogs and salamanders respond to their environment. Although threats posed by emerging infectious disease shape much of our current work, potential projects are not limited to this topic. We welcome new lab members who wish to pursue graduate studies in all related research areas.

Projects in our laboratory currently underway include:

1. How did amphibian chytrid fungus spread from Asia and what are its effects? 2. How does adaptive immunity to the chytrid pathogen evolve? 3. What is the role of innate immunity in conferring disease resistance? 4. Identification of microbiome correlates of disease resistance and tolerance. 5. Life-history effects of infection and investment in immune responses. 6. Genomic analyses of behavioral strategies to cope with infection. 7. How do pesticides and herbicides impact disease resistance? 8. What are the genetic underpinnings of social recognition?

To answer these questions, our laboratory makes use of modern methods to study population genetics, genomics and transcriptomics.

Students are treated as independent investigators and are encouraged to propose and follow up on new ideas. We keep up-to-date on current research developments with weekly lab meetings.

Graduate teaching assistantships with competitive stipends and full tuition waiver are available to all graduate students. Research assistantships also are available when funds permit.

Oklahoma State University is a Carnegie Tier 1 research university with excellent facilities for research and instruction. The Department of Integrative Biology is a growing department with 24 faculty and over 65 graduate students, all working on interrelated themes in ecology, evolution, and environmental stress. Collaborations among research groups within the department, and with partner research groups in the USA and internationally, are encouraged. Interactions with other labs enhance the depth and breadth of our students' graduate careers.

Oklahoma State University is located in Stillwater, rated the friendliest college town in America. The close-knit college community offers a low cost of living, diverse restaurants, a thriving music scene, and a local airport served by several daily commercial flights. Not far away, two major metropolitan areas (Tulsa and Oklahoma City) provide access to trendy shopping, dining, and cultural activities. Because of its mid-continent location that spans a broad expanse of habitats, from deciduous forest to semi-arid grasslands, Oklahoma comprises a rich tapestry of prairie and forest ecosystems which support an exceptional level of biodiversity.

For further details, or to discuss possibilities, please contact

Professor Bruce Waldman Department of Integrative Biology 501 Life Sciences West Oklahoma State University Stillwater, Oklahoma 74078 Email: Bruce.Waldman@okstate.edu

“bw@bronze.lcs.mit.edu” <bw@bronze.lcs.mit.edu>

OklahomaStateU HerbariumInformatics

The Oklahoma State University Herbarium has an opening for a graduate student (PhD or MS) to be advised by Dr. Mark Fishbein (http://plantbio.okstate.edu/-faculty/faculty/135-bios/392-dr-mark-fishbein) starting in August 2020. The position is supported by the NSF-ADBC funded project “American Crossroads: Digitizing the Vascular Flora of the South-Central United States, conducted by the Texas Oklahoma Consortium of Herbaria (TORCH) Thematic Collections Network (https://www.nsf.gov/awardsearch/-showAward?AWD_ID=1902085). The graduate student will participate in all aspects of herbarium digitization, including imaging, databasing, and georeferencing, and will assist with mentoring undergraduate students at OSU and regional universities. The student will be supported by a combination of research and teaching assistantships. The ideal applicant will have some experience working with natural history collections and associated databases. Preference will be given to applicants who have an interest in conducting thesis or dissertation research making use of digitized collection data.

Applicants should contact Dr. Fishbein (mark.fishbein@okstate.edu) and apply here: https://-gradcollege.okstate.edu/apply/ Applications completed before January 15, 2020 will receive the highest consideration. Applicants from groups traditionally underrepresented in the sciences and academia are especially encouraged to apply.

Mark Fishbein Department of Plant Biology, Ecology & Evolution

”Fishbein, Mark“ <mark.fishbein@okstate.edu>

OxfordU PlanarianEvolution

The SalGo lab, Aboobaker lab and Jackson lab at the Department of Zoology of Oxford University invite joint applications for a PhD in the area of life history theory, population/community ecology, ecological modelling, and parasitology. The project will examine the drivers of alternative life history strategies using flatworms as model organisms. Flatworms (Platyhelminthes) are small acoelomate organisms that lack specialised circulatory or respiratory organs and have a single digestive cavity opening. In the UK, where this project will take place, flatworms are typically found under rocks in freshwater habitats. With over 25,000 known species, flatworms display a great deal of variation in life history strategies and conservation status. Some flatworm species reproduce strictly asexually by fission, while others can reproduce both sexually and asexually; some species are short-lived, while others, through their ability to regenerate, can live extremely long lives and potentially avoid physiological senescence altogether. In addition, some flatworms in the UK are invasive, while others are believed to be narrow endemics.

This PhD project could take (i.e. we expect the prospective candidate to take the project in innovative directions) any mixture of experimental, theoretical and field work approaches to (i) examine the factors that have contributed to the evolution of the fascinating flatworm life history traits (e.g. How did the mechanisms that allow regenerative life histories and asexuality evolve?); and (ii) test how these life history strategies might now allow them to persist in a world characterised by anthropogenic environmental change (How robust are flatworm life history strategies to changes in the environment? How do multiple stressors impact the diversity of life history strategies in flatworm communities?). The student will capitalise on the world-leading expertise in flatworm biology, regenerative biology, experimental biology, and ecological modelling at the Department of Zoology of the University of Oxford. A range of quantitative methods (mathematical theory and statistics), field and laboratory experimental manipulations, including mesocosms, will be applied. Plausible hypotheses to test using a combination of approaches include the role of abiotic (e.g. global warming, pollution, habitat loss), and biotic stressors (e.g. predators, parasites, cannibalism) in the shaping of life history strategies and demographic/community outcomes.

Funding: Applicants will need to obtain funding to cover tuition fees and living expenses. There are a wide range of funding opportunities at Oxford, which include two Doctoral Training Programmes (DTP): the NERC DTP and the BBSRC DTP. Details on both are found here (https://www.environmental-research.ox.ac.uk and http://www.ox.ac.uk/admissions/graduate/courses/interdisciplinary-bioscience). However, we note that students'Â eligibility for funding from these DTPs are limited to UK/European citizens. Interested non-UK/non-European citizens are welcome to propose and seek alternative funding support from their home countries.

The applicant should have at least an upper second-class undergraduate degree (or equivalent overseas qualification; see http://www.fulbright.org.uk/going-to-the-usa/pre-departure/academics) in a relevant subject (e.g. biology, evolution, ecology), and either postgraduate experience at the MSc level (or similar), or alternative research experience (e.g. laboratory assistant, fieldwork assistant). Non-native English speakers must be able to provide proof of excellent oral and written communication skills. Experience in laboratory and fieldwork settings, as well as programming are strongly encouraged.

Location: The University of Oxford Department of Zoology, OX1 3SZ, Oxford, UK

General contact info: Interested candidates are encouraged to contact Dr Rob Salguero-GÂÂmez (rob.salguero@zoo.ox.ac.uk) with (1) a max 1 page statement letter detailing overall research interests and specific interests in this project, and (2) a 2 page CV.

General info on PhD applications to Oxford: Details on PhD application at the Department of Zoology of the University of Oxford can be found here: https://www.ox.ac.uk/admissions/graduate/courses/dphil-zoology?wssl=1 More info on the advisory team: Assoc Prof R. Salguero-Gomez - https://www.zoo.ox.ac.uk/people/dr-rob-salguero-gomez Prof Aziz Aboobaker - https://www.zoo.ox.ac.uk/people/professor-aziz-aboobaker

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PennsylvaniaStateU GallWaspEvolution

Graduate student and postdoc opportunities to study gall wasp (Cynipidae) evolution at Penn State.

Background: Gall wasps comprise thousands of species that manipulate host plant development to create tumor-like structures, called galls, in which wasp larvae feed while being protected from predators and the outside environment. These galls exhibit diverse architectures and develop in specific locations on host-plant species depending on the wasp species that initiated the gall. While wasps are likely using molecular signals to alter plant development to generate these novel structures, the mechanisms are unknown. Through our NSF-funded project (grant number 1856626), we aim to shed light on the evolution of gall wasps and their galls using phylogenomic data, examine molecular mechanisms of gall induction, and to develop new tools for research on these wasps in North America. Multiple opportunities are available to pursue some combination of phylogenomics, taxonomy, informatics, genomics, transcriptomics, and chemical ecology with project PIs.

Qualifications: Interested students/postdocs should have a passion for discovery, interest in biodiversity, strong background in biology and molecular research, and, given the large scale of this project, good organization skills and attention to detail.

How to apply: This position will based in University Park, PA in the Hines and/or Deans Labs and involve a team of project investigators including Drs. Andrew Deans, Heather Hines, John Tooker (all PSU), Seán Brady (Smithsonian), and Matt Buffington (USDA SEL). Please email a statement of interest and CV to Andrew Deans (ard19@psu.edu) or Heather Hines (hmh19@psu.edu).

https://sites.psu.edu/frost/graduate-student-opportunities/ // Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status. You can find our departmental diversity statement on our website: https://ento.psu.edu/diversity-statement //

"Deans, Andrew Robert" <ard19@psu.edu>

Ploen MathematicalBiology

https://www.mpg.de/14073947/phdmathbio PhD position (m/f/d) - Mathematical Biology (3 years)

The Research Group "Stochastic Evolutionary Dynamics" at the Max Planck Institute for Evolutionary Biology, Plön, is looking for a PhD student (m/f/d) to join the research group. The *PhD position in Mathematical Biology (3 years)* has the topic "Evolutionary dynamics of antibiotic resistance on plasmids".

The evolution of antibiotic resistance poses a severe threat to modern healthcare. Clinically relevant resistance is often encoded on plasmids. Plasmids are extra-chromosomal DNA elements that can be transmitted vertically or be transferred horizontally between cells. The location of resistance genes on plasmids can lead to special evolutionary dynamics. The aim of the project is to develop mathematical models for the evolution and spread of resistance on plasmids. On the mathematical side, the analysis will mainly be based on branching process theory, complemented by deterministic ODE systems and stochastic computer simulations.

The position is part of a DFG-funded Research Training Group (RTG) on "Translational Evolutionary Research". The program brings together 14 research groups from several institutions to study how insights from evolutionary biology can be applied to solve problems in medicine, food production, and wildlife conservation. Projects are organised in tandems who work on related topics. The tandem partner of the proposed project is Professor Tal Dagan (University of Kiel). The student would hence closely interact with a research group that focuses on experimental evolution and data analysis.

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

Working environment

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

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

*Pl**ö**n*

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

Application

Interested students should send their application (motivation letter, CV, copies of certicates, contact details of two references) by email to uecker@evolbio.mpg.de. Please use the *code PhD2019-2* in the subject line.

The Max Planck Society strives for gender and diversity equality. We welcome applications from all backgrounds. The Max Planck Society is committed to employing more disabled individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

For further questions, please get in contact with Dr. Hildegard Uecker. Application deadline is December 15, 2019. However, the position will remain open until filled by a qualified candidate.

Contact:

Dr. Hildegard Uecker Research group Stochastic Evolutionary Dynamics Department of Evolutionary Theory Max Planck Institute for Evolutionary Biology

Website: web.evolbio.mpg.de/stochdyn Email: uecker@evolbio.mpg.de Phone: + 49 4522 763-536

– Dr. Sabrina Koehler

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Portugal MetaGenomics

We are currently accepting applications to fill a 24 months contract for a PhD researcher under the project “ENVMETAGENOMICS ”eDNA: from rare species detection to whole-community diversity using high-throughput sequencing“.

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

a) Demonstrated scientific and/or professional experience in the area of Bioinformatics or Comparative Genomics.

b) The candidate must also have experience in the analysis of next-generation sequencing data (genomics and/or transcriptomics), preferentially of eukaryotes, with expertise in bash, R, Python or other relevant programing language.

c) Wet laboratory experience in molecular genetics will be considered a plus.

d) Knowledge of Iberian freshwater ichthyofauna will be considered a plus.

For more details about this call, please use the following link: http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=121727 *Application deadline: 10 Dezembro 2019*

– Ana Veríssimo, PhD Researcher

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

http://orcid.org/0000-0003-3396-9822 Ana Verissimo <verissimoac@gmail.com>

StAndrewsU CrowBehaviour

StAndrews.NewCaledonianCrow.PhD

PHD STUDENTSHIP: TOOL CRAFTING IN NEW CALEDONIAN CROWS

SUMMARY

New Caledonian crows are renowned for their ability to manufacture complex foraging tools from plant materials. For example, using an elaborate sequence of actions, they craft hooked stick tools from branching vegetation, and using a completely different technique, they cut tapered leaf tools from the barbed edges of screw-pine leaves. Professor Christian Rutz's research group has been studying the behavioural ecology of New Caledonian crows since 2005, focussing on a suite of seven established study sites, including some with marked crow populations. Building on some of the group's recent advances, this PhD project will provide a detailed investigation of the tool-manufacture behaviour of wild crows. There is considerable flexibility with regards to specific study objectives, but the successful candidate is likely to conduct both field observations and aviary-based experiments with temporarily-captive subjects, with excellent scope for collaboration with other group members and external project partners. This fully-funded PhD project offers exciting opportunities for a highly motivated student to join a dynamic research group, to conduct topical research on the behavioural ecology of one of the most accomplished non-human tool users, and to receive training in state-of-the-art field-ornithological research methodologies.

CENTRE FOR BIOLOGICAL DIVERSITY

The Centre for Biological Diversity (CBD) at the University of St Andrews provides a highly interactive and stimulating environment for doctoral students, with particular strengths in animal behaviour and evolution. The successful candidate would benefit from frequent interactions with postgraduates, postdocs and PIs, including lab chats, seminars, and discussion groups.

CONTACT

Informal enquiries (with CV) can be addressed to Professor Rutz (christian.rutz@st-andrews.ac.uk), but all applications must be submitted via the School's online portal.

FUNDING NOTES

Eligibility requirements: Upper second-class degree in Biology or a related area.

Funding: Fees and stipend is provided for 3.5 years.

SELECTION CRITERIA

- excellent academic track record
- excellent analytical, writing and communication skills
- demonstrable skill and enthusiasm for behavioural research and fieldwork
- high degree of self-motivation and independence
- ability and willingness to live and work overseas, for extended periods of time and sometimes under challenging field conditions
- clean driving licence
- prior research experience is an advantage

FULL ADVERT ON FINDAPHD

https://www.findaphd.com/phds/project/tool-crafting-in-new-caledonian-crows/?p112599 Christian Rutz <cr68@st-andrews.ac.uk>

TexasAMU DeNovoGenesEvolution

PhD Positions in Brassicaceae de novo gene evolution and function

The Casola and Pepper labs at Texas A&M University seek candidate PhD students to work on de novo gene evolution. This project will combine comparative genomics, machine learning approaches and reverse genetics to study the evolutionary dynamics and biological impact of de novo gene in Brassicaceae, with a special focus on Arabidopsis thaliana and Brassica spp.

Prospective students should email a short description of research interests and a CV to Claudio Casola (ccasola@tamu.edu) or Alan Pepper (apepper@bio.tamu.edu). Students are encouraged to get in touch as soon as possible in order to be eligible for funding opportunities through the Ecology and Evolutionary Biology interdisciplinary program https://eeb.tamu.edu/graduate-program/prospective-students-2/. For full consideration, applications for Fall 2020 to the EEB program should be received by December 9, 2019.

Individuals from underrepresented groups in STEM are particularly encouraged to apply.

Dr. Claudio Casola Assistant Professor Department of Ecosystem Science and Management Texas A&M University https://agrilife.org/casolalab/ Dr. Alan Pepper Professor Department of Biology Texas A&M University https://www.bio.tamu.edu/faculty-page-alan-pepper/ "Casola, Claudio" <ccasola@tamu.edu>

TexasAMU InvertPopulationGenomics

A Ph.D. assistantship is available in the Hogan Lab at Texas A&M University - Corpus Christi (TAMUCC). The student will join an NSF Macrosystems-funded project to study population genomics of vernal pool branchiopods. The project is using reduced representation genome sequencing (RADseq) to assess patterns of genetic diversity and gene flow among populations across the central United States by wind driven processes and animal vectors (birds) as well as determining genome-by-environment correlations. The Ph.D. student will join a team of researchers that includes Dr. Jim Thorp (University of Kansas), Dr. Kevin McCluney (Bowling Green State University), and Dr. Chris Patrick (Virginia Institute of Marine Science), and others.

The student will develop population genomic datasets from spatial and temporal samples from five study populations, including patterns of diversity and signatures of selection, and genetic drift. The student will also lead field work in Texas to sample vernal pool ecosystems for invertebrates, as well as contribute to the maintenance of mesocosm experiments at TAMUCC. Extensive opportunities for collaboration across the multi-institutional team, including within the HoBi Lab and Marine Genomics Lab at TAMUCC.

The position is ideally suited to researchers with a background in population genomics, bioinformatics, population and community ecology. No experience in vernal pool ecology is required, though experience with RAD library preparation, RADseq analysis pipelines, analysis of population genetics data, and database management are highly sought after. Applicants with evidence of productivity, strong oral and written communication abilities, and enthusiasm are especially encouraged to apply. The successful applicant will be an independent, motivated person who communicates well and enjoys working in a collaborative team.

Assistantship details The Ph.D. assistantship in TAMUCC's Marine Biology (MARB) program will begin in Fall 2020. RA funds and partial tuition support at available. Competitive assistantships are also available through the MARB program. Assistantship includes health insurance and other benefits. Funding for conference travel are available.Applicants ideally will have an MS degree prior to starting in Fall 2020.

Application process Review of applications will begin on December 6, 2019 and will continue until the position is filled. Interested candidates should email Dr. J. Derek Hogan (james.hogan@tamucc.edu). In your email please include: 1) a oneÂ'-page cover letter describing your interest in the position and your relevant skills you possess. The letter must address your experience in RAD library preparation, RAD analysis pipelines, and analysis of population genetic data; 2) a CV including education history, publications, conference presentations and grant/scholarship funding; and 3) the names and contact information for three scientists familiar with your research work.

Texas A&M University - Corpus Christi TAMUCC is located in Texas' coastal bend on the Gulf of Mexico. TAMUCC has recently been ranked as a tier 2 research university by the Carnegie Classification of Institutions of Higher Education. The Marine Biology program is the largest Ph.D. program on campus and consists of approximately 30 research faculty and 50 graduate students engaged in research in marine, estuarine, freshwater, and terrestrial research in the fields of ecosystem, community, and population ecology, evolutionary biology, biogeography, microbial ecology, developmental genetics, restoration ecology, and biomedical research. Corpus Christi is known for an active outdoor life-style including salt-water fishing, wind surfing, sailing, and sea kayaking. The city is 2.5 hours from San Antonio, and 4 hours from cultural centers including Houston and Austin Texas.

J. Derek Hogan Associate Professor Department of Life Sciences Texas A&M University - Corpus Christi Corpus Christi, Texas, 78412 USA

"Hogan, James" <James.Hogan@tamucc.edu>

TexasAMU MarineMicrobiomeDiversity

Ph.D Assistantship - Marine Biology (Botany)

Agency/Location: Texas A&M University at Corpus Christi, TX

Responsibilities - A PhD assistantship position is available under the advisement of Dr. Barnabas Daru in the direction of Marine Biology. The successful applicant will be working on projects in the Marine Biology program and has a chance to study the use of herbarium specimens as sources of big data for understanding the distributions and diversity of marine plant microbiomes. The project includes the use of pressed herbarium specimens of marine plants (seagrasses and mangroves) as sources of big data by analyzing the diversity of microbiomes, with the aim of understanding how climate change and urbanization have affected the microbiomes of marine plant species along coasts and estuaries of North America spanning the past 120 years. Student will obtain Ph.D. degree through the Marine Biology Program, an interdisciplinary degree program combining the strengths of three universities within the Texas A&M University (TAMU) System; TAMU-Corpus Christi, TAMU-Galveston, and TAMU-College Station.

Qualifications 'V (1) B.S. or M.S. in biological sciences, botany, environmental science, marine science, microbiology or related field. (2) Basic knowledge in plant biology, molecular biology, and microbiology. Experience/knowledge with herbarium specimens, DNA extraction and bioinformatics is a plus. (3) GPA =3.0. (4) 1100 (or 310 in new scoring system) on the verbal and quantitative sections and 3.5 in analytical writing of the GRE.

Closing Date 'V December 31, 2019

Contact 'V Send cover letter, resume, unofficial transcripts and GRE scores to: Dr. Barnabas Daru, through email: barnabas.daru@tamucc.edu

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Barnabas Daru (PhD)

Assistant Professor of Biology Department of Life Sciences Texas A&M University - Corpus Christi Phone: +1 361 825 3489 Email:Barnabas.Daru@tamucc.edu Lab Website:https://barnabasdaru.com "Daru, Barnabas" <Barnabas.Daru@tamucc.edu>

UAberdeen 2 SocialInsectAdaptation

2 PhD positions on social insects and environmental change

Two PhD positions to work on social insects are available in the Lab of Functional Genomics & Sociobiology at the University of Aberdeen, under the supervision of Dr Fabio Manfredini.

The first position deals with the "Origin and maintenance of plasticity in response to thermal stress in invasive and declining ants".This is a 4 year PhD project, part of a competition funded byEASTBIO BBSRC DTPand in collaboration withDr Lesley Lancaster(University of Aberdeen),Dr JenniStockan(The James Hutton Institute) andDr Nathan Bailey(Univeristy of St Andrews). The deadline for application is Sunday, January 05, 2020.

The second project instead will investigate "The cost of being a fussyeater 'V Oligolectic pollinators and environmental change". This is a 3.5 years project, part of a competition funded byQUADRAT NERC DTPand in collaboration withDr Lorraine Scott(Queen's Univeristy Belfast).The deadline for application is Friday, January 24, 2020.

You can find full details about the two projects and how to apply here:

https://fmanfredini79.wixsite.com/manfredini/-functional-genomics-sociobiology Or you can contact Dr Fabio Manfredini directly if you have any question: Email fmanfredini79@gmail.com, Twitter@fmanfredini79

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Fabio Manfredini (BSc; MSc, PhD)

Postdoctoral Research Associate School of Biological Sciences Ecology and Evolutionary Biology Royal Holloway, University of London Egham, TW20 0EX

Cell.: +44 07852416104 e-Mail: fabio.manfredini@rhul.ac.uk Skype: fabio.manfredini2 Webpage: www.fmanfredini79.wixsite.com/manfredini Fabio Manfredini <fmanfredini79@gmail.com>

UAlmeria Spain EcoEvolutionaryBioinformatics

Possibility for PhD position on eco-evolutionary bioinformatics (University of Almería and EEZA-CSIC, Almería, Spain)

Deadline to accept candidates: November 10th 2019

Are you a recently-graduated computer scientist who happens to be interested in nature, animals, animal behavior, ecology, evolution, the environment? or specific topics, such as the extinction of the dinosaurs, or how to improve biological pest control?

Then you could be interested in this opportunity to apply for a 4-year PhD scholarship to work on improving a Next-Generation Individual-Based model, Weaver, and bring it to the next level: parallel computing. With parallelization we will be able to scale up simulations to include larger and more complete ecosystems including up to tens of millions of individuals. We seek for a highly motivated computer scientist from EU countries, and will only consider applicants having completed (or currently on their last year of) a MS in Computer Sciences, preferably on parallel computing or similar disciplines.

The candidate should have finished his/her undergrad after January 1st 2016, and hold top academic qualifications (i.e., within the top 10% of his/her undergraduate graduating class).

Annual salary (before taxes): 1st year: 16,027.58Â€; 2nd year: 17,279.5Â€; 3rd year: 21,599.48Â€; 4th year (having defended the PhD): 28,640.91Â€; 4th year (without PhD defense): 21,599.48Â€.

Success of the candidate will be elegible after a nationwide open competition based on their academic qualifications, research experience, theresearch team and the quality of his/her proposed research. More details on the call will be delivered upon contacting the research team.

Contact: Jordi Moya-Laraño (jordi@eeza.csic.es); Leocadio G. Casado (leo@ual.es); Juana López-Redondo (jlr526@ual.es).

References: Bilbao-Castro, J.R., Barrionuevo, G., Ruiz-Lupión, D., Casado, L.G., Moya-Laraño, J.: Weaver: a multiagent, spatial-explicit and high-performance framework to study complex ecological networks. In: Bajo, J., Hallenborg, K., Pawlewski, P., Botti, V., Sánchez-Pi, N., Duque Méndez, N.D., Lopes, F., Julian, V. (eds.) PAAMS 2015. CCIS, vol. 524, pp. 139-150. Springer, Cham (2015)

Grimm, V.; Ayllón, D. & Railsback, S.F. (2017). Next-Generation Individual-Based Models Integrate Biodiversity and Ecosystems: Yes We Can, and Yes We Must. Ecosystems, 20: 229-236. Moya-Laraño, J.; Verdeny-Vilalta, O.; Rowntree, J.; Melguizo, N.; Montserrat, M., Laiolo, P. 2012. Climate Change and eco-evolutionary dynamics in food webs. Adv. Ecol. Res. 47:1-80.

Moya-Laraño, J.; Bilbao-Castro, J.R.; Barrionuevo, G.; Ruiz-Lupión, D.; Casado, L.G., Montserrat, M.; Melian, C.; Magalhaes, S. 2014. Eco-evolutionary spatial dynamics: rapid evolution and isolation explain food web persistence. Adv. Ecol. Res. 50:75-143.

Jordi Moya-Laraño

Functional and Evolutionary Ecology Estación Experimental de Zonas Ãridas - CSIC Carretera de Sacramento s/n La Cañada de San Urbano 04120-Almería Spain

phone:34 950281045 ext. 419 email: jordi@eeza.csic.es www.eeza.csic.es/foodweb De: Jordi Moya Laraño Enviado: domingo, 27 de octubre de 2019 9:32 Para: evoldir@evol.biology.McMaster.CA Asunto: PhD position in eco-evolutionary bioinformatics Asunto: PhD position in eco-evolutionary bioinformatics

UAuckland InvasionGenomics

Genomics of rapid adaptation: the expansion and evolution of the invasive common myna and common starling in New Zealand

A PhD scholarship, funded by a New Zealand Royal Society Marsden Fund Grant, is available with Dr Anna Santure and Dr Annabel Whibley in the School of Biological Sciences, University of Auckland, New Zealand. This project is an exciting opportunity to use genomics and evolutionary genetics approaches to understand the evolution of two globally invasive species, the common myna (*Acridotheres tristis*) and common starling (*Sturnus vulgaris*). There is evidence that both species have adapted rapidly in the invasive ranges, despite what we assume to be very low founding genetic diversity. Common myna and common starling are two of only three bird species on the global 'top 100' invasive species list, and offer unique replicated systems to identify genomic differences between invasive and native source populations. Changes to morphology and gene expression will be correlated with identified genomic changes in genes and regulatory elements to infer the genomic basis of rapid adaptation.

We are looking for a candidate with a strong background in genetics and bioinformatics, statistics, computer science or similar, as well as a passion for evolutionary biology and ecology.

The PhD position requires the applicant to be eligible for admission to the PhD programme at the University of Auckland (see https://www.auckland.ac.nz/en/-for/future-postgraduates/how-to-apply-pg/apply-for-a-doctorate/phd-entry-requirements.html; please note the English language proficiency requirements). Candidates should ideally have a GPA of 7 or above (see https://www.gpecalculator.auckland.ac.nz/#/ for a grade conversion calculator); international students are welcome to apply.

This project is a collaboration with Prof Rebecca Johnson and Dr Richard Major at Australian Museum and Dr Lee Ann Rollins at the University of New South Wales. To apply for this position, please email Dr Anna Santure (a.santure@auckland.ac.nz) with your cv, names and details of two referees, your academic transcript, and a short statement of interest. I welcome informal enquiries. The PhD scholarship is available from 1 April 2020 and covers tuition fees and provides an annual tax free allowance of NZD$27,500 for three years. The closing date is 6 December 2019.

Anna Santure <asanture@gmail.com>

UBath ExperimentalEvolutionCRISPR

We are seeking a highly motivated and enthusiastic PhD student to work on the evolution of transcriptional regulation of CRISPR-Cas in a naive bacterial host.

Deadline: Sunday 2nd December 2019

Enquiries and application: https://www.findaphd.com/-phds/project/swbio-dtp-phd-project-horizontal-transfer-of-antiviral-defences-between-bacterial-species/?p114158 Project Description: Horizontal transfer of antiviral defences between bacterial species The discovery of CRISPR-Cas has arguably been one of the most influential discoveries in biology of the past decades. CRISPR-Cas systems that are encoded on bacterial genomes protect against viral and plasmid infections. This has been utilised to safeguard industrial fermentations, and recently been exploited to eradicate antimicrobial resistance plasmids from microbial communities under laboratory conditions. Furthermore, the recent development of CRISPR-Cas genome editing is facilitating ground-breaking strategies in science, agriculture, medicine and pest management. Many of these applications require that the genes encoding CRISPR-Cas are stably expressed across many generations. Yet, long-term studies that examine genetic and transcriptomic stability of these systems are lacking. Based on classical evolutionary theory, we hypothesise that we can predictably manipulate the way CRISPR-Cas gene regulation evolves in bacteria following the synthetic or natural transfer of CRISPR-Cas genes to a naïve bacterial host. An ability to predictably evolve CRISPR-Cas gene regulation would be truly ground-breaking, and would have clear implications for the use of these systems in industry and in the development of strategies for eradicating antimicrobial resistance. Throughout this interdisciplinary project, the student will receive extensive training in experimental evolution, molecular microbiology, genetics and modelling. The student will be based in the Taylor lab in the Milner Centre for Evolution at the University of Bath with opportunities to work in the Westra and Buckling labs at the ESI, Cornwall campus of the University of Exeter, and with the Roger lab in the Department of Mathematical Sciences at the University of Bath.

Location: This project will be conducted under the direct supervision of Dr Tiffany Taylor with co-supervision from Prof Edze Westra. Based primarily at the Department of Biology and Biochemistry at the University of Bath (UK) in the new Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/). The Milner Centre is a new research centre focused on doing ground breaking research that addresses major questions in evolutionary biology. There will also be some time spent in the Westra lab at the Univesity of Exeter's ESI in Cornwall (UK) (http:/-/www.exeter.ac.uk/esi/). The University of Exeter's Environment and Sustainability Institute (ESI) is an interdisciplinary centre leading cutting-edge research into solutions to problems of environmental change.

Requirements: We are looking for a biology graduate who has a strong interest in microbiology, molecular biology and evolution. Applicants must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in an appropriate area of science or technology. Some practical experience in microbial molecular techniques is highly desired, but training will be provided. The successful candidate will be enthusiastic, highly motivated, independent, have experience in microbiology, molecular biology or evolutionary biology (or a combination), and have a relevant degree. The applicant must meet the standard University of Bath English language requirements, details of which can be found here: http://www.bath.ac.uk/study/pg/apply/english-language/index.html . Planned start date: October 2020 (4 year PhD)

For informal enquiries please contact Dr Tiffany Taylor at: T.B.Taylor@bath.ac.uk

Funding Notes: This is a competition funded project by the South West Bioscience Doctoral Training Partnership (SWBio DTP), the selection process can be found here: https://www.swbio.ac.uk/programme/selection-process/ Funding is available to UK and EU nationals who have established UK residency (EU nationals must have ordinarily lived in the UK throughout the three years preceding the start of the studentship). Applicants from EU countries who do not meet the residency requirements may still be eligible for a fees-only award. However, the four core universities (Bath,

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UCalifornia LA MicrobiomeEvolution

Graduate student:UCLA.MicrobiomeEvolution

Graduate student position atUCLAon the evolutionary dynamics of the microbiome.

A PhD position starting in Fall 2020 is available in the lab of Dr. Nandita Garud in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles. We are broadly interested in understanding the evolutionary dynamics of natural populations with a current focus on the microbiome. The lab develops statistical and computational methods to gain insight into evolutionary processes from population genomic data.

Students will have substantial input in the specific nature of their research project. However, the project should broadly fit within the lab's goals of learning about adaptation in natural populations and evolutionary dynamics in the microbiome. As this is a computational lab, prior experience in in programming in R, Perl, or Python, and shell scripting is preferred.

Additional information can be found at:http://garud.eeb.ucla.edu The Ecology and Evolutionary Biology department atUCLAoffers a cutting-edge research environment with many opportunities for collaboration. The lab will have affiliations with the Microbiome Center atUCLAand the Institute for Quantitative and Computational Biology atUCLA.

Interested candidates should apply to the EEB program atUCLAby December 1 and specify Dr. Nandita Garud as a Prospective Faculty Advisor (https://www.eeb.ucla.edu/grad_onlineappl.php). Direct inquiries are also welcome at ngarud@ucla.edu.

Nandita Garud <nandita.garud@gmail.com>

UColorado Denver SeasonalPlasticityAdaptation

The Ragland lab at the University of Colorado, Denver, is recruiting a PhD student for Fall 2020. Our group is interested in the process of adaptation to variable environments at multiple levels of organization, from genes, to physiology, to organismal performance. Current projects include the study of rapid adaptation of seasonal timing in insects, the overwintering physiology and adaptive potential of bark beetle forest pests, and the evolution of adaptive (and maladaptive) plasticity. In addition to studies leveraging genomic and transcriptomic approaches, we are increasingly incorporating techniques from developmental biology to understand the regulation of phenology through developmental rate modulation. Students with interests in any of these areas are welcome to apply.

More information about the lab and our current research is available on our website and through our full publication list on google scholar: https://raglandlab.wordpress.com https://scholar.google.com/citations?user=8iUPFR0AAAAJ&hl=en Interested students should contact Greg Ragland (gregory.ragland@ucdenver.edu) directly prior to the application deadline, 1 December 2019. Our lab is in the Department of Integrative Biology (https://clas.ucdenver.edu/integrative-biology/), a diverse group of faculty, postdocs, and students with interests spanning molecules to ecosystems. Between the downtown and Anschutz Medical campuses, CU Denver houses a number of biology-related departments with access to state-of-the-art core facilities and computing infrastructure. Financial packages will be competitive, and highly qualified students may be considered for research assistantships through current NSF grants and/or fellowships through University sources.

GREGORY.RAGLAND@ucdenver.edu

UDebrecen ShorebirdEvolution

Sex role evolution and demography in shorebirds PhD studentship based in Debrecen, Hungary 2020-2024

Supervisors: Prof Tamás Székely (Debrecen University) and Dr VojtÃKubelka (Debrecen Uni.)

Deadline of application: 15 December 2019

We are interested in: Sex roles (i.e. courtship, competition for mates, pair bonding and parenting) are among the most diverse social behaviour. Recent research is uncovering key elements of sex role variation, but significant gaps remain. Appropriate sexual behaviour is essential for reproduction, and thus understanding the causes and implications of sex roles are at the core of evolutionary biology and fundamental for the study of life history evolution, physiology and population biology. Understanding sex roles and demography (reproduction and mortality rates) is also important for biodiversity conservation since disruptions to normal sexual behaviour due to environmental changes reduce the viability of wild populations. Our team was awarded an project of Hungarian Science Foundation, the ÃLVONAL Shorebird Science: https://elvonalshorebirds.com/ to investigate sex role evolution in shorebirds.

This PhD project will focus on sex role behaviour in shorebirds. Using behavioural observations in wild populations it will investigate causes of display behaviour, pair bonding and parenting. The PhD student will test whether (i) sex role behaviours are induced by ambient environment, demographic parameters or social environment, (ii) explore the relationship between different sex role components, and (iii) test the fitness implications of sex role variations.

The ideal candidate: has a strong interest in evolutionary biology, behavioural ecology and field biology, and willing to work in remote areas, e.g. South Africa, South America or Arctic Russia or elsewhere. He/she needs to have a solid background in data analyses preferably in R, and statistical modelling. A condition of the application is a Master degree (or equivalent) in biology, zoology or similar subject. Experience in field ornithology and bird ringing is desirable but not essential. The studentship will start in September 2020. We are preferably seeking candidates willing to raise their own funding. Note that for students from eligible countries the Stipendium Hungaricum offers a scholarship programme (www.stipendiumhungaricum.hu).

Are you interested? Contact Dr VojtÃKubelka (kubelkav@gmail.com). Applications includes: a CV (max 3 pages) and a max 2 pages cover letter with personal motivation and the name and contact details of two references (both in English) should be sent to Dr Kubelka before deadline.

References Carmona-Isunza, M C, C Küpper, M A Serrano-Meneses & T. Székely. 2015. Courtship behavior differs between monogamous and polygamous plovers. Behavioral Ecology & Sociobiology 69: 2035-2042. Cunningham, C, J. E. Parra, L. Coals, M. Beltrán, S. Zefania & T. Székely. 2018. Social interactions predict genetic diversification: an experimental manipulation in shorebirds. Behavioral Ecology 29: 609-618. Eberhart-Phillips, L. J., Â, T. Székely, Â 2018. Demographic causes of adult sex ratio variation and their consequences for parental cooperation. Nature Communications 9 (1651). Kubelka V., Âálek M., Tomkovich P., Végvári Z., Freckleton R. P. & Székely T. 2018: Global pattern of nest predation is disrupted by climate change in shorebirds. Science 362: 680-683. Liker A., Freckleton R. P. & Székely T. 2015: The evolution of sex roles in birds is related to adult sex ratio. Nature Communications 4 (1587). Vincze, O., A. Kosztolányi, Â & T. Székely. 2016. Parental cooperation in a changing climate: fluctuating environments predict shifts in care division. Global Ecology and Biogeography 26: 347-358.

Fanni Takács <fannitakacs.94@gmail.com>

UEastAnglia 2 InsectEvolution

Reproductive interference for insect control

A collaborative PhD project with Profs Tracey Chapman (UEA, UK), Dr Wilfried Haerty (The Earlham Institute, UK) and Prof Luke Alphey (The Pirbright Institute, UK).

You will train at the interface of fundamental reproductive biology, bioinformatics and genetic engineering, to develop proof-of-principle for the use of reproductive interference as complementary new method for insect control. Insect pests are a persistent and growing threat to human livelihoods and health because they damage economically important crops and spread disease. The pressing global challenge of combating such pests is being exacerbated by the evolution of resistance, the diminishing availability of pesticides and by climate change. The student will focus on reproductive interference ' whereby courtship and copulation of one species / population is interrupted or disturbed by another. In the context of insect control this is often referred to as Âsatyrization' and it works because the consequences (particularly costs) of hybrid mating can lead to the competitive exclusion of a harmful species (or population) by a more benign one.

Please contact tracey.chapman@uea.ac.uk for further questions!

To apply, see:

https://biodtp.norwichresearchpark.ac.uk/projects/-reproductive-interference-for-insect-control/ Application deadline Nov 25th 2019!

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Gifts that keep on giving: maternal effects and insect pest control

A collaborative PhD project with Prof Tracey Chapman and Dr Phil Leftwich (UEA, UK), Dr Wilfried Haerty and Dr Will Nash (The Earlham Institute, UK) and Dr Tim Harvey Samuel (The Pirbright Institute, UK).

You will train at the interface of genetic engineering and fundamental biology to understand the role of maternal RNAs in early development. Variation in the diversity and levels of maternal RNAs are key to understanding evolutionary adaptation and plasticity, as well as aiding in the development of next generation gene drive systemsfor insect control. Successful early embryonic development occurs as a result of a precise balance between the effects of both embryonic and maternal genomes. Very little of this process is known in key insect pests and it is of particular importance for effectively tackling serious agricultural pests such as the medfly (Ceratitis capitita). This is an extreme generalist whose larvae can thrive in over 350 different host fruits, many of which are of global economic importance.

Please contact tracey.chapman@uea.ac.uk for further questions!

To apply, see:

https://biodtp.norwichresearchpark.ac.uk/projects/-gifts-that-keep-on-giving-maternal-effects-and-insect-pest-control/ Application deadline Nov 25th 2019!

"Tracey Chapman (BIO - Staff)" <Tracey.Chapman@uea.ac.uk>

UEdinburgh 2 EvolutionaryRescue

I am currently recruiting up to two PhD students to join my new group at the Institute of Evolutionary Biology, University of Edinburgh, starting October 2020. Our interdisciplinary research involves mathematical (especially stochastic) modelling and experimental tests using bacteria to address fundamental and applied questions in evolutionary biology, particularly with applications to infectious diseases. The currently proposed projects will primarily involve modelling and/or computation. Students from diverse backgrounds (e.g. mathematics, physics, biology) are welcome to apply. Depending on funding scheme, application deadlines start from 5 January 2020 and interested candidates (particularly those from outside the UK) are encouraged to contact me as soon as possible to discuss opportunities.

Project 1: Evolutionary rescue or the emergence of antibiotic resistance in time-varying environments. * As part of the NERC E4 DTP (for students eligible for UKRI funding, i.e. UK or UK-resident EU students): https://www.ed.ac.uk/e4-dtp/how-to-apply/our-projects?item=892 * For university and external scholarships (for international students): https://www.findaphd.com/phds/project/emergence-of-antibiotic-resistance-in-time-varying-environments-and-the-optimisation-of-antibiotic-dosing/?p113424 Project 2: Evolutionary consequences of mutation rate variation in bacteria. * As part of the EASTBIO DTP (for students eligible for UKRI funding): https://www.findaphd.com/phds/project/-eastbio-evolutionary-consequences-of-mutation-rate-variation-in-bacteria/?p113425 * For university and external scholarships (for international students): https://www.findaphd.com/phds/project/evolutionary-consequences-of-mutation-rate-variation-in-bacteria/-?p113423 Motivated students who are interested in working on other topics in microbial/pathogen evolution, infectious disease dynamics, adaptation to environmental change, stochastic population dynamics or mutagenesis are also welcome to contact me to discuss possibilities.

For further details on eligibility and funding opportunities, and to formally submit an application, please follow the links from the appropriate project advertisement above. For more information about the department, please see https://www.ed.ac.uk/biology/evolutionary-biology For more information about my research, please see https://www.ed.ac.uk/profile/helen-alexander and https://scholar.google.com/citations?user=jRW2Z7QAAAAJ To express interest or request further information, candidates are strongly encouraged to contact me, including a CV and a brief explanation of their research interests.

Dr. Helen Alexander Royal Society University Research Fellow Institute of Evolutionary Biology, University of Edinburgh Helen.Alexander@ed.ac.uk

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

ALEXANDER Helen <Helen.Alexander@ed.ac.uk>

UEdinburgh GenomicsBreeding

Dear colleagues,

We have placement for two fully-funded PhD positions in the EASTBio Doctoral Training Programme competition - www.eastscotbiodtp.ac.uk. UK and European students are eligible for this programme.

The positions are in:

1) Efficient and sustainable genomic breeding in turkeys

Detailed description: www.findaphd.com/phds/project/eastbio-efficient-and-sustainable-genomic-breeding-in-turkeys/?p114312 Supervisors: Gregor Gorjanc and Andreas Kranis Industry partner: Aviagen

2) Design of breeding programs to improve honeybee health and production

Detailed description: www.findaphd.com/phds/project/eastbio-design-of-breeding-programs-to-improve-honeybee-health-and-production/?p114336 Supervisors: Tom Freeman and Gregor Gorjanc Industry partner: AbacusBio

These are 4-year studentships to start in October 2020. The studentships cover fees, stipend, research training, limited research costs and a small travel/conference allowance. Successful students will join the EASTBIO training programme and undertake enhanced subject-specific, core bioscience and generic skills training and placement (3 to 18-months) with their industrial partner.

Application deadline is the 5th of January 2020. Please follow the instructions at www.eastscotbiodtp.ac.uk/how-apply-0 . Prospective candidates are encouraged to contact us by e-mail.

With regards!

University of Edinburgh Gregor Gorjanc, PhD Roslin Institute Chancellor's fellow in Easter Bush Data Driven Innovation for AgriTech Midlothian twitter: @GregorGorjanc EH25 9RG mail: gregor.gorjanc <at> roslin.ed.ac.uk Scotland, UK skype: ggorjan

Gregor Gorjanc <gregor.gorjanc@roslin.ed.ac.uk>

UEdinburgh ParasiteEvolution

A studentship on The evolutionary ecology of disease transmission: how will vector control programmes change parasite life histories? is available in the Reece Lab, University of Edinburgh, UK.

More details can be found here, including eligibility criteria and how to apply [deadline 10th Jan 2020]:

https://www.findaphd.com/phds/project/the-evolutionary-ecology-of-disease-transmission-how-will-vector-control-programmes-change-parasite-life-histories/?p114770 The Reece lab uncovers the strategies parasites have evolved to cope with the challenges of their lifestyle and to exploit the opportunities it brings, by asking what makes a successful parasite and what are the evolutionary limits to their success?. Specifically, we investigate how parasites maximise "survival" and "reproduction". These fitness components underpin the severity and transmission of diseases.

Most disease research focuses on interactions between parasites and their hosts. Analogous studies of interactions between parasites and vectors have been largely neglected, despite the fact that vectors are responsible for spreading disease. Clearly, to fully understand the evolution of vector-born parasites it is necessary to ask how they solve the challenges of living in hosts and in vectors. This is especially important for malaria parasites whose vectors are changing in response to vector-control programs (e.g., bed nets, insecticides). Whilst the evolutionary responses of malaria-transmitting mosquitoes to vector-control are being monitored, the knock-on consequences for parasite evolution have been overlooked. Just like drugs or vaccines administered to hosts, vector-control represents an ecological perturbation aimed at reducing parasite fitness. History clearly illustrates that attempts to reduce the survival and/or transmission of malaria parasites is usually met with counter-evolution (e.g., drug resistance mutations and phenotypic tolerance). Parasite counter evolution to vector-control may be constrained or facilitated, depending on the amount of genetic variation and plasticity underpinning parasite phenotypes. Anticipating parasite evolution will inform monitoring strategies for current control programs as well as uncovering novel new vector-control strategies.

For informal enquiries, please contact Sarah [sarah.reece@ed.ac.uk]

Professor Sarah Reece Chair of Evolutionary Parasitology

Institute of Evolutionary Biology & Institute of Immunology and Infection Research, School of Biological Sciences, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3FL Scotland, UK Tel +44 131 650 5547 Fax +44 131 650 6564

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Sarah.Reece@ed.ac.uk

UEdinburgh UStirling PlantPopulationGenetics

PhD Position available, supervised by Matthew Hartfield (University of Edinburgh) and Mario Vallejo-Marin (University of Stirling). Title: Dissecting the causes of reproductive mode variation in the yellow monkeyflower (Mimulus guttatus).

Project Description: Perennial plants exhibit a wide variety of reproductive modes, from exclusively sexual reproduction through seeds, to relying almost entirely on asexual propagation. Various theories exist to explain the evolutionary and ecological advantages of these reproductive modes, but testing theories can be hampered by a lack of empirical data. The facultative sexual plant Mimulus guttatus (yellow monkeyflower) is an exciting model system for investigating the evolution of different reproductive modes, as there is a large amount of variation in the relative contribution of sexual and asexual reproduction, with populations spanning different environments and ecological niches. By investigating genetic diversity across populations and linking it to the local reproductive mode across environments, we can ask: are different modes (sex or asex) associated with specific ecogeographic regions? To what extent is the reproductive mode affected by local ecological conditions, compared to large environmental factors such as climate? How does reproductive mode (sex, asex) and mating'Vsystem (selfing, outcrossing) interact?

The PhD project will use UK populations of Mimulus guttatus as a model system for investigating the evolution of reproductive modes, and how they interact with the mechanisms of natural selection. The student will generate new genomic data from previously'Vcollected samples to quantify the extent of self-fertilisation and clonal reproduction in natural populations. These data will allow us to investigate how the evolutionary history differs between regions exhibiting different reproductive modes. The project will put the student at the forefront of developing an exciting new model system for evolutionary genetics study.

The expected start date is October 2020.

More details about the project, including application details, are available from the following links:

- BBSRC EASTBIO and NERC E4 funding is available to UK nationals, or EU nationals who have been resident in the UK for three years prior to the start date. Deadlines are the 5th January 2020 and 9th January 2020 respectively. Further details and application instructions: https://www.findaphd.com/phds/-project/eastbio-dissecting-the-causes-of-reproductive-mode-variation-in-the-yellow-monkeyflower-mimulus-guttatus/?p113464 .https://www.ed.ac.uk/e4-dtp/-how-to-apply/our-projects?item=848 . - For those who wish to apply for funding via other schemes (e.g., the Darwin Trust), the deadline is the 5th January 2020. Further details and application instructions: https://www.findaphd.com/phds/project/dissecting-the-causes-of-reproductive-mode-variation-in-the-yellow-monkeyflower-mimulus-guttatus/?p113463 . Interested students can get in contact to ask for more details.

Matthew Hartfield m.hartfield@ed.ac.uk https://-matthartfield.wordpress.com The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

m.hartfield@ed.ac.uk

UExeter CardiffU EvolutionaryBiology

Competition amongst endemic lizard species on a tropical island (Round Island, Mauritius)

To apply visit: https://www.findaphd.com/phds/-project/nerc-gw4-dtp-case-studentship-competition-amongst-endemic-lizard-species-on-a-tropical-island-round-island-mauritius/?p112900 Supervisors:—Cardiff University - Prof. William Symondson, Dr. Ian Vaughan, Dr. Pablo Orozco-terWengelCASE Partner - Dr. Nik Cole (Durrell Wildlife Conservation Trust and Mauritius Wildlife Foundation)DTP Partner - Dr. Gavin Broad (Natural History Museum, London)

Project Description:—Round Island, Mauritius, hosts a community of rare endemic lizard species. Their environment was cleared of most vegetation by introduced goats and rabbits (now eliminated). A partnership between the Durrell Wildlife Conservation Trust, Mauritian Wildlife Foundation and the Government's National Parks and Conservation Service has permitted the restoration of habitat and with it the recovery of the reptile-dominated vertebrate community (Cole et al. 2018). The reptile species occupy a landscape going through plant community recovery, but little is known about availability of the invertebrate prey. The skinks and geckos have proved to be remarkably resilient to environmental change, although some species were extirpated from the island's reptile community. It is likely the reptiles originally adapted to different niches, including trophic niches that allowed them to avoid direct competition. One species, the Telfair's skink, is a generalist, consuming a wide range of different taxonomic groups (Brown et al. 2014). Other species may have narrower niche axes and be more specialised. Understanding the feeding niche of the reptiles may help explain differences in population recovery and guide restoration management to enhance the success of planned reptile reintroductions.

The main aims/methods of this project are: - To analyse the diets of the lizard species that have survived on Round Island. Collect lizard faecal samples from across the island and use High Throughput Sequencing (HTS) of plant and invertebrate DNA.- To DNA barcode as many invertebrate species on Round Island as possible (we have already barcoded all the plants). Invertebrates will be identified by the student at the Natural History Museum. Once we have the barcodes we can interpret the output from HTS and identify who is eating what.- To analyse for prey choice and competition. Compare what lizards are eating with available food (Vaughan et al. 2018) and use dietary overlap tests to assess dietary similarity.- To analyse differences in the abundances of lizard and invertebrate species in different plant communities. Apply/develop a range of invertebrate and reptile survey techniques. Look for areas of more advanced regrowth of the vegetation to predict changes to the island food web structure in the future (Macfadeyn et al. 2011).- To analyse the diets of reptile species that are to be reintroduced to Round Island's reptile community. Use prey overlap tests to evaluate whether any of these species are likely to compete with Round Island species.

The project will be co-supervised by Dr Nik Cole (CASE Partner) from Durrell Wildlife Conservation Trust and the Mauritian Wildlife Foundation, and by Dr Gavin Broad (DTP Partner) of the Natural History Museum. Their expertise was critical to the development of this project and will be invaluable to the student.

Applicants will need to have a strong academic record with expertise relevant to this project. Molecular Ecology expertise would be ideal but is not a prerequisite. Must be able to work in the field on a rugged tropical island for extended periods and also be good in the lab. Possession of a clean driving licence would be an advantage for accessing mainland sites on Mauritius.

How to apply: You should apply to the Doctor of Philosophy in Biosciences with a start date of October 2020, including: an upload of your CVa personal statement/covering lettertwo references (applicants are recommended to have a third academic referee, if the two academic referees are within the same department/school)current academic transcripts.

In the research proposal section of your application, please specify the project title and supervisors of this project and copy the project description in the text box provided. In the funding section, please select 'I will be applying for a scholarship/grant' and specify that you are applying for advertised funding from NERC GW4+ DTP.

If you wish to apply for more than one project please email us.

The deadline for applications is 16:00 on 6 January 2020.

Shortlisting for interview will be conducted by 31 January 2020.

Shortlisted candidates will then be invited to an institutional

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UExeter MaternalPaternalEffectsCrickets

Competitively funded PhD position on paternal and maternal effects in crickets. Based at the Centre for Ecology and Conservation at the Cornwall Campus of the University of Exeter.

Team: Dr Bram Kuijper (UExeter), Prof Chris Bass (UExeter), Dr Sinead English (UBristol) and Dr Barbara Tschirren (UExeter)

More information: http://www.exeter.ac.uk/studying/funding/award/?id=3719 Deadline for applications: Sunday December 2, 2019

* Project Background * While it is well known that mothers transfer 'V next to their genes 'V various non-genetic factors to their young (e.g., hormones, DNA methylation variants and small RNAs), fathers in most animals are thought to transfer nothing but genes to offspring. However, this view is now increasingly untenable given recent studies which show that fathers influence offspring phenotypes via DNA methylation or small RNAs. A clear example of such paternal influences occurs in the cricket Teleogryllus oceanicus (e.g., https://doi.org/10.1002/evl3.124), in which fathers transfer a spermatophore (a large clump of foam) to females during mating which affects offspring viability. The aim of this project is to understand how maternal and paternal effects interact: for example, do paternal effects enhance maternal effects and vice versa, or do they inhibit each other? How do paternal effects respond to selection versus maternal effects?

* Potential projects * Below we suggest three possible components. Students are welcome to design the contents of this PhD project according to their own interests.

Computational models of paternal effects: as we still have a limited understanding of whether paternal effects are a general phenomenon in the animal kingdom, this part of the project allows the student to learn computational techniques with which to model the evolution of paternal effects across a range of biological scenarios. Such models allow you to make general predictions about the ecological contexts and molecular mechanisms that are most conducive to paternal effects.

Selection experiments of paternal versus maternal effects and their interaction: with these computational predictions in hand, we then create selection lines of Teleogryllus oceanicus to assess how maternal and paternal effects interact. We can do so by artificially selecting for diverging spermatophore characteristics, so that lines become different in features such as spermatophore size and transcriptome profile. Using other lines, we can also artificially select for different characteristics of ova. Ultimately, by crossing spermatophore and ova selection lines, we can then achieve much-needed insight on how maternal and paternal effects interact in shaping the transcriptome and subsequent survival of the developing zygote.

Transcriptome bioinformatics: using state-of-the-art bioinformatics techniques we analyze the gene expression levels in spermatophores and ova of these selection lines to assess divergence in paternal versus maternal effects.

* Start Date * October 2020.

* Funding * This is a project funded by the South West Bioscience Doctoral Training Partnership (SWBio DTP). The selection process can be found here: https://www.swbio.ac.uk/programme/selection-process/ Funding is available to UK and EU nationals who have established UK residency (EU nationals must have ordinarily lived in the UK throughout the three years preceding the start of the studentship).

Applicants from EU countries who do not meet the residency requirements may still be eligible for a tuition-fees-only award. However, a limited number of fully-funded four year studentships available (1-2 studentships per university), which might well be worth a try. For more info on eligibility: https://www.swbio.ac.uk/programme/eligibility/ We would also welcome externally funded applicants, for example through international PhD fellowships: https://www.swbio.ac.uk/programme/how-to-apply/external-funded-applicants/ * More information * For more information and to apply, visit http://www.exeter.ac.uk/studying/funding/award/?id=3719 https://www.findaphd.com/phds/project/epigenetic-interplay-how-maternal-and-paternal-effects-interact-in-australian-crickets-phd-in-biosciences-swbio-dtp/?p113887 Dr Bram Kuijper Stella Turk Building Centre for Ecology & Conservation

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UGeorgia EvolutionaryBiology

The University of Georgia is seeking graduate students to join a large community of ecology and evolutionary biology researchers through the Integrated Life Sciences (ILS) program.

Admission through the ILS program allows new graduate students to explore research across 14 participating Ph.D. graduate programs, including over 50 laboratories with diverse ecology and evolutionary biology interests. Over their first semester in the program, graduate students can choose rotations among laboratories from nearly all life science departments.

The application deadline for Fall 2020 admission to the ILS program is December 2, 2019. To learn more about the ILS program and research at the University of Georgia, please visit the website at:

http://ils.uga.edu Potential students are encouraged to explore the ecology and evolutionary biology research underway at UGA through the ILS program and to get in contact with faculty whose research they are interested in:

http://evolutionary.genetics.uga.edu/EvoEcol.html Athens, Georgia is a vibrant college town and is consistently ranked one of the top places to live.

Please contact us with any questions.

Michael White Evolution and Ecology ILS Group Representative Assistant Professor of Genetics whitem@uga.edu

Michael White <whitem@uga.edu>

UGuelph PlantEvolution

Graduate student positions in plant evolutionary ecology at the University of Guelph

I am looking for graduate students (MS or PhD) interested in studying the effect of pollinator declines on floral evolution in native wildflowers.

For more information on my lab, check out:

www.christinamariecaruso.com Students will have considerable freedom to develop their projects, and could start in either Fall 2020 or Winter 2021.

Interested candidates should email me at carusoc@uoguelph.ca. Please include a statement of interest, CV, and transcript (unofficial is fine). Because of funding restrictions, preference will be given to candidates who are Canadian citizens or landed immigrants.

Christina M. (Chris) Caruso Associate Professor

Department of Integrative Biology

University of Guelph

Guelph, OntarioN1G 2W1Canada

Christina M. (Chris) Caruso Associate Professor Editor-in-Chief, International Journal of Plant Sciences

Department of Integrative Biology,University of Guelph,Guelph, Ontario N1G 2W1 Canada 519-824-4120 x52030 carusoc@uoguelph.ca christinamariecaruso@gmail.com www.christinamariecaruso.com Christina Caruso <christinamariecaruso@gmail.com>

UHouston EcologyEvolution

GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston (UH) welcomes applications for its graduate program in Ecology & Evolutionary Biology for Fall 2020. The following faculty in the areas of Ecology and Evolutionary Biology have opportunities available for their labs:

Alex Stewart (astewar6@central.uh.edu): Mathematical biology Blaine Cole (bcole@uh.edu): Evolution and social behavior Dan Graur (dgraur@uh.edu): Molecular evolutionary bioinformatics Diane Wiernasz (dwiernasz@uh.edu): Sexual selection Erin Kelleher (eskelleher@uh.edu): Evolutionary genetics and genomics Kerri Crawford (kmcrawford3@uh.edu): Community ecology Rebecca Zufall (rzufall@uh.edu): Evolutionary genetics Ricardo Azevedo (razevedo@uh.edu): Evolutionary genetics Rich Meisel (rpmeisel@uh.edu): Evolutionary genetics and genomics Steve Pennings (spennings@uh.edu): Community ecology Tony Frankino (frankino@uh.edu): Evolution of complex traits

If you are interested, you should look at the relevant faculty members' web sites and then contact them directly for more information:

http://www.uh.edu/nsm/biology-biochemistry/people/-faculty/faculty-alpha/ For more information regarding the Evolutionary Biology and Ecology graduate program at UH see:

http://www.bchs.uh.edu/graduate/prospective-students/ http://www.uh.edu/graduate-school/-prospective-students/how-to-apply/ If you have any questions regarding the application process, please contact:

Ms. Rosezelia Jackson (biograd@central.uh.edu)

The early deadline for application of prospective students is February 1st, 2020. Evaluation will continue after that date, but students are encouraged to apply as early as possible.

Ricardo B. R. Azevedo, PhD Associate Professor Associate Chair for Graduate Affairs Dept. Biology & Biochemistry University of Houston 369 Science & Research 2 Houston, TX 77204-5001 Tel: 713-743 4149 Fax: 713-743 2636 Email: razevedo@uh.edu

"razevedo@Central.UH.EDU"
<razevedo@Central.UH.EDU>

UHull UK BeeGenomics

For details please contact Dr James Gilbert (james.gilbert@hull.ac.uk). To apply, and for more details: https://panorama-dtp.ac.uk/research/-nutrigenomics-and-the-resilience-of-bees-in-a-changing-climate/ Deadline: 6 Jan 2020 Eligibility: UK and EU students only Funding: UK (NERC, Competition-funded)

Ecosystem stability and global food security depend upon healthy populations of bees, our foremost pollinators. Bees provide pollination services worth hundreds of billions of pounds annually. Honeybees and bumblebees are our most important managed pollinators, but the UK is home to ~245 species of wild solitary bees which collectively perform most pollination.

Unfortunately, bee populations are declining, with multiple causes. Key to bee survival and fitness is nutrition; all bees feed offspring with pollen gathered from the landscape. But human influences such as agricultural intensification are altering nutritional landscapes for bees [3,4], and fundamentally affecting gene expression, growth and reproduction. Most of what we know about bee nutrition comes from studies in social bees like honeybees or bumblebees [5,6], where nutrition influences caste determination, development, pathogen resistance and others. However, the nutritional ecology of other bees, particularly solitary bees, is largely unstudied. Unless these bees can detect and respond to changes in nutritional landscapes, their fitness will be reduced 'V a scenario we term a "nutritional trap".

Human activity is also changing climates and raising average temperatures. Temperature affects animals'Â metabolic rate, physiology, digestion, and nutrient assimilation, as well as gene expression. Dr Gilbert'Âs recent work [7] has identified the need to store enough carbohydrate and fat to survive the winter as potentially critical for solitary bees'Â nutritional ecology. But we know little about how this is regulated, how climate change will affect bees, and how bees will deal with changing nutritional landscapes in a future filled with uncertainty.

We are now, for the first time, in a position to understand not just whether but also how different nutritional landscapes and climates affect bees. This exciting cross-institutional project combines field ecology with cutting edge molecular approaches to address a crucial knowledge gap about how bees are being affected by human-altered nutritional landscapes. This project addresses issues relevant for pure ecological science, conservation biology, agriculture and crop science. At Hull, Dr Gilbert'Âs lab has pioneered rearing protocols for the economically and ecologically important solitary bee, Osmia bicornis. This work is providing an unprecedented window onto bee nutritional ecology. At Leeds, Dr Duncan'Âs lab uses a variety of cutting-edge molecular tools to understand how bees are influenced by their environment. Dr Duncan has conducted groundbreaking work on how nutrition affects gene expression in developing bees, as well as recent work on the environmental and molecular control of reproduction in O. bicornis. The student will capitalise on this timely opportunity to synthesize the research interests of these two research groups and create collaborative links between institutions. The candidate will be integrated into both lab groups and will benefit from the infrastructure and connections at both universities.

Differences in larval nutrition in the honeybee results in gene expression changes and ultimately adult bees with different reproductive potential and lifespan. Using careful manipulations within controlled laboratory environments, the student will first establish how dietary macronutrients affect the fitness of solitary bee larvae in response to changes in rearing temperature. Then, they will use high-throughput sequencing technology to examine genome-wide expression profiles of larvae receiving different diet and temperature treatments, to understand the molecular and physiological mechanisms underlying bees'Â responses to landscape and climate change. Nutritional cues are known to alter gene expression [8], but to date studies have focussed largely on a few genes, and only in honeybees. The student will compare larvae receiving different treatments in (1) choices larvae make about which nutrients to consume, (2) correlates of fitness such as body size and overwinter survival, and (3) expression of growth- versus diapause-related genes. Outcomes: The findings will, firstly, shed light on the optimal nutrition for bees 'V both currently, and in a warmer future. They will help inform active measures such as wildflower strips to conserve and promote these vital pollinators as the climate changes. Secondly, results will also show the physiological effects of different nutritional landscapes upon bees, now

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ULethbridge Canada EvolutionSalamanders

The Lee-Yaw lab at the University of Lethbridge in Alberta Canada is looking to recruit 1-2 graduate students to work on the evolutionary ecology of range limits.

Current, priority projects in the lab are focused on the long-toed salamander and include:

1) Wildfire effects on genetic diversity and population connectivity

The frequency and severity of wildfires are increasing around the world, making it imperative to understand the effects of these events on wildlife populations and species of conservation concern in particular. In collaboration with Parks Canada, the Lee-Yaw lab is investigating the effects of the 2017 Kenow Wildfire on long-toed salamanders in Waterton Lakes National Park. Long-toed salamanders occur at the edge of their range in Alberta where they are considered a species of Special Concern. The Kenow Wildfire was a severe disturbance event affecting 40% of vegetated areas in the park including many of the breeding ponds used by this species. Taking advantage of pre- and post-fire samples from across the park, we will assess changes in genetic diversity and patterns of gene flow in response to the fire. This work includes opportunities for fieldwork in the stunning setting of Waterton Lakes National Park and surrounding areas of the Rocky Mountains. The project will involve molecular lab work and modelling landscape connectivity with GIS data. This project is best-suited for an MSc student, although could be extended to a PhD. Applicants should have a background or coursework in evolution, population biology, and/or ecology. Molecular lab experience is a strong assets, as is field experience, familiarity with R, and/or experience working with GIS datasets.

For more information on this project, visit: https://julleeyaw.weebly.com/wildfire-project.html 2) Genomic perspectives on range limits

I am seeking a motivated PhD student to collect and analyze genomic data (ddRADseq and/or transcriptome data) for the long-toed salamander. This species is found throughout the Pacific Northwest and is comprised of several, genetically distinct subspecies. The boundaries between subspecies afford an opportunity to study parapatric range limits involving hybridization while the species' eastern range limits in the foothills of the Rocky Mountains represent an opportunity to study limits to adaptation and range limits along elevational gradients. Tissue samples from across the species' range are available. A number of dissertation projects involving these samples are possible, including testing genetic explanations for range limits, examining hybrid zone dynamics and cytonuclear interactions, and testing biogeographic hypotheses of historical range dynamics. Prior experience in the molecular lab is essential and priority will be given to candidates who have experience with next-generation sequencing (library preparation and SNP calling). Protocol optimization and bioinformatics will be done in collaboration with other labs and may involve opportunities to travel. There is scope to pair the genomic data with other types of data (field or lab experiments, or GIS modelling) depending on the student's interests and progress.

Other projects within the scope of my research program may be considered depending on funding.

General inquiries should be sent to Julie Lee-Yaw (julie.leeyaw@uleth.ca). Applications should be sent by December 20. Please use the subject line "Graduate Studies" and include 1) a brief statement of research interests, 2) relevant experience, 3) a current CV, 4) unofficial copies of academic transcripts, and 5) intended start data and whether you are seeking a MSc or PhD. U of L deadlines for applying to graduate school are February 1 (for a May start date) and May 1 (for fall start). All students are encouraged to apply for external funding. Please note that I am currently unable to provide stipend support for international tuition fees: I would be happy to consider students from outside of Canada who have their own funding or who are eligible for U of L graduate awards.

The Lee-Yaw lab is committed to diversity and inclusion and welcomes applications from students with diverse backgrounds, perspectives, and experiences.

Additional Information:

Lee-Yaw Lab: https://julleeyaw.weebly.com/ U of L Biological Sciences: https://www.uleth.ca/artsci/-biological-sciences U of L Graduate Studies: https://-www.uleth.ca/future-student/graduate-studies/ Julie A. Lee-Yaw

Department of Biological Sciences

University of Lethbridge

"Lee-Yaw, Julie" <julie.leeyaw@uleth.ca>

UMaine CoastalAnimalGenomics

As part of a new, collaborative NSF-funded research and training program in environmental DNA (eDNA) and coastal ecosystem sustainability, the Cammen and Kinnison labs at the University of Maine are recruiting a PhD student to study food web connectivity of a recovering ecosystem in Maine using eDNA. The student will be expected to conduct both field work and molecular analyses towards understanding trophic networks in connected freshwater, estuarine, and marine ecosystems that have been the focus of targeted recovery efforts over the past several decades. Focal study species may include harbor seals, gray seals, and alewife. Molecular approaches may include metabarcoding and qPCR to assess spatiotemporal variation and connectivity of aquatic ecosystems, characterize predator diet, and evaluate genetic diversity of eDNA-sampled populations.

The student will be co-advised by Drs. Kristina Cammen (http://cammenlab.org) and Dr. Mike Kinnison (https://umaine.edu/evoappslab/people/dr-michael-kinnison/). Graduate students can join our labs through the School of Marine Sciences or Ecology and Environmental Sciences programs at the University of Maine, located in Orono, an hour to the ocean and an hour and a half to Maines highest peak. Students will also participate in cross-program grad training, professional development, and communicating science to the public through a robust education and outreach program supported by Maine-eDNA. For more information about the NSF-funded Maine-eDNA program, see our website here: https://umaine.edu/edna/ The successful candidate must have a strong background in aquatic ecology and/or molecular ecology. Preferred candidates will have demonstrated experience with genetics, genomics, and/or bioinformatics. Prior experience with environmental DNA will be particularly beneficial. Individuals who are intellectually curious, responsible, willing to learn, and have attention to detail are encouraged to apply. An M.S. in a related field is preferred, but qualified candidates with extensive experience will be considered.

The selected candidate will receive up to 4 years stipend, plus tuition and health insurance coverage, with annual renewal based on satisfactory degree and program progress. As part of the National Science Foundations and our commitment to broadening participation, we especially encourage women, underrepresented minorities, first-generation students, veterans, and students with disabilities to apply.

To apply, please send 1) a cover letter describing your qualifications including any prior experience working in interdisciplinary teams, why you are interested in pursuing a PhD through the Maine-eDNA program, and how your research interests relate to employing eDNA-based ecological inference to understand processes related to ecosystem recovery; 2) a resume/CV; 3) GRE scores and unofficial transcripts; and 4) contact information for three references. All application materials should be sent to kristina.cammen@maine.edu with eDNA PhD Student Search as the subject line of your email. All applications received before December 15, 2019 will receive full consideration for the first round of application review. The position will begin between June and September 2020.

The University of Maine is an EEO/AA employer and does not discriminate on the grounds of race, color, religion, sex, sexual orientation, including transgender status and gender expression, national origin, citizenship status, age, disability, genetic information or veterans status in employment, education, and all other programs and activities. Please contact the Director of Equal Opportunity, 101 N. Stevens Hall, Orono, ME 04469 at 207-581-1226 (voice), TTY 711 (Maine Relay System), or equal.opportunity@maine.edu with questions or concerns.

– Kristina Cammen Assistant Professor of Marine Mammal Science School of Marine Sciences

5735 Hitchner Hall, Rm 151A University of Maine Orono, ME 04469

Email: kristina.cammen@maine.edu Phone: 207-581-2820 cammenlab.org

Kristina Cammen <kristina.cammen@maine.edu>

UMemphis Biodiversity

The Center for Biodiversity Research at the University of Memphis (Department of Biological Sciences) is recruiting graduate students for 2020. Our Biodiversity Scholars Program offers research and stipend awards for exceptionally qualified candidates. Apply by February 1, 2020 for full consideration. Please see our website for more information (www.umbiodiversity.org).

Duane McKenna PhD William Hill Professor of Biology Department of Biological Sciences Director, Center for Biodiversity Research Co-Director, Agriculture & Food Technologies Research Cluster, FedEx Institute of Technology University of Memphis Memphis, TN 38152

"Duane McKenna (dmckenna)" <dmckenna@memphis.edu>

UMuenster 12 EvolutionaryBiology

The DFG funded Research Training Group "Evolutionary Processes in Adaptation and Disease" (EvoPAD) at the University of Münster, Germany, invites applications for 12 PhD Positions in biology, medicine, and philosophy (salary level E13 TV-L, 65%).

The positions are fixed term for 36 months, and the expected starting date is 1 April 2020. Currently, the regular working time for full (100%) employment is 39 hours and 50 minutes per week. The DFG-funded Research Training Group "Evolutionary Processes in Adaptation and Disease" (EvoPAD, GRK 2220) unites biological, medical, and philosophical research at the University of Münster. The core idea is to use the theory of evolution to understand processes leading to adaptation and/or disease. The PhD students will make use of evolutionary thinking to address basic and medical questions.

EvoPAD doctoral researchers will perform cutting-edge research in an interdisciplinary environment. Our multidisciplinary qualification program is tailored to individual career tracks, and offers opportunities for international cooperation, summer schools, and courses covering evolutionary and population genetics, bioinformatics, experimental design, philosophy of science, and bioethics. EvoPAD offers a family friendly and international atmosphere.

For project descriptions please visit: https://www.uni-muenster.de/EvoPAD/application/index.html < http://www.uni-muenster.de/EvoPAD/application/%20 >

Requirements

§outstanding Master's or equivalent degree in Biology, Biomedicine, Bioinformatics, Biotechnology, Philosophy or related fields.

§proven qualifications with particular relevance to EvoPAD projects.

§capacity to formulate and solve research problems and effectively interpret research results.

§willingness to interact with colleagues in an interdisciplinary setting.

§motivation to manage a PhD project and to participate in our multidisciplinary qualification program.

§fluency in written and spoken English.

How to apply The application should include:

§CV including information about former academic education and degrees, professional experience, publications, fellowships/awards, conference contributions, languages, and further relevant skills and abilities.

§cover letter stating the candidate's expectation from EvoPAD and motivation to join the project.

§master's thesis abstract.

§two letters of recommendation.

The University of Münster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. We also welcome applications from candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered, unless other project-related reasons apply.

Applications should be sent by email as one PDF file (max. 5 MB) to the EvoPAD Coordinator Dr Kristina Wensing (evopad@uni-muenster.de) by 13 December 2019. Please indicate in the cover letter the project that you would like to apply for and give a second choice (if wanted).

Shortlisted candidates will be interviewed via Skype between 9 - 14 January 2020. The most promising candidates will then be invited to Münster to take part in an admissions workshop on 6 & 7 February 2020.

— Dr Kristina Wensing

Coordinator of the Münster Graduate School of Evolution < https://www.uni-muenster.de/Evolution/mgse/ > Coordinator of the DFG Research Training Group 2220 "Evolutionary Processes in Adaptation and Disease" < https://www.uni-muenster.de/EvoPAD/ > Westfälische Wilhelms-Universität Münster Hüfferstr. 1a, D-48149 Münster, Germany

Phone: +49 251 83-21252 E-Mail: mgse@uni-muenster.de or evopad@uni-muenster.de

"Kristina Wensing, MGSE" <mgse@uni-muenster.de>

UNESP SaoPaulo DrosophilaGenomics

Candidates interested in doing PhD in genomics area using Drosophila

I am selecting a candidate who has the profile and interest to do a doctorate in the area of Genetics and Evolutionary Biology, in the Postgraduate Program in Biosciences in Sāo José do Rio Preto / Sāo Paulo Brazil (https://www.ibilce.unesp.br/) . There is possibility of a doctoral fellowship support by CAPES or FAPESP and also a cotutela with the Museum of Paris . The research project to be developed will use Drosophila sturtevanti aiming to study genome and phylogenetic relationships in the Drosophila saltans group.

It is important that the candidate has developed his master's degree using some molecular biology techniques and has knowledge of some bioinformatics programs.

Those interested should send CV lattes and a letter of recommendation, if possible from their advisor, by November 8st, to Email lilian.madi@unesp.br.

– *Profa Dra Lilian Madi-Ravazzi* Departamento de Biologia UNESP-IBILCE Rua Cristovâo Colombo, 2265 CEP 15054-000 Sāo José do Rio Preto-Sāo Paulo

Lilian Madi Ravazzi <lilian.madi@unesp.br>

UNevada Reno InsectEvolution

Graduate student positions in multi-sensory integration during search behavior

The van Breugel lab at the University of Nevada, Reno is hiring graduate students for Fall 2020 to work on multi-sensory integration in insects during search behavior (flies/mosquitoes). Our research lab leverages modern engineering and genetic tools available in the fly to study fundamental questions in ecology and neuroscience, such as the role of temporal and spatial memory in search/foraging.

The lab is very interdisciplinary and you will have opportunities to learn techniques that include field work, wind tunnel experiments, 2-D and 3-D real-time tracking, optogenetics & virtual reality, and robotics. More information about the lab can be found here:https://www.florisvanbreugel.com/ . The position is fully funded through a combination of RA and TA appointments.

The Reno area is a diverse and growing hub for technology, the arts, science, and the outdoors. We have riverside parks, lots of summer festivals, skiing is only 30 min away, and it's almost always sunny, but rarely gets uncomfortably hot or cold.

Students can apply throughEcology/Evolution or Integrative Neuroscience. Ideal applicants will have some experience with programming (python preferred), an interest in tinkering and building things, and a fascination with how animals work, but any combination of those skills and interests will be considered.

For more information, please contact me atfvanbreugel@unr.edu(after taking a look at my website).

Floris van Breugel | http://www.florisvanbreugel.com Assistant Professor of Mechanical Engineering & Graduate Program for Neuroscience Palmer 226, University of Nevada, Reno

Wildlife and Landscape Photography

Galleries:http://www.ArtInNaturePhotography.com/ Blog:http://www.ArtInNaturePhotography.com/wordpress/ Floris Van Breugel <fvanbreugel@unr.edu>

UNorthCarolina Greensboro EvolutionMammalParasites

The McLean Lab (https://www.mclean-lab.org/) at University of North Carolina Greensboro (http://www.uncg.edu/) is recruiting graduate students at PhD and Masters levels to investigate community ecology of paired mammalian-parasite systems. We are especially interested in investigating the structure and complexity of mutli-host, multi-parasite networks and working to understand their responses to past and present environmental change.

Research in the McLean lab bridges mammalian ecology and evolution and relies on an integrative toolkit including fieldwork and specimen collection, phylogenomics, phylogenetically-informed community analyses, distribution modeling, and biodiversity informatics. Prospective applicants will be encouraged to develop research projects that apply these tools to mammal-ectoparasite community ecology in one of the ecological contexts we work in, including: the Southern Appalachians, Great Basin Desert, and Gobi Desert (Mongolia). Students will begin graduate school in August 2020, with the option to work as a field technician on lab project(s) during summer 2020.

To inquire about positions, please email Bryan McLean (b_mclean@uncg.edu) no later than November 15th and describe: a) the broad research questions you are most passionate about in ecology and evolution, 2) how these fit with previous research in the McLean lab, 3) a summary of academic and research experiences, and 4) an updated CV.

Students accepted into the Environmental Health Science (EHS) PhD program at UNCG will be provided a tuition waiver and a competitive stipend. Additional competitive fellowships are available by specific application. *Note: In order to apply for the program you must have taken the GRE, and applicants with a first language other than English must also submit scores on the Test of English as a Foreign Language (TOEFL). The deadline for application to the Environmental Health Science PhD program is 15 December 2019 and the deadline for the MS Program is 31 March 2020.

For more information about the UNCG Graduate Program in Biology, please visit:

https://biology.uncg.edu/graduate/mission/ . For more information about the HIGH quality of life and LOW cost of living in Greensboro, please visit:

https://www.greensboro-nc.gov/i-want-to https://realestate.usnews.com/places/north-carolina/greensboro Bryan McLean <bryansmclean@gmail.com>

UNorthCarolina Greensboro LifeHistoryInformatics

The McLean Lab (https://www.mclean-lab.org/) at University of North Carolina Greensboro (http://www.uncg.edu/) is recruiting graduate students at PhD and Masters levels to investigate life history responses of North American small mammals to global change. Our lab combines historic data streams (e.g., museum specimens) with new field surveys and collections to understand environment-life history dynamics and the potential for change in key life history traits (reproduction, phenology, body size and shape) through time. This research is highly integrative, and we value students with broad interests in natural history, mammalogy, specimen-based research, and biodiversity data analysis.

Research in the McLean Lab bridges mammalian ecology and evolution and relies on an integrative toolkit including fieldwork and specimen collection, phylogenomics and landscape genomics, trait evolution, and biodiversity informatics. Prospective applicants will be encouraged to develop research projects that leverage these or new tools. Students will begin graduate school in August 2020, with the option to work as a field or lab technician on field or informatics projects during summer 2020.

To inquire about positions, please email Bryan McLean (b_mclean@uncg.edu) no later than November 20th and describe: a) the broad research questions you are most passionate about in ecology and evolution, 2) how these fit with previous research in the McLean lab, 3) a summary of academic and research experiences, and 4) an updated CV.

Students accepted into the Environmental Health Science (EHS) PhD program at UNCG will be provided a tuition waiver and a competitive stipend. Additional competitive fellowships may be available by application. *Note: In order to apply for the program you must have taken the GRE, and applicants with a first language other than English must also submit scores on the Test of English as a Foreign Language (TOEFL). The deadline for application to the Environmental Health Science PhD program is 15 December 2019 and the deadline for the MS Program is 31 March 2020.

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https://biology.uncg.edu/graduate/mission/ . For more information about the HIGH quality of life and LOW cost of living in Greensboro, please visit:

https://www.greensboro-nc.gov/i-want-to https://realestate.usnews.com/places/north-carolina/greensboro bryansmclean@gmail.com

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UParis Sud AppleAdaptation

Title: Fruit tree responses to climate changes in a context of domestication??

Amandine Cornille??s group (http://moulon.inra.fr/index.php/fr/equipes/group-leader-amandine-cornille-young-atip-avenir-team) and St??phane Bazot??s group (https://www.ese.u-psud.fr/en/team-members/stephane-bazot/) are recruiting a graduate student at Master 2 level to investigate fruit tree responses to climate changes in a context of domestication.??

Lab address??: Laboratoire ??cologie Syst??matique et ??volution Bat 362 Universit?? Paris Sud 91405 Orsay, FRANCE

Supervisors??: Amandine Cornille (amandine.cornille@inra.fr) and St??phane Bazot (stephane.bazot@u-psud.fr)

Project summary Will populations be able to cope with the rapid climate changes? This question is critical and timely given the increasing pace of human induced changes. This is particularly true for crop wild relatives which in addition to climate changes may often be threatened by crop-to-wild gene flow following the domestication of their cultivated relative. Fruit trees have major economic and ecological roles, yet the study of their response to climate change has been surprisingly neglected. The project will therefore assess the capacities of the two major wild apple contributors to the cultivated apple genome using an unprecedented multi-layer approach (genomic, gene expression, ecophysiology) applied to a transplant experiment in controlled conditions. The project will bring new insight in how fruit tree species respond to climate changes in a context of domestication. This is not only an academic exercise as wild fruit tree crop relatives render multiple ecosystem services and are often emblematic species in their respective ecosystems. They have also a high potential genetic diversity for improvement of future breeding programs in context of climate changes.

Master project The candidate will be involved in the assessment of the adaptive and plastic capacities at the ecological level of the two major crop wild apple relatives. The project involves the transplant of wild apple seedlings from these two species in four different climate conditions simulated in a national controlled climate simulator experimental station (ECOTRON). 1) The candidate will lead the launching of the experiment in two out of the four climatic conditions (i.e. ECONTRON celles) during spring 2020 by transplanting crop wild apple seedlings originating from Eurasia and will measure several phenotypic traits. The germination date and growth rate of each plant will be measured three times a week. Various functional traits which are proxies of the condition of the plant (i.e. chlorophyll content, carbon/nitrogen balance, and flavonol and anthocyanin content measured with the Dualex?? pincel) will be measured once a week the last two weeks of the experiment. 2) He/She will analyze an already available dataset that was generated during summer 2019 for the two other conditions.

Methodology : Statistical analyses (linear and mixed models, R), ecophysiology, phenotypic measurement

Profile preferred for the candidate: Ideally, the candidate will have skills in ecology and evolution or at least will show strong interest in these fields. He/she will not necessarily be familiar with apple model.

Supervision??: Amandine CORNILLE - Charg??e de Recherche CNRS CR2 G??n??tique Quantitative et Evolution - Le Moulon Ferme du Moulon 91190, Gif.sur.Yvette, France mail??: amandine.cornille[at]gmail.com Google Scholar profile : https://scholar.google.com/citations?user=EqIE2h8AAAAJ&hl=fr Personal page : http://moulon.inra.fr/index.php/fr/equipes/dygap/355 Group page??: http://moulon.inra.fr/index.php/fr/equipes/group-leader-amandine-cornille-young-atip-avenir-team St??phane Bazot Laboratoire ??cologie Syst??matique et ??volution Bat 362 Universit?? Paris Sud 91405 Orsay Personal page: https://www.ese.u-psud.fr/en/team-members/stephane-bazot/ Duration : 6 months, january 2020 ?? june 2020 or february 2020 ?? july 2020, starting dates are flexible, contact Amandine CORNILLE and St??phane BAZOT for further discussions.

Fixed indemnisation: 3500 euros for 6 months (577 euros/month).

References Cornille A., Antolin F., Garcia E., Vernesi C., Fietta A., Brinkkemper O., Kirleis W., Schlumbaum A., Rold??n-Ruiz I. (2019) A Multifaceted Overview

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UPlymouth PollinatorGenomics

Ph.D PROJECT AVAILABLE: Hard-wired for success? Unravelling genomic signatures in pollinators University of Plymouth and the Earlham Institute, UK

Key information:

This project has been shortlisted for funding by the ARIES NERC Doctoral Training Partnership, and will involve attendance at mandatory training events throughout the course of the PhD. Successful candidates who meet UKRI's eligibility criteria will be awarded a NERC studentship - UK and EU nationals who have been resident in the UK for 3 years are eligible for a full award. This studentship will start on 1st October 2020, and the closing date for applications is 12:00 on 7th January 2020. Shortlisted applicants will be interviewed on 18/19 February 2020.

For further information, please contact Mairi Knight, mairi.knight@plymouth.ac.uk

Background: Many pollinator species, recognised as essential for ecosystem function, are undergoing rapid declines. One recent exception is the 'Tree Bumblebee' Bombus hypnorum: expanding its range into and across the UK in <20 years, it is now one of our most common species.

Building on previous work from the supervisory team, and in collaboration with the Earlham Institute, this project will investigate key genomic differences between this and other bumblebee (Bombus) species to substantially improve our understanding of the factors contributing to its success, along with the declines of others. The project's focus is a genomic comparison of Bombus species from within the UK and continental Europe. Initial work has identified genomic regions of interest in B. hypnorum that may be indicative of its ability to adapt to anthropogenically altered landscapes. However, current data are preliminary and lack essential phylogenetic comparison.

Methodology: This is a timely and exciting opportunity to generate a highly novel, and substantial, genomic dataset to test hypotheses as to whether the observed genomic differences are unique to B. hypnorum, or shared among Bombus species (some evidence suggests elevated resilience in the wider Pyrobombus sub-genus). In addition to fulfilling the specific aims, the data generated will offer the student significant scope to guide the project's further direction through characterisation of genomic signatures and differences across this important pollinator group.

Training The project will equip the successful student with state-of-the-art genomic techniques as well as bioinformatic and modelling skills that are highly transferable and increasingly essential across a wide range of academic and applied biological disciplines. The student will also gain important soft skills (e.g. communication, team working, problem solving). He/she will be based in Plymouth, spending short periods at the other Institutions as relevant.

Person Specification The successful candidate will have a biology-based degree, an academic interest in evolutionary ecology, and be enthusiastic about pursuing a laboratory- and computer-based project. Ideally, he/she will have some basic molecular ecology experience (e.g. DNA extraction, PCR) and interest in genetic and evolutionary analysis. Experience of genome sequencing and bioinformatics is not essential as full training will be provided.

Dr Mairi Knight mairi.knight@plymouth.ac.uk School of Biological and Marine Sciences University of Plymouth Plymouth PL4 8AA UK

Jonathan Ellis <jonathan.s.ellis@plymouth.ac.uk>

UQuebec Abitibi-Temiscamingue ForestPopGenetics

A PhD opportunity in population genetic and dendrochronology: Understanding adaptation of sugar maple at its northern distribution limit Context: The sugar maple is a dominant species of the Eastern North-American temperate forest, which is expected to migrate northward as a result of global warming. Populations at the edge of their range should be therefore the first to benefit from climate change. Genetic makeup of frontier populations, however, may affect species capacity to adapt to changing environment. Specifically, it is hypothesized that a low genetic diversity of such populations may limit ability of the species to respond to increases in the length and average temperature of the growing season.

The doctoral project will seek to assess the role of genetic makeup in the future dynamics of maple distribution range and will study regeneration and growth of frontier maple populations in Eastern Canada. For the study of maple regeneration the project will examine the variability in genetic diversity across different age cohorts within populations. For the study of tree growth, the project will rely on the analysis of growth response to climatic changes, as recorded in the tree rings, and assessments of genetic variability within frontier maple populations.

PhD student. We are looking for an ambitious and highly motivated PhD student with a completed master degree in forest ecology, population genetics/genomics, climatology, geography, or ecosystem modelling. Documented experiences with dendrochronology, forest genetics, and large relational databases are strong assets during the evaluation process. The knowledge of R is a must. The candidate should be fluent in English and has a good ability to formulate himself/herself both orally and in writing. Knowledge of French and Chinese is a strong asset. A record of scientific publications is highly valued. We put a great emphasis on personal characteristics of the successful applicant, solid work ethics, and in particular the ability to independently manage a large volume of laboratory and analytical tasks and to meet reporting and publication deadlines. The candidate is expected to be physically fit and capable of conducting field work in remote yet aesthetically superior environments. It is expected that the student will spend between six to twelve months with a project partner, South China Botanical Garden of the Chinese Academy of Sciences in Guangdong.

Location. The student will be based at the Forest Research Institute of the University of Quebec at Abitibi-Temiscamingue (IRF UQAT, Rouyn-Noranda QC). The student will become a member of the Chair in Sustainable Forest Management and the Center for Forest Studies. The IRF team enjoys a highly dynamic and truly international research environment. The city of Rouyn-Noranda is very active culturally and offers a high quality of life thanks to its tourist attractions (Film Festival, Music Festival Emerging, World Guitar Festival to name a few) and a large number of outdoor activities which include hiking, camping, canoeing, skiing, and snowshoeing (http://www.ville.rouyn-noranda.qc.ca/; http://tourismerouyn-noranda.ca /).

Beginning of studies: January 2020 Funding: a fellowship of Can$ 21,000 per year for a total of three years. An internship of 6 months to 1 year in China is planned during the duration of the doctorate.

Supervision: Yves Bergeron, Igor Drobyshev (IRF UQAT) & Jianguo Huang (Chinese Academy of Sciences) Interested candidates must apply by e-mail (yves.bergeron@uqat.ca & igor.drobyshev@uqat.ca) by sending (1) a cover letter outlining their academic background and research experience, as well as (2) a detailed CV including name and contact information of two references.

"Godbout, Julie (DRF)" <Julie.Godbout@mffp.gouv.qc.ca>

USaskatchewan EvolutionLymeDisease

PhD in Ecology of mixed strain infections in the Lyme disease pathogen Department of Veterinary Microbiology, WCVM, University of Saskatchewan

Position: One PhD position is available in an NSERC-funded research lab at the University of Saskatchewan to investigate the ecological factors that maintain the strain diversity of Borrelia burgdorferi, the tick-borne pathogen that causes Lyme disease (LD). We will use experimental infections with a lab LD system (mice, ticks) to determine how interactions between different B. burgdorferi strains inside the vertebrate host and the tick vector influence the transmission and fitness of this multi-strain tick-borne pathogen.

Location: The University of Saskatchewan is one of the 15 top research universities in Canada. The WCVM is the premiere veterinary school in Western Canada and has state-of-the-art facilities. The faculty in the Department of Veterinary Microbiology are biologists and veterinarians who study pathogens and parasites across a wide range of biological disciplines (molecular biology, physiology, and ecology). The Voordouw Tick & Lyme Lab has research funding from NSERC and the SHRF.

Job requirements: The position requires an independent, highly motivated, enthusiastic, and scientifically curious individual with a strong background in any of the following fields: infectious diseases, microbiology, immunology, ecology, or evolutionary biology. Molecular techniques (qPCR, ELISA, Western Blots), experience working with rodents, statistical data analysis skills and writing skills are useful. The applicant must have a Master's degree. Successful students are expected to be competitive and apply for a diversity of internal scholarships.

Start date: The position is available as early as May 2020. The salary is set by the Department of Veterinary Microbiology and the University of Saskatchewan College of Graduate and Postdoctoral Studies.

Application requirements: Please submit: (1) a 1-2-page cover letter indicating your research interests and why you are interested in the position, (2) your CV (including a list of publications), (3) University transcripts, and (4) two letters of reference. Submit your complete application package via email to: maarten.voordouw@usask.ca. The application deadline is 31 December 2019 (or until the position is filled).

Professor Maarten J. Voordouw Department of Veterinary Microbiology, WCVM, University of Saskatchewan Saskatoon, Saskatchewan, Canada Email = maarten.voordouw@usask.ca Work phone = 306 966-7245 Website: https://researchers.usask.ca/maarten-voordouw/ maarten.voordouw@usask.ca

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UStAndrews EvolutionaryQG

Evolutionary quantitative genetics in the wild: behaviour, growth and fitness in Soay sheep

Project Description

Contemporary natural selection frequently appears to favour the evolution of increased body size. However, corresponding evolutionary responses of body size, of magnitudes predicted by evolutionary quantitative genetic theory, are frequently not observed. The nature of evolutionary constraints in the evolution of many traits, particularly body size, thus present an important problem at the confluence of current evolutionary theory and data from wild populations. This PhD project will use cutting edge technology (3D accelerometers) to collect types of behavioural data that are not generally available in evolutionary quantitative genetic studies, to test hypotheses about behavioural trade-offs that could underly evolutionary stasis in body size.

The Soay sheep of St Kilda, in the Outer Hebrides, Scotland, provide an excellent system for evolutionary quantitative genetic studies of wild populations. The population has been subject to an intensive individual-based study for approximately 35 years, during which time extensive phenotype, fitness, and pedigree data have been collected. These basic data have supported an extremely productive research program in the evolutionary quantitative genetics of wild populations. The current PhD project will use accelerometery data loggers to collect detailed behavioural data. This will allow for tests for trade-offs among different behaviours (e.g., feeding, resting, moving, agonistic interactions) that could underly variation in body size and constrain its evolution.

The PhD will offer experience in field work in a remote location, the use of novel technologies for data logging, experience with modern statistics, and a chance to engage with current formal evolutionary theory. The School of Biology at the University of St Andrews is home to a large group of graduate students engaged in a wide variety of research projects. The school provides a highly supportive environment, and structured support throughout the course of PhD study.

Informal inquiry is encouraged; please contact Michael Morrissey, michael.morrissey@st-andrews.ac.uk

St Andrews postgraduate research application website here: https://www.st-andrews.ac.uk/pgr/home.htm Funding: Fees and stipend is provided for 4 years.

References

Falconer, D.S., and T.F.C. Mackay. 1996. Introduction to Quantitative Genetics, 4th ed. Longmans Green, UK.

Hansen, T.F., and D. Houle. 2004. Evolvability, stabilising selection, and the problem of stasis. Chapter 5 in: M. Pigliucci and K. Preston, eds. Phenotypic integration: studying the ecology and evolution of complex phenotypes. Oxford University Press. Unpaywalled pre-print here: https://www.bio.fsu.edu/~dhoule/Publications/-HansenHoulestasisfinal.pdf Hunter, D.C., J.M. Pemberton, J.G. Pilkington, and M.B. Morrissey. 2018. Quantification and decomposition of environment-selection relationships. Evolution 72: 851-866.

Kingsolver, J.G. and D.W. Pfennig. 2004. Individual-level selection as a cause of Cope's rule of phyletic size increase. Evolution 58: 1608-1612.

Michael Morrissey Royal Society University Research Fellow and Reader in Evolutionary Biology University of St Andrews michael.morrissey@st-andrews.ac.uk

Michael Morrissey <mbm5@st-andrews.ac.uk>

USussex FlowerEvolution

* PhD position available to study plant plasticity and local adaptation to new pollinators after range expansion at the University of Sussex, UK *

Supervisor: Maria Clara Castellanos (http://-www.sussex.ac.uk/lifesci/plant-evolutionary-ecology-lab)

I am looking for an enthusiastic student interested in plant-pollinator interactions and evolutionary biology. The PhD project will focus on how plants can rapidly adapt to new pollinator environments. Our work with a developing study system in recently colonised environments (Digitalis purpurea, the common foxglove) shows that floral morphology can change in a few generations under new pollinators (including larger bees and hummingbirds in tropical mountains) but we still know relatively little about how this occurs. The project will use this exciting model system to examine how adaptation to new pollination environments takes place, and in particular, the potential role of phenotypic plasticity in the process. We will use a combination of approaches that include: 1) experimentally testing for local adaptation using translocation experiments in the field, 2) measuring plastic variation in floral traits in the greenhouse using quantitative genetics, 3) measuring pollinator-mediated selection on floral traits, including male components of fitness using novel techniques to track pollen grains. There will be scope for developing further new ideas within this system.

This 3.5-years fully funded studentship is open to UK and EU citizens. The project will have a significant field component in the UK and abroad (e.g. South and Central America), so it is essential that applicants are committed and available to spend time in the field. For fieldwork in the UK and abroad, a driving licence and driving experience are essential. Experience with plant growing and some knowledge of Spanish are a plus.

For further details on the project and the application process, please visit https://www.sussex.ac.uk/study/-fees-funding/phd-funding/view/1133-PhD-Studentship-for-School-of-Life-Sciences .The student will be part of the vibrant Evolution, Behaviour and Environment subject group within the University of Sussex (http://-www.sussex.ac.uk/lifesci/ebe/). Our campus is located within a national park, 10 minutes from the lively seashore city of Brighton.

The closing date for applications is January 31st 2019. Applications should be submitted through Sussex University's graduate application system: http:/-/www.sussex.ac.uk/study/phd/apply. Please include a CV, statement of interest and the names and email addresses of two academic referees. On the application system use Programme of Study - PhD Biology. For enquiries about the application process contact Emma Chorley (mailto:lifesciphd@sussex.ac.uk). The expected starting date is May 2020.

Feel free to email me for informal inquiries: Maria Clara Castellanos - m.c.castellanos@sussex.ac.uk

"m.c.castellanos@sussex.ac.uk"
<m.c.castellanos@sussex.ac.uk>

UtahStateU EvolutionaryGenomics

The Gompert lab in the Department of Biology at Utah State University (USU) is seeking a highly motivated and enthusiastic PhD student to study the ecological causes and evolutionary genetic consequences of fluctuating selection and contemporary evolution. Research in the lab addresses fundamental questions in evolutionary genetics. We are particularly interested in the genetic architecture of ecologically important traits, the determinants of genetic variation and molecular evolution in natural populations, and the nature and evolution of species boundaries and barriers to gene flow. This specific position is funded through a NSF CAREER award to Gompert. A stipend will be provided via a mixture of teaching and research assistantships. Review of applicants will begin November 25, 2019. The start date for the PhD project is fall 2020.

In the struggle for existence, organisms interact with each other and with their environment. Variation in climate, weather, and species interactions can cause variation in the direction and strength of natural selection. Differences in selection across space cause local adaptation. However, whether seasonal, yearly or longer-term fluctuations in selection are equally important for evolution is unknown. Selection that varies over time can cause rapid evolution. It can also erode or maintain variation for individual traits or genes, but may or may not be an important factor in evolutionary dynamics more broadly. In this NSF-funded project, the Gompert lab will use computer simulations, experiments, and genome sequencing of populations sampled across multiple generations to fill this knowledge gap.

We are looking for a PhD student interested in collaborating on the project. The PhD student will develop computational methods to quantify the prevalence, causes and targets of fluctuating selection from population genomic time-series data. Additional components of the PhD student's dissertation will be tailored to the student's interests and background. Possible project include: (i) developing theory on the consequences of fluctuating selection, (ii) studying the evolutionary genomic consequences of fluctuating selection in quasi-natural selection lab experiments (with cowpea seed beetles), or (iii) identifying the causes and consequences of fluctuating selection (or contemporary evolution) using population genomic time-series from natural populations of Lycaeides butterflies.

The successful candidate should have previous training in evolutionary biology, population genetics, applied math and statistics, or computational biology. Some proficiency with R (or other language, e.g., C) or experience working with population genomic data is preferable, but not essential. Students with or without a Master's degree are encouraged to apply. We welcome and encourage enthusiastic and open-minded applicants from any nation, ethnicity, gender, sexual orientation or socioeconomic class. For more information about the Gompert lab, including a statement of mentoring philosophy and expectations, please visit the lab website at https://-gompertlab.com/ . USU is a public land-grant research university in Logan, Utah (USA). The Department of Biology and USU offer excellent opportunities for education, training, funding, and collaboration. Graduate students in the department have the option of pursuing a PhD in Biology or in the inter-departmental Ecology program. Located in the Rocky Mountains, the Logan area also offers exceptional opportunities for outdoor recreation.

Interested students should e-mail me (zach.gompert@usu.edu) with the following:

1. A cover letter describing the student's background and training, goals and reasons for pursuing a PhD, and the specific reasons why this opportunity is of exceptional interest. 2. A CV, including contact information for three academic references. 3. A writing sample. This could be in the form of a published or draft manuscript, an undergraduate thesis, or some other substantial document that constitutes scientific writing.

zachariah.gompert@aggiemail.usu.edu

UTennessee Knoxville EvolBiology

The Department of Ecology and Evolutionary Biology (EEB) at the University of Tennessee, Knoxville, is seeking applications from prospective graduate students who wish to pursue a research-based Masters or PhD degree. Our ecology program is among the top 10% for research impact in North America (Keville et al., 2017). We pride ourselves on supporting the professional growth and career success of our students, as evidenced by their excellent track record of important scientific discoveries, publications in top journals, participation in international scientific meetings, receiving prestigious national and international funding, and placement in their desired career pathways (whether that leads them to top research and/or teaching institutions, positions in public/governmental agencies, or private industry - see

https://eeb.utk.edu/wp-content/uploads/2018/11/-image002.png).

Our faculty work across a broad range of exciting questions in a collaborative, collegial department. We investigate interactions within and between levels of biological organization; our study systems span from genes to ecosystems (see

https://eeb.utk.edu/people-2/faculty/ and a few brief examples at the end of this message). We integrate experimental, survey, theory, modeling and statistical approaches with a rich tradition of natural history in pursuit of these topics.

While we encourage students to pursue independent funding opportunities, our policy is to admit students only when we are confident we have funding support available for the full duration of their studies (provided adequate progress in the program). We provide funding to both Master's and PhD students through teaching assistantships, regardless of their citizenship. Our goal is to recruit a diverse pool of students on a range of metrics, including background, career stage, and research interests.

Our program relies on the strong mentorship bond between student and advisor(s). We therefore give very strong preference to candidates who have already communicated with their potential advisor(s) before submitting their application. Our deadline for applications is Dec 1st, 2019, so we suggest reaching out to potential advisors at least 2 weeks before submitting your application to allow for low-stress communication.

Read more about us at https://eeb.utk.edu/ and find our application instructions and materials at

https://eeb.utk.edu/graduate-studies/application-information/ . If you need help with the online application, please contact the Graduate Admissions Staff assigned to EEB. For other questions, please contact Prof. Nina Fefferman, Chair of the Graduate Admissions Committee.

Brief examples of some of the foci of strength in our program include (but are not limited to) the large numbers of faculty who work as quantitative bioscientists in a variety of fields, http://www.nimbios.org/qb, and conservation biology, https://consci.utk.edu/. There are also many faculty members working on predictive ecological and evolutionary frameworks for the outcome of plant-soil-microbial interactions under global change.

Nina Fefferman <nina.h.fefferman@gmail.com>

UToronto Scarborough GenomicsSymbiosis

The Wang lab in the Department of Biological Sciences at University of Toronto Scarborough is looking for graduate students interested in genomics and symbiosis between microbial fungi and insects to start in Fall 2020. Interested applicants should apply through the Ecology and Evolutionary Biology graduate program at University of Toronto (deadline Jan. 7th, 2020).

Major efforts in the lab include: 1) assembling high-quality fungal genomes using long-read sequencing data, 2) developing phylogenomic markers for molecular systematics of early-diverging fungi, 3) investigating population genomic structure of insect-associated fungi, and 4) examining experimental evolution and gene expression preference of insect gut-dwelling fungi. We use combined approaches in field collection, host-microbe interactions, and bioinformatics. For additional information on our research activities, please check our recent papers at http://individual.utoronto.ca/yanwang/-publications.html. The Wang lab is strongly committed to equity, diversity, and inclusion in the workplace.

Qualifications:

Applicants should have research interests and relevant experience in either Mycology, Entomology, or Bioinformatics. A Master of Science degree is generally eligible for entrance into our Ph.D. program. A bachelor's degree in either Biology or Science is required before Fall 2020 for the M.Sc. or direct-Ph.D. programs. More details can be found at http://www.eeb.utoronto.ca/-grad/prosp.htm . For inquiries, please contact Dr. Yan Wang at yanxw.wang@utoronto.ca. Please include your most recent CV and a brief research statement (less than 1 page) summarizing your research interests and experience. Further information can also be found at

http://individual.utoronto.ca/yanwang/contact.html . The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas.

Yan Wang, PhD

Assistant Professor (starting Jan. 1st, 2020) Department of Biological Sciences & Department ofEcology and Evolutionary Biology University of Toronto Scarborough Science Wing, Room 542 1265 Military Trail,Toronto, Ontario M1C 1A4 http://individual.utoronto.ca/yanwang/@funganomics http://www.eeb.utoronto.ca/people/G-faculty/Yan_Wang.htm Yan Wang <yanxw.wang@utoronto.ca>

UTulsa AnimalColoration

The Toomey Lab in the Department of Biological Sciences at the University of Tulsa (TU) is seeking PhD students to investigate animal coloration and color vision beginning Fall 2020. Our work is broadly integrative, bringing together genomic, transcriptomic, molecular biological, biochemical, and behavioral approaches to investigate how animals see color, produce colorful displays, and how these traits have evolved. You can learn more about our research at: mbtoomey.net.

If you are interested in joining the lab, please email Dr. Matthew Toomey (mbtoomey@gmail.com) with a brief cover letter describing your research interests and experiences and a CV or resume that includes contact information for three references.

You can learn more about our department here: https://engineering.utulsa.edu/biological-science/ Learn more about life in Tulsa: http://roottulsa.com/ Matthew Toomey <mbtoomey@gmail.com>

UWisconsin Madison DrosophilaAdaptation

University of Wisconsin-Madison MS and PhD positions on molecular adaptation of invasive spotted wing Drosophila

Position Description: MS and/or PhD research assistantships are available in the Molecular Ecology Lab at UW Madison (https://molecularecology.russell.wisc.edu/) to assess how invasive fruitflies adapt to novel environments. Insect pests can be viewed as model systems in which to explore fundamental concepts in ecology and evolutionary biology. They are especially promising candidates to study mechanisms of rapid evolution at the genetic level, as many insect pests have shown a remarkable ability to cope with pesticides, novel climatic space, and novel host plants. While there are significant challenges in determining adaptation at the genetic level and in finding ways to forecast future changes, there are strong incentives (ecological, economic and social) to do this research. Students will combine population genomics approaches with field ecology and manipulative experiments to understand the evolutionary mechanisms of adaptation. Training will focus on the use of population genomics and physiological approaches to relate spatial and temporal variation in the environment to adaptive genetic variation. The start date for the project is September 2020.

Information on University, Department, Lab, and City: The University of Wisconsin-Madison is one of the major research universities in the United States. This project will be supported in the Department of Entomology and under the supervision of Dr. Sean Schoville and Dr. Christelle Guedot, with additional supervision from Dr. John Pool (Department of Genetics). Madison consistently ranks as one of the best places in the United States to live, work, and study. It is Wisconsin's capital city, with a vibrant population of approximately 230,000 that combines small town charm with a variety of leisure and cultural opportunities.

Stipend/Salary: Current annual stipend levels are $24,816 per year before taxes, plus tuition remission and health care benefits. Financial support is available for two years. More information about UW Madison's competitive graduate school can be found here: https://grad.wisc.edu/investing-in-graduate-assistants/ Qualifications: A BS or BA degree in entomology, biology or a related discipline is required.

We are looking for motivated students interested in pursuing a MS or PhD degree at UW-Madison. Students with an MS degree will be given preference in admissions to the PhD program. The preferred candidate will have prior research experience and have some knowledge of population genetics. Candidates should have interests in entomology, evolutionary ecology, and working in both the field and laboratory. Excellent writing and verbal communication skills are expected, as well as the ability to work collaboratively.

Application Process: Interested applicants are asked to apply here: https://grad.wisc.edu/apply/ The application deadline is December 1, 2019. The University of Wisconsin-Madison is an equal opportunity/affirmative action employer. We promote excellence through diversity and encourage all qualified individuals to apply.

Sean Schoville University of Wisconsin-Madison Department of Entomology 1630 Linden Drive 637 Russell Labs Madison, WI 53706 Office phone: 608-262-2956 http://labs.russell.wisc.edu/molecularecology Sean Schoville <sean.schoville@wisc.edu>

UZurich PlantAdaptation

PhD position in plant adaptation

A PhD position is available in my group at the Department of Systematic and Evolutionary Botany, University of Zürich, for a period of four years. The position is to study the evolutionary consequences of interactions between plants and insects. Most studies on plant evolution use either an ecological approach to study mechanisms leading to future evolutionary change, or study patterns of past evolution using phylogenetic approaches. In this project, we will conduct experimental evolution using fast cycling Brassica plants to investigate real-time adaptation in plants. This approach has been proven highly successful in past experiments, and enables to study in detail the process of ongoing evolution. As selective, variable biotic environment, different communities of pollinators and herbivores will be used. During 5 generations, groups of plants will be under selection by these insects, and their adaptive evolution will be studied. Afterwards, selection treatments will be swapped to study the potential of plants to reverse their evolutionary trajectory, as required during adaptation in dynamic environments. Plant traits under adaptive evolution will be studied using selection analysis, phenotyping, as well as molecular and bioinformatics tools. The work will be primarily based in the greenhouse and lab. You should have a Master (or comparable) degree in any field of biology and a thorough interest in evolutionary biology. Prior experience with plants and/or insects is an advantage. Proficiency in English both orally and written is a must. The successful candidate will work in an exciting research environment focusing on patterns and process of plant evolution. Our department is located in the botanical gardens and houses modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zürich has a very broad coverage of organismal and molecular biology, and several research groups work on evolutionary topics (www.lifescience-zurich.ch). The city also offers excellent quality of life through cultural programs and infrastructure, as well as an attractive surrounding.

If you are interested in the job, please send me by e-mail (florian.schiestl@systbot.uzh.ch) a letter describing your motivation, C.V., copy of degrees, publications (manuscripts), and e-mail addresses of two academic referees, by 15th of January 2020. Please send all documents in a single file. If you have any further questions, don‘t hesitate to contact me.

Prof. Dr. Florian P. Schiestl Director, Department of Systematic and Evolutionary Botany and Botanical Gardens University of Zürich Zollikerstrasse 107 CH-8008 Zürich, Schweiz e-mail: florian.schiestl@systbot.uzh.ch Tel. +41 44 63 48409 Fax. +41 44 63 48403

“florian.schiestl@systbot.uzh.ch” <florian.schiestl@systbot.uzh.ch>

UZurich PlantEvolution

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

RESEARCH PROJECT: Plant symbiosis with nitrogen-fixing cyanobacteria is a unique form of mutualistic association. It has independently evolved in diverse, yet isolated lineages, from a few species of bryophytes, ferns, cycads, to a small genus of flowering plants. Compared to rhizobia, cyanobacteria are less dependent on the host, and therefore hold a promising translational potential toward installing nitrogen-fixing symbiosis onto crop plants. However, very little is known about the genetic regulation in plant-cyanobacteria symbiosis. The major difficulty to study such symbiosis had been the lack of tractable genetic systems for the host plant species. Because of this, most of the research has solely focused on the model cyanobiont Nostoc punctiforme, and how the plant partners initiate and maintain symbiosis still remains largely unknown. The recent groundwork by PI and project partners on hornworts, a group of bryophytes capable of cyanobacteria symbiosis, has made hornworts a promising model system. The complete genome of the hornwort Anthoceros agrestis is sequenced and annotated. More importantly, protocols for genetic transformation as well as targeted gene knockout have been developed. By leveraging the tractable systems established for both host (A. agrestis) and symbiont (N. punctiforme), this proposed research will take the first step to uncover the genetic underpinnings of plant-cyanobacteria symbiosis. This project has two specific objectives, aiming to identify the metabolites and the genes that are essential for symbiosis. The first objective focuses on the putative chemical signals exchanged during symbiosis initiation - the hormogonium inducing factor from the plant. The exact identities of this signal have been unknown, but will be determined using comparative metabolomics, structural analyses combined with a large-scale forward genetic screen. The second objective is to dissect the genetic control of symbiotic association through time course RNA-seq experiments. A systems approach will be taken to discover and prioritize candidate genes from both partners, and their functional involvements validated by reverse genetics. By integrating metabolomics, gene network analyses and genetic manipulations, this research will provide the first mechanistic overview on the interaction between hornworts and cyanobacteria, from the early communications to the symbiotic maintenance. The outcome will greatly complement what is known about plant interactions with rhizobia and AM fungi, and address whether the common symbiosis pathway also extends to cyanobacteria symbiosis. In addition, given the multiple origins of cyanobacteria symbiosis in plant tree of life, future work can build upon this hornwort study to examine other plant lineages, thereby testing if there is a unified molecular mechanism behind plant-cyanobacteria symbiosis. Furthermore, the essential genes and metabolites identified through this research will lay the foundation for future efforts to assess and design crop-cyanobacteria symbiosis.

This project is founded by a Swiss National Science Foundation (SNSF) grant to Peter Szovenyi. 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 metabolomic, reverse genetic and bioinformatic work and requires advanced skills in handling, analyzing and interpreting high-throughput metabolomic, next-generation sequencing and RNA-seq data. Good skills in assembling vectors, carrying out genetic transformations and microscopy are also required. 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 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 four 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 motivation, copies of relevant publications (published or submitted)

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VIB Gent PlantComputationalTools

The Comparative Network Biology lab, led by Klaas Vandepoele, of the VIB Center for Plant Systems Biology is home to an enthusiastic, diverse and international group of researchers in the field of plant bioinformatics. Beyond our expertise in plant genomics, comparative genomics and scientific creativity, we are looking for a new team member: PhD student 'Computational Tools for Network Biology in Plants'

Job description - Fully funded PhD position with the aim to obtain a doctorate at Ghent University. In this project, the candidate is expected to - i. develop new computational methods to accurately build gene regulatory networks in different plants (model species & crops) with varying levels of genome complexity - ii. develop and evaluate methods to translate networks between model and crop species using different experimental data sources - Reporting of results through publications in peer-reviewed international journals. - Attending and presenting your results at international scientific events. - Access to a diverse set of training programs at UGent / VIB (both scientific & soft skills)

Profile - MSc in Bioinformatics, Computer Science, Engineering, or similar. - Good programming (Python, JavaScript and/or PHP) and Linux skills are a must - Experience with tool/web-development (for example, JavaScript frameworks like React, Vue, of Angular) is a plus. - You are enthusiastic about scientific research, computational biology, and want to learn more about advanced biological concepts. - You have good communication and writing skills. - You are proficient in English.

How to apply? Submit your application online (https://vibvzw.jobsoid.com/j/23481/phd-student-computational-tools-for-network-biology-in-plants) and please include a letter of motivation, a detailed CV and contact info of 2 references (including e-mail addresses and phone numbers). Applications will be accepted until the position is filled.

Klaas Vandepoele - Professor Comparative Network Biology VIB-UGent Center for Plant Systems Biology Ghent University Technologiepark-Zwijnaarde 71 - 9052 Ghent - Belgium Tel. +32(0)9 331 38 22 www.psb.ugent.be Genome editing, cutting-edge technology for a sustainable agriculture

Klaas Vandepoele <Klaas.Vandepoele@psb.vib-ugent.be>

WageningenU CovertVirusInfectionsInInsects

PhD position: Hide and Seek: The transmission, mechanism and impact of covert virus infections in insects

We are recruiting a motivated PhD student to join the Laboratory of Virology, Wageningen University, the Netherlands, supervised by Dr. Vera Ros.

The project focuses on covert virus infections in insects: latent/persistent infections that do not cause any visible signs of disease. Insects are increasingly mass reared in large scale facilities due to a growing demand for insects for food and feed, biological pest control, pollination and waste management. This intensification leads to a rise in disease outbreaks that frequently result in a complete collapse of production systems. These outbreaks are caused by insect-specific pathogens, including viruses, that may already be present in a covert state within the reared insects. Such covert virus infections can suddenly develop into overt (symptomatic) infections under stress conditions. Within this project we aim to elucidate the (molecular) mechanisms underlying transmission and maintenance of covert virus infections in insects and to determine the impact of covert infections on host fitness and immunity. The project involves 2 PhD students, and the PhD student we are now recruiting for will mainly focus on the role of the host immune system, including RNA interference pathways, in maintaining the covert state. Furthermore, he/she will use molecular tools to verify identified mechanisms. As model system, baculoviruses infecting caterpillars will be used. The pathology of covert baculovirus infections has been intensively studied in larval stages, however, the effect of covert baculovirus infections and how these viruses are passed on throughout the host life cycle has received little attention.

The prospective PhD student will be part of a research team and will collaborate with other PhD students and postdocs on this project and related projects.

To apply and to see further information and requirements: https://www.wur.nl/en/vacancy/PhD-position-The-transmission-mechanism-and-impact-of-covert-virus-infections-in-insects.htm Dr. ir. Vera I.D. Ros Assistant Professor

Laboratory of Virology | Plant Sciences Group | Wageningen University | Droevendaalsesteeg 1 | 6708 PB Wageningen, The Netherlands | +31-317-484461 | vera.ros@wur.nl | www.vir.wur.nl "Ros, Vera" <vera.ros@wur.nl>

WesternWashingtonU EvolutionaryBiology

Masters of Science in Biology Western Washington University

The Biology Department at Western Washington University has openings for graduate students starting Fall 2020. Faculty members in the department offer a wide range of expertise, from molecular biology to ecology. Graduate students are eligible for teaching assistantships, which fund the majority of tuition and provide a stipend of $12,411 per academic year. WWU is located in Bellingham, WA, a coastal city north of Seattle at the base of Mt. Baker in the northwestern part of the state. We strongly advise interested students to contact potential advisors in their area of specialty to get more details about individual labs.

APPLICATION DUE DATE: Feb. 1, 2020

More information can be found at: The Biology Dept: https://cse.wwu.edu/biology/biology-graduate-program The WWU Graduate School: http://www.wwu.edu/gradschool/App_Reqs_Deadlines.shtml by contacting Dr. David Hooper, Biology Graduate Program Advisor, hooper at wwu.edu and by contacting the individual faculty, below.

Potential advisors

Shawn Arellano: Marine invertebrate larval ecology and deep-sea ecology. The Arellano lab has opportunities to study larval biology and larval ecology in deep-sea, methane-seep organisms as part of an NSF-funded project. Some sea-time will be required, and research training opportunities may include larval culturing and embryology, larval physiology and behavior techniques, use of oceanographic equipment, microscopy, and/or molecular ecology approaches. https://wp.wwu.edu/arellanolab/ Lina Dalberg: The Dahlberg Lab uses the model organism C. elegans to probe the neurobiological, cellular, and behavioral role for proteins involved in a ubiquitin-dependent processes called Endoplasmic Reticulum Associated Degradation (ERAD). Student projects will use a variety of techniques, including fluorescence microscopy, behavioral assays, and biochemical characterization to investigate how ERAD targets neural receptors for degradation. A second, NSF-funded project focuses on improving metacognitive skills in undergraduate Biology students; students interested in this project should have experience (via coursework or research) in education and pedagogy research. https://cse.wwu.edu/biology-faculty/dahlbec Deb Donovan: Research in the Donovan lab is focused on restoration aquaculture of our native pinto abalone, Haliotis kamtschatkana. Pinto abalone populations have declined precipitously in the last few decades and we collaborate with the Puget Sound Restoration Fund and with government agencies to restore populations in the Salish Sea. Student projects could focus on any aspect restoration, including optimizing rearing of juveniles at the hatchery, outplanting larval or juvenile abalone, or monitoring abalone at outplant sites. Students work closely with hatchery personnel to identify projects that align with student interest and that contribute meaningfully to abalone restoration. https://cse.wwu.edu/biology-faculty/donovad Nick Galati: Cilia are evolutionarily ancient, hair-like projections that generate hydrodynamic force and process extracellular information. Algae use undulating cilia to swim through and sample aqueous environments. Protists coordinate hundreds of cilia in a wave-like motion while relaying chemical information to the cell interior. Nematodes sniff around soil using cilia that sprout from sensory neurons. In vertebrates, one individual cilium protrudes from the cell surface. This cilium, called a primary cilium, acts like an antennae to relay signals from the extracellular environment, which influences cellular process such as cell division and migration. The goal of our lab is to understand how cells build cilia, with a specific focus on how individual proteins to traffic to and from a structure at the base of cilia, called the basal body. Much like traffic cameras and GPS illuminate vehicular traffic patterns, we aim to create a spatial map of protein movement to and from cilia as they assemble and sense the environment. To do this, we combine high-resolution fluorescence microscopy with digital image analysis to detect and quantify ciliary protein trafficking in space and over time. Our analyses are primarily conducted in mammalian cells and in the protist Tetrahymena. https://cse.wwu.edu/biology-faculty/galatid David Hooper: Plant Community and Ecosystem Ecology: effects of riparian restoration on nutrient retention in mixed use watersheds. I will be accepting one graduate student in fall 2020 to work on a modeling project

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WestvirginiaU PlantEvolution

The Barrett Lab in the Department of Biology at West Virginia University is seeking highly motivated Ph.D. or M.S. students for admission in Fall 2020. Our lab focuses on using genomic approaches to study systematics and evolution of plants, as well as plant-microbial interactions.

Specifically, we are looking to recruit two graduate students to join an NSF-funded project on the genomics of rapid adaptation in an invasive plant species, “Consortium for Plant Invasion Genomics (CPING): Combining Big Data and Plant Collections to Understand Invasiveness.” This is a highly collaborative project between universities in nearly all EPSCoR states, with focal hubs in five states (WV, LA, AL, KS, and SD). Multiple years of support for students is available.

Project: At WVU, we will focus on Japanese stiltgrass (Microstegium vimineum), a horrible invasive weed that threatens eastern US forests, yet presents a fascinating opportunity to study rapid evolution of invasiveness.

Research will involve: sequencing a high-quality reference genome; fieldwork and common garden experiments to study evolution in the invasive range; genotyping to study the number of invasions and gene flow dynamics across space and time using contemporary and herbarium specimens; evidence for adaptive polymorphisms; and the role of epigenetics (e.g. transposable elements) in invasiveness. In addition, our project will focus on a nationwide effort in the USA to train researchers in genomic and bioinformatic techniques.

Students with skills in field biology, genomic lab techniques, and bioinformatics are strongly encouraged to apply. Experience with computer scripting languages useful in bioinformatics (e.g., Python, Perl, R, or UNIX) is preferable.

Dr. Barrett's Google Scholar profile: https://scholar.google.com/citations?hl=en&user=zm0PEwYAAAAJ&view_op=list_works&sortby=pubdate Campus resources at WVU include: WVU Genomics Core Facility, housed in the Biology Department: http://genomics.as.wvu.edu/ High Performance Computing: http://it.wvu.edu/research/research-computing/high-performance-computing The WVU Evansdale Greenhouse Facility: https://www.davis.wvu.edu/about-davis-college/centers-initiatives/wvu-evansdale-greenhouse Fernow Experimental Forest: http://www.nrs.fs.fed.us/ef/locations/wv/fernow/ WVU Earl Core Arboretum: http://arboretum.wvu.edu/ WVU Herbarium: http://www.biology.wvu.edu/facilities/herbarium Ecotron and greenhouses: http://biology.wvu.edu/about/facilities/ecotron-and-greenhouses WVU and Morgantown: *West Virginia University* is a large, diverse university with R1 status. The *Department of Biology* has core research strengths including plant & microbial genomics, ecology, neuroscience, and other areas. *Morgantown* is a vibrant, diverse college town/small city, situated in the foothills of the Allegheny Mountains, ~1.5 hours from Pittsburgh, PA, and ~3 hours from Columbus, OH and Washington, D.C.

Outdoor activities abound in and around Morgantown, and throughout WV and neighboring MD, PA, and VA. Fishing, rafting, kayaking, hiking, skiing, biking, etc., are within a short drive of the city limits.

*Requirements and deadlines: While the Department of Biology has a rolling application and review process during the academic year, to be considered for nomination for university fellowships and scholarships, all application materials must be submitted online no later than December 1.

Application details can be found here: https://biology.wvu.edu/students/graduate-students/admission Some useful links: WVU Biology website: http://biology.wvu.edu/ WVU Graduate Education: http://graduate.wvu.edu/future-students/application-process/apply Please contact me (Craig Barrett, cfb0001@mail.wvu.edu); for questions about out graduate program, please contact or our graduate chair, Jennifer Hawkins (Jennifer.Hawkins@mail.wvu.edu).

WVU, the Department of Biology, and the Barrett Lab are committed to diversity: women, members of minorities, first-generation college students, students with disabilities, and veterans are strongly

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Jobs

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ArizonaStateU VertebrateCollectionsManager

Prior direct inquiries via email to nico.franz@asu.edu are strongly encouraged. Excerpts from full positing:

Research Specialist: Vertebrate Collections Manager and Co-Manager of Digital Data Collections

The School of Life Sciences at Arizona State University (https://sols.asu.edu/) is seeking a full-time Research Specialist who will act as Vertebrate Collections Manager and Co-Manager of Digital Data Collections. The relative weight of each task can vary, within boundaries, and depending on the candidate's particular research and curation interests and qualifications. The position is part of a dynamic, collaborative Biocollections and biodiversity informatics group of faculty, staff, students, volunteers, and other researchers that recently relocated into a unified, 24,000 sq. ft. facility. This new and highly accessible infrastructure is located ca. 2 miles from the main ASU Tempe Campus, and forms part of ASU's BioKIC 'V Biodiversity Knowledge Integration Center (https://biokic.asu.edu/). As of 2018, our facility and personnel also constitute the primary Biorepository for NEON, the National Ecological Observatory Network (https://biorepo.neonscience.org).

The ASU Vertebrate Collections focus mainly on documenting vertebrate diversity in the Southwest U.S. and Sonoran Desert Region; and comprise the following four collections. (1) Ichthyology Collection; built most prominently by Wendell Minckley, with 24,000 registered lots (70% online) and more than 1,000 stained specimens. (2) Herpetology Collection; with 36,000 specimens (90% online). (3) Ornithology Collection; with 1,000 specimens (80% online). (4) Mammalogy Collection; with 9,000 specimens (95% online). These research collections are complemented by teaching collections located in the same facility. They are now also being complemented by annual additions of 20,000 vertebrate specimens, samples, and DNA extractions being received and accessioned by the continental-scale NEON Biorepository. A related, 3,500 sq. ft. cryo collections infrastructure addition will be completed in 2020. Although the NEON Biorepository has independently supported personnel, curatorial and managerial responsibilities are frequently coordinated across all collections.

BioKIC is a leading promoter of the Symbiota software platform (http://symbiota.org/) and of related biodiversity data representation and analysis tools, and is involved in co-/managing and hosting an increasing range of biodiversity data portals that also feature vertebrate occurrence records. We therefore seek a candidate with a strong background and/or willingness to become highly skilled in biodiversity informatics, database and portal management, and digitization workflows. We also strongly encourage the candidate to develop an active field- and collections-based research program at a level commensurate with the position, and possibly including systematic, biodiversity inventory, and ecological forecasting-related themes. The successful candidate will work in close collaboration with curators, collection managers, students, and researchers affiliated with the Biocollections and the School of Life Sciences. Contributing to our diverse biodiversity/data learning programs is strongly encouraged. A wide range of applicant profiles will be considered.

For more information and to apply:

1. Go to https://cfo.asu.edu/applicant 2. Select "Non- / ASU employees" (as applicable) 3. Search for position "56752BR"

Nico M. Franz, Ph.D. Professor & Curator of Insects Founding Director - BioKIC Director of Biocollections

School of Life Sciences, PO Box 874108 Arizona State University, Tempe, AZ 85287-4108

Office: (480) 965-2036; Fax: (480) 965-6899 E-mail: nico.franz@asu.edu iSearch: https://isearch.asu.edu/profile/1804402 BioKIC: https://biokic.asu.edu/ Nico Franz <nico.franz@asu.edu>

CaliforniaStateU MontereyBay EvolutionaryBiology

Our department at California State University, Monterey Bay is currently looking for an evolutionary biologist with expertise in population genetics. If you're interested in coming to work at an inclusive, mid-sized minority-serving institution on the coast, please take a look at the job description (see below) and apply at https://csumb.peopleadmin.com/postings/5520, if you are interested.

Feel free to contact Aparna Sreenivasan (asreenivasan@csumb.edu)if you have any questions.

Job Announcement:

The Department of Biology and Chemistry in the College of Science at California State University, Monterey Bay seeks an evolutionary biologist with expertise in population genetics and strong computational skills to fill a tenure track assistant professor position. The applicant should be a dedicated teacher capable of successfully involving undergraduates in research. The successful candidate will work with other faculty to develop undergraduate curricula, professional outreach programs, and extramural research or programmatic funding. Additional information on the College and Biology Department can be found at https://csumb.edu/biologychemistry/biology-bs, the university and its vision at about.csumb.edu/vision-statement, and our exceptional undergraduate research program at uroc.csumb.edu.

RESPONSIBILITIES

- Teach upper division evolutionary biology & population genetics - Develop and teach upper division advanced evolutionary biology course (e.g. bioinformatics, systems biology, molecular ecology or a new upper division course in genomics or other computationally intensive branch of biology) - Develop and maintain a research program that provides opportunities for undergraduates - Occasionally teach genetics or help with lower division instruction - Contribute to the development of this growing department

MINIMUM QUALIFICATIONS

Ph.D. in biology or related field by the time of appointment Expertise in Evolutionary Biology Expertise in Population Genetics Demonstrated excellence in teaching

PREFERRED QUALIFICATIONS

- Expertise in a computationally intensive field of study that can be applied to projects suitable for the undergraduate research environment - Experience mentoring student research and/or internships - Desire and ability to teach and mentor students from diverse cultural, ethnic, educational, and economic backgrounds - A record of writing successful proposals for extramural funding - Experience with course and curriculum development

Powered by an inspiring Founding Vision Statement, California State University, Monterey Bay (WWW.CSUMB.EDU) is a comprehensive, mid-sized four-year university whose staff and faculty help transform student lives by emphasizing project-based learning, requiring service learning, and promoting multicultural and global perspectives on and beyond the campus community. CSUMB is both an MSI and HSI and has a vibrant, diverse student body of nearly 7000 students and growing. Our faculty and staff, many of whom live in campus housing, appreciate living and working about one mile from the shores of the beautiful Monterey Bay. As one of the 23 campuses in the California State University (CSU) system, we offer excellent benefits, including housing, and competitive salaries for our faculty and staff. During our 25th Silver Anniversary Celebration in 2019-20, we will complete two major building projects: the College of Arts, Humanities and Social Sciences and the Student Union. By 2030, CSUMB's sustainability initiative is to be carbon neutral.

Regards, Nate Jue

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Nathaniel K. Jue, Ph.D. Assistant Professor School of Natural Sciences California State University, Monterey Bay Seaside, CA 93955 www.csumb.edu/juelab Nathaniel Jue <njue@csumb.edu>

CityUNewYork EvolutionaryEcol

Assistant Professor in Urban Ecology at Queens College of The City University of New York

Job Title: Assistant Professor in Urban Ecology (tenure track)

Job ID: 21392

Location: Queens College of the City University of New York

Full/Part Time: Full-Time

Regular/Temporary: Regular

FACULTY VACANCY ANNOUNCEMENT

The Biology Department at Queens College CUNY invites applications for a full-time, tenure track Assistant Professor Position in Urban Ecology beginning September 1st, 2020. The successful candidate is expected to teach electives; participate in introductory courses; and develop advanced courses in his/her area of expertise. The candidate is also expected to establish an active research program, and share responsibilities for committees and other departmental functions. Candidates who use integrative approaches to conduct field and laboratory research in general ecology, evolutionary ecology, habitat restoration, and conservation biology with a strong urban focus preferred. The Biology Department's community includes 18 full-time faculty members, 35 Masters and PhD candidates, and approximately 250 Biology majors. For details of curricula, faculty research interests, and departmental resources, please log onto our website: https://www.qc.cuny.edu/academics/degrees/dmns/biology/Pages/default.aspx QUALIFICATIONS

The successful candidate should:

hold an earned doctoral degree or equivalent with doctoral or postdoctoral experience in urban ecology.

show evidence or promise of success as an educator at the college or university level.

provide evidence of scholarly achievements.

demonstrate the ability to design, carry out and support an active research program involving students and the potential to leverage external funding.

adopt novel approaches to asking questions in their field that assess multiple levels of organization (molecular, physiological, geographical, etc.).

demonstrate the ability to work with colleagues in research and carry out departmental functions.

COMPENSATION

CUNY offers faculty a competitive compensation and benefits package covering health insurance, pension and retirement benefits, paid parental leave, and savings programs. We also provide mentoring and support for research, scholarship, and publication as part of our commitment to ongoing faculty professional development.

CLOSING DATE

Open until filled with review in December 22, 2019

HOW TO APPLY

-Go to cuny.jobs

-In the box under “job title/ keyword”, enter “21392”

-Click on “Assistant Professor-Urban Ecology”

-Click on the “Apply Now” button and follow the instructions.

Please note that the candidates must upload a cover letter describing related qualifications and experience, resume, and the name and contact information of three (3) professional references as ONE DOCUMENT in any of the following formats: .doc, .docx, or .pdf format

**Please use a simple name for the document that you uploaded, for example: JDoecv (Documents with long names cannot be parsed by the application system.)

APPLY HERE: https://cuny.jobs/queens-ny/assistant-professor-in-urban-ecology/E5982896AEA247C6859F39D250C93056/job/ – John J. Dennehy, PhD Professor of Biology Deputy Executive Officer, Biology PhD Program Queens College and The Graduate Center of CUNY john.dennehy@qc.cuny.edu Office SB D322 (718) 997-3411 Lab SB D343 (718) 997-3419 dennehylab.org https://twitter.com/DrJDennehy John Dennehy <john.dennehy@qc.cuny.edu>

EarlhamCollege 1yr TeachingEvolution

Earlham College: Visiting Assistant Professor of Biology- Ecology, Evolution, and Environmental Science

Description

Earlham College invites applications for a biologist with teaching and research interests in ecology, evolution, and/or environmental science. This is a full-time, one-year appointment in the Biology Department as a visiting professor, possibly renewable for a second year depending on institutional needs. The position begins in August 2020.

The Department seeks an individual who is first and foremost excited about teaching'Xin lecture, seminar classes, laboratory, and research venues'Xto bright and motivated undergraduates in a student-focused department at a nationally ranked small liberal arts college.

Primary Duties and Responsibilities

Teaching responsibilities will include contributing to introductory courses in ecology, environmental science/sustainability, and biodiversity, and upper-level courses in the applicant'Âs area of expertise. Applicants who have an expertise in one or more of the following areas are especially attractive: population and community ecology, conservation, and field research. Typical course load is two courses with labs per semester (12 contact hours). For an expanded description of Earlham College and the Biology Department please visit: http://www.earlham.edu/biology Experience and Qualifications

A Ph.D. is required; teaching or post-doctoral experience is desired.

Application Instructions

Please send a single PDF that includes: (1) cover letter, (2) curriculum vitae, (3) statement of teaching philosophy, (4) statement of research interests, (5) statement on diversity and inclusion, and (6) contact information for three references that can speak to your teaching, research, and communication skills. References should be people who are able to respond (or produce a letter of recommendation) within 1 week after they are contacted.

Please send your application to Kim Allen, Biology Administrative Assistant (biology@earlham.edu). Please do not send application materials via postal mail.

Review of applications will begin on December 1, 2019 and continue until the position is filled.

For additional information, contact Dr. Wendy P Tori, Associate Professor of Biology at: toriwe@earlham.edu.

Earlham College is an Equal Opportunity Employer that seeks applications from candidates who contribute to diversity in terms of race, ethnicity, age, religious affiliation, gender, sexual orientation, gender identity, disability, and veteran status, among other distinctions and contributions. As a College with a Quaker identity, Earlham also is eager to solicit applications from members of the Religious Society of Friends (Quakers). Earlham utilizes E-Verify to confirm employment eligibility for all newly hired employees within the United States.

Wendy P Tori <toriwe@earlham.edu>

EarlhamC VisitingProf EcolEvolEnvSci

Job: EarlhamC.VisitingProf.EcolEvolEnvSci

Earlham College invites applications for a biologist with teaching and research interests in ecology, evolution, and/or environmental science. This is a full-time, one-year appointment in the Biology Department as a visiting professor, possibly renewable for a second year depending on institutional needs. The position begins in August 2020.

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A Ph.D. is required; teaching or post-doctoral experience is desired.

Please send a single PDF that includes: (1) cover letter, (2) curriculum vitae, (3) statement of teaching philosophy, (4) statement of research interests, (5) statement on diversity and inclusion, and (6) contact information for three references that can speak to your teaching, research, and communication skills. References should be people who are able to respond (or produce a letter of recommendation) within 1 week after they are contacted.

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Earlham utilizes [http://www.dhs.gov/e-verify | E-Verify] to confirm employment eligibility for all newly hired employees within the United States.

Lindsey Willett McGee <mcgeeli@earlham.edu>

GeorgeWashingtonU BiodiversityInformatics

Tenure-track Faculty Position in Biodiversity Informatics

Department of Biological Sciences

The George Washington University

The Department of Biological Sciences at the George Washington University (GWU) invites applicants for a tenure-track faculty position in* Biodiversity Informatics (data science)* at the rank of Assistant Professor, to begin as early as the Fall 2020 Semester. We encourage a broad array of applicants working with big data, including but not limited to: i) artificial intelligence applied to biological systems; ii) -omics (genomics, transcriptomics, metabolomics, phenomics, etc.); and iii) evolutionary, ecological, environmental, and global change biology. The successful candidate will complement our existing strengths in multidisciplinary research areas such as Systematics, Evolution, Evo-Devo, Cellular and Molecular Biology, Ecology, Behavior, and Conservation. They will be expected to establish and maintain an externally funded research program comprising graduate and undergraduate students. Teaching duties include undergraduate courses that contribute towards the new undergraduate curriculum in Data Science as well as upper division Biology electives in their area of expertise. We encourage applications from individuals with identities historically underrepresented in STEM, and those who have experience working with diverse student populations.

Office space and start-up funding will be provided. As a computational investigator, no dedicated laboratory space is available, but collaborative opportunities in shared spaces will be available as needed. Institutional resources at GWU include a high-performance computing center, greenhouse, core facilities in genomics, imaging, nano-fabrication, histology, and flow-cytometry. Our location in Washington DC offers superior undergraduate and graduate learning opportunities through access to the GW Computational Biology Institute, the Smithsonian Institution, the National Institutes of Health, and a consortium of universities in the DC area.

Required Qualifications: A completed PhD and postdoctoral training in biological sciences, computer science, mathematics or related fields as well as research accomplishments that integrate biology and data science, as demonstrated by peer-reviewed publications in high quality journals.

Application Procedure: To be considered, complete an online faculty application at http://www.gwu.jobs/-postings/71787 and upload the following documents: (i) cover letter describing interests and qualifications for the position; (ii) curriculum vitae including a full list of publications; (iii) brief research and teaching statements; (iv) three recent publications; (v) diversity statement that highlights past experiences and future plans related to supporting a diverse and inclusive educational community; (vi) and include the names and contact information of three referees. Letters of recommendation from referees will be requested at a later stage for candidates advancing to the second stage of the process. Only complete applications will be considered.

Review of applications will begin on December 4, 2019 and continue until the position is filled, pending final budgetary approval. Employment offers are contingent on the satisfactory outcome of a standard background screening.

The George Washington University is an Equal Employment Opportunity/Affirmative Action employer that does not unlawfully discriminate in any of its programs or activities on the basis of race, color, religion, sex, national origin, age, disability, veteran status, sexual orientation, gender identity or expression, or on any other basis prohibited by applicable law.

Please contact Dr. Alex Pyron (rpyron@gwu.edu) with any questions.

Alex Pyron <rpyron@colubroid.org>

HolarU Iceland QuantGenetics

Assistant professor- position available in the dept. of Aquaculture and Fish Biology

Hólar University's Department of Aquaculture and Fish Biology invites applications for the full time position of an Assistant Professor. We are seeking a highly qualified individual with knowledge and experience in the field of quantitative genetics, ideally with knowledge on animal breeding and aquaculture.

A successful applicant will: - Teach undergraduate and graduate students - Conduct research in their field and supervise graduate students - Take active part in the scientific aspects of the selective breeding program of Icelandic Arctic charr, hosted by the department - Participate in international projects and collaboration - Take active part in the quality work and administration of the Department and the University

Requirements regarding education and qualifications: - Doctoral degree in the field of biology and preferably in quantitative genetics - Experience in research on quantitative genetics, e.g. related to broodstock management and selection - Experience in securing research funding - Good publication track record - Good human relations skills and the ability to collaborate in a modern academic environment - Responsibility, initiative, independent work and organizational ability

The Department of Aquaculture and Fish Biology at Hólar University offers a diploma program in aquaculture and a Master's program in aquatic biology, as well as a Nordic Master's program in Sustainable Production and Utilisation of Marine Bio-resources. In addition, the department staff teaches specialised topics in aquaculture, as a part of the United Nations University's Fisheries Training Program. Furthermore, academic staff in the department supervises PhD and research internship students, mostly from abroad. The department has a strong research profile and is responsible for the national selective breeding program of Arctic charr for Icelandic aquaculture companies. The department has offices and research facilities in VeriÃº in SauÃºárkrókur and on campus at Hólar. The community in Hólar is family friendly, boasts a wealth of history and natural beauty and provides opportunities for different outdoor recreational activities. See www.holar.is and www.holaraquatic.is.

The evaluation of academic merits will be in accordance with the Act on Public Universities No. 84/2008 and regulations on recruitment and promotion of academic staff at Hólar University. Salary is in accordance with the current collective wage and salary agreement between the relevant union, and the Minister of Finance. Otherwise, rights and obligations follow the Act 70/1996 on the Rights and Obligations of Civil Servants.

This is a full time position. Application deadline is December 27th, 2019 and it is preferred that the person hired will be able to start as soon as possible. For further information, please contact the Head of Department of Aquaculture and Fish Biology, Prof. Bjarni Kristófer Kristjánsson, +(354) 455-6386, bjakk@holar.is

Applications should be sent by email to umsoknir@holar.is and marked "Assistant professor aquaculture ". The application should include copies of academic records, CV and copies of publications the applicant wishes to be considered. A cover letter describing previous experience in teaching and research, is required. Furthermore, the cover letter should include ideas for future research and research collaboration. The applicant shall secure references from two individuals that should be sent to the above mentioned email address.

All applicants will be informed when the hiring process is over.

– Dr. Bjarni K. Kristjánsson, Prófessor Hólaskóli - Háskólinn á Hólum/ Hólar University Hólar í Hjaltadal Iceland bjakk@holar.is Phone: +354 4556300 holar.is

Bjarni Kristófer Kristjánsson <bjakk@holar.is>

JohannesGutenbergU SocialEvolution

Job advertisement

The Faculty 10 Biology, Institute of Organismic and Molecular Evolution, Department Behavioral Ecology and Social Evolution at the Johannes Gutenberg University of Mainz is looking for an

Assistant Professor / Junior Group Leader (Akademischer Rat at a University / Bes.Gr. A 13 BBesG) (m/f/d)

Evolution, Behavioral Ecology and / or Genomics of (Social) Insects Reference-No.: 18619-10-A13-ml

starting February 1st 2020 or later.

Employment will be as a civil servant, for initially for 3 years with the possibility of extensions (12-year rule applies).

In case the prerequisites of civil service are not fulfilled, an engagement as a Scientific Assistant (EG 13 TV-L) is possible. More information on potential contract length and conditions can be given upon request. The earliest start of the position will be February 1st 2020, preferably no later than 15.4.2020.

The research focus of the department under the direction of Prof. Dr. Susanne Foitzik lays within evolutionary biology and behavioral ecology of social insects. Our international research team consists of four groups working on the evolution, behavior, transcriptomics, chemical ecology of social insects (https://www.blogs.uni-mainz.de/fb10-evolutionary-biology/research-groups/) and collaboration with the other groups at the department are desirable. Scientific interactions or integration within the Research Training Group ???Gene regulation in Evolution??? (https://www.imb.de/about-imb/joint-research-initiatives/genevo/) would be advantageous.

We are seeking a highly motivated young researcher with a strong background in evolution, behavior and / or genomics to establish a junior research group within the Department of Behavioral Ecology and Social Evolution. Candidates must hold a Ph.D. and postdoctoral experience is necessary. The successful candidate should address evolutionary, behavioral ecological or genomic questions on insects, preferentially social insects. Scientific experience with the newest genetic methods (e.g. Next-Gen Seq, transcriptomics, Genomics, Proteomics. Microbiome, Metabolomics) including bioinformatic analyses is advantageous.

Excellent research conditions are available at new Biocenter I of the JGU with ???State of the Art??? genetic and chemical laboratories in Mainz. Furthermore, several new climate chambers are available for animal maintenance and controlled experiments. A small start-up package may be possible. A NextGen sequencing facility is available on campus. For further information, please contact foitzik@uni-mainz.de.

The successful candidate should have an excellent publication record. Experience with grant acquisition and teaching is advantageous. The candidate should set-up an independent, competitive research group and is encouraged to apply for grants in Germany or the EU (e.g., DFG, ERC). The position comes with a teaching requirement of 4 h per week during the semester in the Master and Bachelor programs. The candidate has the option to acquire a ???Habilitation???. The working language of the lab is English.

Requirements of appointment:

University degree and a PhD in biology (or related field)

a full-time employment of at least two years and six months after university education

The Johannes Gutenberg-University Mainz is interested in increasing the number of women in science. Applications from female scientists are strongly encouraged. Similarly, qualified candidates with disabilities will be preferred.

The University of Mainz (http://www.unimainz.de/-eng/) hosts many excellent scientific institutions, including theInstituteofMolecularBiology(IMB,www.imb-mainz.de) and Mainz is a historic city located on the Rhine River with many students and a rich social and cultural life (http://www.mainz.de/WGAPublisher/-online/html/default/hpkr-5nkek8.en.html).

Interested candidates should send an application (as a single e-mail pdf attachment) containing a CV, a list of publications (including reprints of the three most important publications), research and teaching statements, and contact information of two potential referees to:

Email: foitzik@uni-mainz.de Prof. Dr. Susanne Foitzik Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Biozentrum Hanns Dieter H??sch Weg 15 D-55128 Mainz Germany Tel: +49 (0) 6131 39 27 840

Closing date for the application is November 20th, 2019. Earliest possible starting date is February 1st 2020, later starting dates are negotiable, but participation in teaching during the summer semester 2020 (end April to July) is expected.

Prof. Dr. Susanne Foitzik

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LouisianaStateU QuantitativeBiology

The Department of Biological Sciences and the Center for Computation and Technology at Louisiana State University jointly invite applications for a tenure-track Assistant Professor in Quantitative Biology. The ideal candidate is a biologist conducting hypothesis-driven research using innovative approaches to large-scale analysis. The position is open to all areas of biology, preference will be given to those candidates who actively develop cutting-edge data science techniques including, but not limited to, informatics, data mining, machine learning, artificial intelligence, statistics, and large-scale data visualization. This hire is part of a larger initiative to establish a university-wide program in Interdisciplinary Data Science.

To apply, please visit: https://lsu.wd1.myworkdayjobs.com/LSU/job/LSU—Baton-Rouge/Assistant-Professor–Biological-Sciences-_R00040207 Deadline: 15 November 2019

Brant C Faircloth <brant@lsu.edu>

Madrid BiodiversityEvolution

The Complutense University of Madrid has announced its Plan for Strengthening Departments 2019 (https://www.ucm.es/aefortalecimiento2019), which includes a call for permanent positions for people with an accreditation for teaching at Spanish Universities (Contratado Doctor or higher) and owning the Spanish I3 certification.

The research group Evolutionary Biology and Conservation (www.ucm.es/bcveng) will support competitive candidates, as it has done successfully in previous editions of this and other programs directed to the attraction of talented researchers. Unfortunately, only one proposal per Department is accepted this year. For this reason, we are looking for candidates with competitive CVs (in terms of scientific production, leadership and internationalisation) who can send us their proposals as soon as possible (by sending their CV to jperez@ucm.es no later than December 5, 2019), so that we can score them in the Department.

Javier Pérez-Tris

–

Javier Pérez-Tris Departamento de Biodiversidad, Ecología y Evolución Universidad Complutense de Madrid Tel.: (+34) 91 394 4949 E-mail: jperez@bio.ucm.es Web: http://www.ucm.es/perez-tris La información contenida en este correo es CONFIDENCIAL, de uso exclusivo del destinatario/a arriba mencionado. Si ha recibido este mensaje por error, notifíquelo inmediatamente por esta misma vía y proceda a su eliminación, ya que ud. tiene totalmente prohibida cualquier utilización del mismo, en virtud de la legislación vigente.

Los datos personales recogidos serán incorporados en la actividad de tratamiento 'Correoweb', bajo la titularidad del Vicerrectorado de Tecnologías de la Información, y en él el interesado/a podrá ejercer los derechos de acceso, rectificación, supresión u oposición ante el mismo (artículos 15-21 del Reglamento UE 2016/679 de 27 de abril de 2016).

Antes de imprimir este correo piense si es necesario: el medio ambiente es cosa de todos.

This message is private and confidential and it is intended exclusively for the addressee. If you receive this message by mistake, you should not disseminate, distribute or copy this e-mail. Please inform the sender and delete the message and attachments from your system, as it is completely forbidden for you to use this information, according to the current legislation. No confidentiality nor any privilege regarding the information is waived or lost by any mistransmission or malfunction.

The personal data herein will be collected in the file "Correoweb", under the ownership of the Vice-Rectorate for Information Technologies, in which those interested may exercise their right to access, rectify, erasure or right to object the contents (article 15-21 of Regulation (EU) 2016/679, General Data Protection Regulation).

Before printing this mail please consider whether it is really necessary: the environment is a concern for us all.

JAVIER PEREZ TRIS <jperez@bio.ucm.es>

MainzU Germany EvolutionayGenomics

The Faculty of Biology of Johannes Gutenberg University Mainz invites applications for the position of a Junior Professor for Evolutionary Genomics

(Bes.Gr. W 1 LBesG with tenure track leading to a W 2)

available at the Institute of Organismic and Molecular Evolution (iomE) at the earliest opportunity.

We are seeking an ambitious early-career scientist in the field of evolutionary genomics.

The research focus should be in the area of population genomics or the molecular basis of evolutionary adaptations (in fields such as coevolution in biotic interactions, phylogenomics, genome evolution, evolutionary epigenetics, or the molecular evolution of aging).

The successful candidate is expected to develop an independent and internationally visible research program, supported by sustained extramural funding.

She/he will be embedded in a highly collaborative environment including the three institutes of the Faculty of Biology (http://www.bio.uni-mainz.de/-33_ENG_HTML.php), the research training group GenEvo ("Gene Regulation in Evolution: From Molecular to Extended Phenotypes"; https://www.bio.uni-mainz.de/koordinierte-forschungsprojekte), the SFB 1361 ("Regulation of DNA Repair and Genome Stability; https://www.sfb1361.de/), the Institute of Molecular Biology (IMB; www.imb-mainz.de), the Institute of Biotechnology and Drug Research (IBWF; www.ibwf.de), and other faculties of the natural sciences at Johannes Gutenberg University, as well as the Rhine Main Universities alliance (RMU) with Frankfurt and Darmstadt).

Contributions to the Bachelor and Master in Biology as well as Molecular Biotechnology are expected. The teaching load of W1 professors is reduced compared to tenured professors. Depending on the candidate's qualification and research direction, the associated budget for staff and running costs may considerably exceed the resources normally associated with a junior professorship. A formal association with the Institute of Molecular Biology may be possible. Furthermore, the successful candidate is expected to actively involve himself/herself in academic administration. The professorship is funded by the Tenure Track program of the German federal and state governments. Researchers early in their careers are therefore particularly encouraged to apply.

Applicants must meet the general requirements according to public services law and the Higher Education Act of Rhineland Palatinate (ç 54 Hochschulgesetz - Higher Education Act). The initial contract will run for three years and will be extended for another three years contingent upon a successful interim evaluation. After a final successful evaluation after six years and provided that the general requirements are fulfilled, the candidate will qualify for the appointment to a tenured full professorship (W2).

The State of Rhineland-Palatinate and JGU are committed to intensive personal mentoring for students and, therefore, expect a strong presence of teaching staff at the University. JGU aims to increase the quota of women in research and teaching, and hence encourages female scientists to apply. Disabled candidates with appropriate qualifications will be given priority. Collaborative research management and scientific leadership have become increasingly important in the academic context. For this reason, the Johannes Gutenberg-University has developed general leadership principles (www.personalentwicklung.uni-mainz.de/985.php).

Applications including the usual documents (e.g. CV; copies of certificates; lists of publications and teaching activities; funding record; current research and future research plans; teaching concept) as a single PDF file and separately the form available at www.bio.uni-mainz.de/-1517_ENG_HTML.php should be submitted in electronic form no later than December 11th, 2019 to the Dean, Faculty of Biology (biologie@uni-mainz.de).

Informal requests can be directed to the chairperson of the search committee (Prof. Dr. Martin Kaltenpoth; mkaltenpoth@uni-mainz.de).

You will find the information on data protection in dealing with your application at: https://-www.verwaltung.personal.uni-mainz.de/files/2019/-10/Datenschutz-Bewerber.pdf Job offers and further information also on the Internet: www.verwaltung.uni-mainz.de Prof. Dr. Susanne Foitzik Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Biozentrum Hanns Dieter Hüsch Weg 15 D-55128 Mainz Germany Tel: 49 (0) 6131 39 27 840

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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

Norwich UK ProtistGenomics

Senior Research Assistant / Senior Scientist (Protist Genomics)

Applications are invited for a Senior Research Assistant / Senior Scientist in protist genomics to support the Darwin Tree of Life project at the Earlham Institute (EI), based in Norwich, UK.

Background:

This exciting position forms part of theDarwin Tree of Life Projectto provide high-quality genome assemblies for all eukaryotic species in the British Isles. EI, along with the University of Exeter, will be leading the analysis of protists (single-celled eukaryote) genomes. Protists are often referred to as 'biology's dark matter' as there is so little known about their biology and biodiversity. There are potentially millions of species, yet very few have been described. The project aims to pilot new methods to sample protist biodiversity in the UK and use comparative genomics tools to study the ecology and biology of these enigmatic organisms.

The role:

This role will develop, validate and apply high-throughput methodologies for large-scale sequencing of protist genomes, including cell sorting and automated library preparation, and providing continuous improvements and extensions to current systems; this will involve translating single-cell methodologies into robust, production-scale protocols and generate high-quality data using these protocols.

Candidates with substantial relevant experience will be considered for the Senior Scientist post, at grade SC5. Candidates at an earlier stage in their career will be considered for the Senior Research Assistant post, at grade SC6.

The ideal candidate:

Applicants should possess a PhD or equivalent experience in molecular biology anda good understanding of modern DNA sequencing technologies. Experience in the preparation of next-generation sequencing (NGS) libraries, laboratory automation, and validation of new protocols is essential. Experience in single-cell and/or microbial genomics would be advantageous.

The ideal candidate for the Senior (grade SC5) post will also be familiar with tools and algorithms used for analysis of next-generation sequencing (NGS) data, and have demonstrable experience with fluorescence activated cell-sorting (FACS) analysis platforms and single-cell genomics and/or method development in a genomics context.

Additional information:

Appointments made at the Senior Research Assistant level (grade SC6) will attract an annual salary of 31,625 - 38,575. Appointments made at Senior Scientist level (grade SC5) will attract an annual salary of 39,990 - 48,775. Salaries are dependent on qualifications and experience. This is a full-time post for a period of 3 years.

We welcome applications from candidates seeking part-time or other flexible working arrangements.

Interviews will be held on 12 December 2019.

For further information and details of how to apply, please visit our web site http://jobs.earlham.ac.uk/ or contact the Human Resources team on 01603 450462 or nbi.recruitment@nbi.ac.uk quoting reference 1003808.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

The closing date for applications will be 3 December 2019.

Many thanks,

Steph

Stephanie Coker HR Advisor (Recruitment) Human Resources

NBI Partnership Colney Norwich NR4 7UH

Internal Extension: 2149 Direct Line: 01603 450149

"Stephanie Coker (NBI)" <Stephanie.Coker@nbi.ac.uk>

PrincetonU Panama FieldAssistantsForGreaterAniProject UPDATE

Greetings!

*Please note: Regarding the posting "Job: PrincetonU_Panama.FieldAssistantsForGreaterAniProject ". Due to the high volume of applications received from qualified applicants, we will stop accepting applications for the position after 8 PM EST on 13 November 2019. We apologize if this causes any inconvenience for interested potential applicants, but in order to allow adequate processing time for the large number of submissions received, we have decided the best course of action was to close the submission period prematurely. Thank you for your understanding.

Announcements for the position can be found here: https://wfscjobs.tamu.edu/jobs/field-assistants-greater-ani-project-bci-panama/ https://ornithologyexchange.org/jobs/board/short-term-positions/field-assistants-wanted-for-study-of-greater-ani-behavioral-ecology-for-six-weeks-in-early-2020-r16174/ Cheers, Josh

Joshua B. LaPergola, M.S., Ph.D. Postdoctoral Research Associate in the Riehl Lab Department of Ecology and Evolutionary Biology Princeton University

jl101@princeton.edu; jbl96@cornell.edu personal research site: https://sites.google.com/site/joshlapergola/ Riehl Lab: https://www.christieriehl.com/ Please consider the environment before printing this e-mail or any unimportant document.

“For in the end, our society will be defined not by what we create, but by what we refuse to destroy.” - John C. Sawhill, 2000

“jl101@princeton.edu” <jl101@princeton.edu>

PrincetonU Panama FieldAssistants GreaterAniProject

Field assistants wanted for study of Greater Ani behavioral ecology for six weeks in early 2020!

Two field assistants needed for a six-week study of Greater Ani behavior in central Panama. Field research assistants will primarily participate in adult capturing efforts over an intensive six-week season. Duties will include (but are not limited to) assisting with mist-net set up and operation, processing (color-banding, measuring, etc.) adult Greater Anis, gear maintenance and repair, data entry and management, and occasionally re-sighting banded birds. We are currently looking for:

- Two assistants available to arrive in Panama on January 13, 2020, and depart on February 25, 2020. Applications will be accepted until positions are filled, but preference will be given to those submitted by 18 November.

Location: Barro Colorado Nature Monument, including Barro Colorado Island (BCI; central Panama), Smithsonian Tropical Research Institute. Researchers and assistants will be housed on BCI in Smithsonian facilities.

Job description: The Greater Ani (Crotophaga major) is a cooperatively breeding Neotropical cuckoo with a unique social system: each breeding group consists of up to 10 individuals (typically between 2 and 4 socially monogamous pairs, plus 0-2 nonbreeding “helpers”), which construct a single nest in which all of the females lay their eggs. The Riehl lab at Princeton University has been intensively studying the breeding biology of the Greater Ani in the Barro Colorado Nature Monument since 2006.

Our work will occur during the non-breeding season, with the primary goal of capturing and color-banding as many adult anis as possible. Although preparation and data entry will occur in lab space provided on BCI, nearly all capture efforts will be accomplished via boat. Our primary means of capturing adult anis is to set mist-nets around group and communal roosts so that we can catch birds as they come into roost each night. Because Greater Anis roost primarily in aquatic vegetation or vegetation overhanging water, most nets need to be placed in water. To put it bluntly: you haven’t really mist-netted until you’ve done it from a boat. Setting and operating the nets can be quite challenging so either extensive previous experience with mist-netting, operating a small motorboat in waters similar to those of the Barro Colorado Nature Monument (i.e., lots of submerged stumps to navigate around), or both would position a field assistant for success in this job.

Dates: Start- 13 January, End- 25 February (~6 weeks)

Salary: Airfare to/from Panama and research-related travel within Panama (i.e., getting to/from the airport and the field site) will be covered. Room and board are also fully covered during your stay at the field site. The BCI field station provides primarily dorm-style housing and three meals a day, seven days a week. A small weekly stipend is provided for highly qualified applicants.

Deadline: Preference given to applications received on or before 18 November.

Qualifications: Those with previous field experience, especially those who have achieved competency in mist-netting, and a strong interest in bird behavior are highly preferred. Other important qualifications include: 1. willingness to work long hours in tropical conditions (that means buggy, sweaty, muddy, and often wet), 2.

ability to get along well with and be respectful of others in a relatively cramped environment, 3. ability and willingness to work jointly in the field and to work in an area where encounters with venomous invertebrates are a real possibility (there are plenty of bees, wasps, and ants; some venomous snakes but not usually encountered while we're working), 4. good color vision (essential for distinguishing color-bands), 5. Spanish language competency is helpful but not required, 6. Applicants must have a strong interest in field research as a possible or definite career goal, 7. Field assistants must have a valid passport, 8. Must be able to swim and comfortable working on a boat, and 9. International applicants welcome!

Additional Desired Skills: Experience operating a motorboat of ~5 m in length. Greater Anis nest along shorelines of lakes and rivers, and all the birds we are attempting to catch live along the waterways of the Barro Colorado Nature Monument.

Application instructions: Please send the following: 1) a cover letter (~1 page) detailing your interests and career goals and how you see this position fitting in with them, 2) a resume or CV (please keep to relevant details), 3) the names and contact information (email and phone) of 3 references (ideally with some experience with how you work in a research/field context). Please also indicate the nature of your professional relationship to EACH reference (e.g., field supervisor, academic advisor, professor for a class, etc.).

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QueensU EvolutionaryGenetics

Department of Biology, Queen's University - Molecular Genetics - Assistant Professor

The Department of Biology at Queen's University invites applications for a Tenure-track faculty position at the rank of Assistant Professor with specialization in molecular genetics, with a preferred start date of July 1, 2020.

Queen's is a research-intensive university, with an integrated Biology Department using observational, experimental, and theoretical approaches to address questions on topics from molecules to ecosystems. The department seeks a broadly-trained, molecular geneticist conducting research on any organism. Examples of research areas could include, but are not limited to: developmental biology, genomics and related fields, metabolism, neurobiology, stress biology, or synthetic biology. The successful candidate will complement and broaden the department's existing strengths and expertise and will contribute to teaching in genetics, molecular biology, and related fields. Applicants with a versatile approach and/or strong potential for collaboration with colleagues from diverse fields of biology are especially encouraged to apply.

Candidates must have a PhD or equivalent degree completed at the start date of the appointment. The main criteria for selection are academic and teaching excellence. The successful candidate will provide evidence of high quality scholarly output that demonstrates potential for independent research leading to peer assessed publications and the securing of external research funding, as well as strong potential for outstanding teaching contributions at both the undergraduate and graduate levels, and an ongoing commitment to academic and pedagogical excellence in support of the department's programs. Candidates must provide evidence of an ability to work collaboratively in an interdisciplinary and student-centred environment. The successful candidate will be expected to make contributions through service to the department, the Faculty, the University, and/or the broader community. Salary will be commensurate with qualifications and experience.

People from across Canada and around the world come to learn, teach and carry out research at Queen's University. Faculty and their dependents are eligible for an extensive benefits package including prescription drug coverage, vision care, dental care, long term disability insurance, life insurance and access to the Employee and Family Assistance Program. You will also participate in a pension plan. Tuition assistance is available for qualifying employees, their spouses and dependent children. Queen's values families and is pleased to provide a 'top up' to government parental leave benefits for eligible employees on maternity/parental leave. In addition, Queen's provides partial reimbursement for eligible daycare expenses for employees with dependent children in daycare. Details are set out in the Queen's-QUFA Collective Agreement. For more information on employee benefits, see Queen's Human Resources.

Additional information about Queen's University can be found on the Faculty Recruitment and Support website. The University is situated on the traditional territories of the Haudenosaunee and Anishinaabe, in historic Kingston on the shores of Lake Ontario. Kingston's residents enjoy an outstanding quality of life with a wide range of cultural, recreational, and creative opportunities. Visit Inclusive Queen's for information on equity, diversity and inclusion resources and initiatives.

The University invites applications from all qualified individuals. Queen's is committed to employment equity and diversity in the workplace and welcomes applications from women, visible minorities, Aboriginal peoples, persons with disabilities, and LGBTQ persons. All qualified candidates are encouraged to apply; however, in accordance with Canadian immigration requirements, Canadian citizens and permanent residents of Canada will be given priority.

To comply with federal laws, the University is obliged to gather statistical information as to how many applicants for each job vacancy are Canadian citizens / permanent residents of Canada. Applicants need not identify their country of origin or citizenship; however, all applications must include one of the following statements: "I am a Canadian citizen / permanent resident of Canada"; OR, "I am not a Canadian citizen / permanent resident of Canada". Applications that do not include this information will be deemed incomplete.

In addition, the impact of certain circumstances that may legitimately affect a nominee's record of research achievement will be given careful consideration when assessing the nominee's research productivity. Candidates are encouraged to provide any relevant information about their experience and/or career interruptions.

A complete application consists of:

- a cover letter (including one of the two statements regarding Canadian citizenship / permanent resident status specified in the

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SGN Frankfurt ApterygotaCurator

Job posting ??? Ref. #08-19013

For over 200 years the Senckenberg Gesellschaft f??r Naturforschung (SGN) represents one of the most relevant institutions investigating nature and its diversity. Currently, scientists from more than 40 countries across 11 locations in Germany conduct research in the fields of biodiversity, earth system analysis and climate change.

The Senckenberg Society for Nature Research intends to fill at the Department of Soil Zoology of the Senckenberg Museum of Natural History in G??rlitz, Germany, the position of a

Curator of Apterygota (m/f/d)

(full time)

Your tasks:

?? Assume responsibility for the management and curatorship of the collection of apterygote insects

?? Developing and expanding the collection of apterygote insects, especially Collembola in G??rlitz

?? Conduct collection-based research on the biology of soil organisms with a focus on Collembola

?? Initiate and manage research projects and actively participate in joint projects with other scientists at the department of soil zoology, and beyond

?? Acquisition of third-party funding

?? Developing Edaphobase, the international database on soil invertebrates

?? Actively publish results of your and the department??s research in higher-ranked international scientific journals

?? Academic education of students and supervise practical work in the course of their academic qualification

?? Participation in the publication of scientific journals

?? Participation in activities of the Science and Society program of Senckenberg

Your profile:

?? Doctoral degree in zoology or related field

?? Excellent knowledge of integrative taxonomy and systematics of Collembola and/or analysis concerning environmental influences on Collembolan communities

?? Outstanding research record in biology of Collembola, documented by publications in international peer-reviewed scientific journals

?? Knowledge in (functional) character traits of Collembola

?? Experience in curating and managing zoological collections and databases

?? Knowledge in molecular taxonomy and population genetics would be desirable

?? Interest in collection-based research

?? Experience in the acquisition of third-party funding

?? Fluency in English both spoken and written; good knowledge of German would be an advantage

?? Motivation, engagement and willingness for independent scientific work, teamwork and willingness to lead a subordinate staff

What is awaiting you?

?? An attractive and challenging position in a research institution of international standing

?? A salary that reflects the tasks and responsibilities of the position based on the collective agreement for public service in the state of Saxony (TV-L E 13)

?? Flexible working hours ??? annual special payment ??? company pension scheme ??? 30days holidays

The contract should start as soon as possible and will be initially limited. The Senckenberg Research Institutes support equal opportunity of men and women in management positions and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is G??rlitz, Germany. The employer is the Senckenberg Gesellschaft f??r Naturforschung.

You would like to apply?

Please send your application documents, mentioning the reference of this job offer (Ref. #08-19013) before January 15th, 2020 by e-mail (attachment in a single pdf document), to:

Senckenberg Gesellschaft f??r Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

For more information, please contact Prof. Dr. Willi Xylander, phone: +49 3581 ??? 4760 ??? 5100.

Stellenausschreibung - Ref. #08- 19013

Die Senckenberg Gesellschaft f??r Naturforschung (SGN) wurde 1817 gegr??ndet und z??hlt zu den wichtigsten Forschungseinrichtungen rund um die biologische Vielfalt. An den elf Standorten in ganz Deutschland betreiben Wissenschaftlerinnen und Wissenschaftler aus ??ber 40 Nationen modernste Forschung auf internationaler Ebene. Am Standort G??rlitz befindet sich das Senckenberg Museum f??r Naturkunde inmitten der historischen Altstadt.

F??r ihren Standort in G??rlitz ???Museum f??r Naturkunde??? in der Abteilung Bodenzoologie sucht die Senckenberg Gesellschaft f??r Naturforschung mit Hauptsitz in Frankfurt am Main zum n??chstm??glichen Zeitpunkt eine/n

Sektionsleiter (m/w/d) f??r Apterygote Insekten (Vollzeit)

Ihre Aufgaben:

?? Leitung der Sektion Apterygota in der Abteilung Bodenzoologie

?? Entwicklung des Sammlungs- und Forschungsprofils der Sektion

?? Forschungst??tigkeit zur Gemeinschafts??kologie von Bodentieren sowie zur Systematik von Collembola

?? Wissenschaftliche Betreuung, Bearbeitung und Entwicklung der bedeutenden Sammlung ???Apterygote Insekten??? am SMNG

?? Initiierung und Leitung von Forschungsprojekten und aktive Beteiligung an gemeinsamen Forschungsprojekten der Abteilung

?? Einwerbung von Drittmitteln

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SouthAfrica StationManager StripedMouseProject

Please poste the following for me on evoldir. Thanks a lot, Carsten

1 position as station manager (starting February 2020)

1 position as research manager (starting August 2020)

at the striped mouse project in South Africa

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project in February 2020 as station manager and a second student to start in July/ August 2020 as research manager until at last November 2021 and for a maximum of 3 years. This position is suitable for somebody who would like to gain experience in field work and scientific management. Managers get free accommodation at the station and a compensation to cover their daily costs. Travel costs can be refunded by up to an additional R 16 000 / year. As such, the position compensates for all arising costs but does not represent a legal employment.

The station manager and the research manager work closely together and both managers share many responsibilities. However, each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained). The new manager will be instructed by the present managers, with the current station manager leaving in May 2020 and the current research manager in November 2020.

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You must have a drivers licence and you must love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science!

Skills needed: Good experience in field work and good knowledge of behavioural ecology or a similar field of research. Experiences in working with small mammals, radio-tracking, blood sampling, and living at a remote location are of advantage. Handyman skills are of advantage and needed for the station manager position.

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

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

Shared duties of managers at SKRS

Striped mice:

* Trapping * Observing * Radio-tracking, putting on radio-collars * Blood sampling

Collect data for specific research projects (to be determined).

Primary duties station manager / secondary duties research manager

* Technical support research station:

* Water system incl. sewage system * Solar system * Gas bottles replacement * House and furniture

o Running of the respirometry laboratory

o Management of the captive colony

o Management of the research station car

o Management of bank account and cash box

o Management of research station supplies

Primary duties research manager / secondary duties station manager

* Data:

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

Compensation:

* Free accommodation.

* A monthly compensation of R 4000 for the first three months, raising to R4700 per month afterwards, which is sufficient to pay all costs of living (approx. 3500/month). The compensation can gradually raise up to R5400/month. * For travel costs, R16 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after November 2021 and will not be paid if the person leaves earlier than agreed. * You will become an honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. * Scientific co-authorship will be possible if the manager contributes to the success of projects by not only collecting the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

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

* The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to

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SouthwesternOklahomaStateU HumanEvolution

The Department of Biological Sciences at Southwestern Oklahoma State University has a tenure-track position available for the Fall 2020 semester. We are seeking a biologist committed to excellence in teaching Human Anatomy, Human Physiology, majors and non-majors biology courses, and upper-division electives in the candidate's area of expertise. The candidate will contribute to a growing research program involving undergraduate students and will work with biology faculty to integrate research experiences into the curriculum. Startup funds and research space are available. The candidate is expected to participate in department and university service. Our department values collegiality and participation in its mission to provide excellent undergraduate training in biology. Additional information about the department can be found at: https://www.swosu.edu/academics/biology/index.aspx . Evolutionary Biologists with any kind of organismal expertise are encouraged to apply!

Questions regarding the position can be sent to Rickey Cothran (rickey.cothran@swosu.edu).

Link to job advertisement: https://jobs.swosu.edu/postings/2966 Rickey Cothran, PhD Associate Professor Department of Biological Sciences Southwestern Oklahoma State University

"Cothran, Rickey" <rickey.cothran@swosu.edu>

TempleU LabManager BiodiversityPhylogenomics

Biodiversity and Phylogenomics Laboratory Manager

The Center for Biodiversity (http://www.biodiversitycenter.org) at Temple University (Philadelphia) is interested in hiring a Biodiversity and Phylogenomics Laboratory Manager. The successful applicant will be skilled in phylogenomics, including sequence capture methods and data analysis. They will be responsible for carrying out research in biodiversity and maintaining a molecular biology laboratory, including a frozen tissue collection, collecting and analyzing DNA sequence data, and working with students and other users of the laboratory. A bachelor's or master's degree is preferred.

The Center for Biodiversity is adjacent to the Institute for Genomics and Evolutionary Medicine (iGEM), both located within Temple's Science, Education, and Research Center (SERC) on the main campus. It is affiliated with the Department of Biology and College of Science and Technology.

Temple has exceptional research strength in biodiversity, evolutionary genomics, and ecology. Interested persons should send an e-mail to temple.biodiversity@gmail.com, stating their interest in this position, and attach a curriculum vitae that also contains contact information for three references. The e-mail may be addressed to the director, S. Blair Hedges (http://www.hedgeslab.org). Review of applications will begin on December 20th and continue until the position is filled.

Temple University is located in the heart of historic Philadelphia and is the sixth largest provider of graduate school education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is the birthplace of America and home to many academic and research institutions as well as numerous cultural attractions.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community (AA, EOE, m/f/d/v).

"sbh@temple.edu" <sbh@temple.edu>

UAntwerp Bioinformatics SupportManager

The Faculty of Sciences is seeking to fill a full-time (100%) vacancy in the UAntwerpen Department of Computer Science for a

Bioinformatics Support Manager

https://www.uantwerpen.be/en/jobs/vacancies/ap/2019bapfwetef289/ Biomina (biomedical informatics network Antwerpen) is a multi-disciplinary consortium that unites life scientists and data scientists in the Antwerp region in the area of bioinformatics and medical informatics. To address the rapidly growing needs for bioinformatics expertise in many life science projects, we are establishing a bioinformatics and biomedical informatics service facility. The Bioinformatics Support Manager is the daily lead of this service facility.

The Adrem Data Lab (Department of Computer Science) is at the forefront in developing and applying data mining and machine learning methods to make sense of large scale data. A large fraction of the group is currently working on solutions specifically tailored to life science data. Many of these data processing solutions are also used in life science research projects.

Job description

Together with the local bioinformatics community you establish and manage a bioinformatics service facility towards academic life science researchers as well as to external clients. You lead the standardization and integration of local bioinformatics platforms and infrastructure for genomics, proteomics and metabolomics. You coordinate bioinformatics training, seminars and networking events for researchers in Antwerpen. You support the maintenance and usage of bioinformatics hardware and software. You manage collaborations and contribute to the bioinformatics component in life science research projects. Profile and requirements

You have a Master degree in Bioinformatics or in life sciences and you can demonstrate at least four years hands-on experience in bioinformatics, medical informatics or biomedical data mining. A doctoral degree is an extra advantage. You are experienced in data processing pipelines for at least one type of omics data. Familiarity with machine learning, pattern discovery and AI techniques is a plus. You have strong statistical, computational and programming skills (preferably in Python and R). You demonstrate a collaborative, service-oriented attitude. Proven experience in supporting life scientists with bioinformatics expertise is a plus. Your academic qualities comply with the requirements stipulated in the universitys policy. You are quality-oriented, conscientious, creative and cooperative. You are a team player who can build bridges between disciplines, and you have strong interdisciplinary communication skills. You are fluent in academic English (speaking and writing).

We offer

a contract according to your qualifications for a period of one year, with a possibility of renewal, within the Adrem team and the biomina consortium; the starting date of the appointment can be immediately (pending administrative procedures), but can be adapted; an exciting, dynamic and stimulating multi-disciplinary working environment in an enthusiastic, fast-growing team, located in the green outskirts of the vibrant city of Antwerp; plenty of opportunities to improve and extend you skill set, in diverse areas, ranging from new omics data processing techniques to data science and AI. How to apply?

Interested candidates are invited to send a strong motivation letter highlighting relevant previous work, a detailed CV (including honours, grades, skills, publications,) and contact info of two references to Kris Laukens (kris.laukens@uantwerpen.be). Please mention Manager_BIOMINA2019' in the subject of your mail.

A pre-selection will be made amongst the submitted applications. More information about the application form can be obtained from prof. Kris Laukens (kris.laukens@uantwerpen.be).

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

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

Hannes Svardal <Hannes.Svardal@uantwerpen.be>

UAntwerp VertebrateEvolution

Research professor, Vertebrate Functional & Ecological Morphology and Biomechanics As part of its dynamic research policy and supported by the possibilities offered by the Flemish Government through the resources of the Special Research Fund (BOF), the University of Antwerp's Faculty of Sciences is seeking to fill a vacancy in the Department of Biology for a Full-time Research professor (TTZAPBOF) in the area of Vertebrate Functional & Ecological Morphology and Biomechanics.

The Biology Department at the University of Antwerp is internationally known for its research on the morphology, physiology, behaviour and ecology of vertebrate animals. An overarching goal is to understand how animals adapt to changing environments within and across generations. Within this context, your research will tackle the relationship between animal form and function - examining how and how fast animal morphology evolves to meet requirements posed by the environment. As such, your research connects to two research spearheads of the University of Antwerp: 'Ecology and Sustainable Development' and 'Neurosciences'. Preference will be given to applicants working on the functional morphology and biomechanics of the musculo-skeletal apparatus, which constitutes an important interface with the environment.

Job description The assignment consists of lecturing duties, scientific research and academic service to society. During a period, limited to five years (duration of the temporary appointment in tenure track), scientific research will be the main activity. You are expected to acquire and manage external funding and to establish an international collaborative network. You play an active role within the department and you bring in expertise that fits and expands the research of the Functional Morphology (FunMorph) research group (animal performance, dynamics of the musculo-skeletal system, biomechanics) and that is complementary to that of researchers of the Evolutionary Ecology (EVECO), the Behavioural Ecology & Ecophysiology (BECO) and the Systemic Physiological and Ecotoxicological (SPHERE) research groups, enabling and promoting interdisciplinary research.

You are expected to explore opportunities for, and set up collaboration with partners of the Faculty of Sciences (e.g. Biomedical Physics) or other Faculties (e.g. Applied Veterinary Morphology, Rehabilitation Sciences and Physiotherapy).Your research preferably makes use of the department's unique facilities, while maintaining and expanding the necessary technical and instrumental support. You will be assigned lecturing duties mainly in the field of zoology, the first 5 years limited to a maximum of 30 hrs/semester.

Profile and requirements You hold a doctoral degree (PhD) in Biology. You are an enthusiastic scientist with minimally 2 years of post-doctoral experience. You have an excellent track record in terms publications, the acquisition of research grants and supervising PhD students. You have leadership skills allowing you to establish a strong research line within the department and to supervise PhD students. Your academic qualities comply with the requirements stipulated in the university's policy < https://www.uantwerpen.be/en/about-uantwerp/organisation/mission-and-vision/three-core-tasks/research/ > The focus in your teaching corresponds to the educational vision < https://www.uantwerpen.be/en/about-uantwerp/organisation/mission-and-vision/three-core-tasks/education/ > of the university. Scientific communication is carried out in English, so knowledge in Dutch language is not a prerequisite, but a commitment to learning the Dutch language is expected within five years after your appointment (CEFR B2, as soon as you take on teaching duties as a course unit coordinator CEFR C1). The University of Antwerp supports international staff members on an integration trajectory and offers tailor-made language coaching in compliance with Flanders' statutory.

We offer §a full-time tenure-track position as a lecturer: the scientist will be appointed on a temporary basis for a maximum of five years. After two and 4 years there will be an assessment of performance based on criteria that will be specified at the time of appointment; based on these assessments, the researcher may be promoted to the rank of senior lecturer with tenure with limited lecturing duties for another period of five years, in order to strengthen the research curriculum; the University of Antwerp advocates gender equality. Woman are therefore strongly encouraged to apply. Equally qualified handicapped applicants will be given preference; the date of appointment will be 1 October 2020

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UCalifornia LosAngeles ConservationGenomics

The UCLA La Kretz Center for California Conservation Science seeks applicants for an Associate Director to help administer and coordinate the activities of the California Conservation Genomics Project (CCGP), a UC-wide project using conservation genomics to protect endangered, threatened and ecologically important species in California. This full-time position is based at UCLA and would begin as soon as a qualified candidate is identified and available.

Under the supervision of the Director of the UCLA La Kretz Center for California Conservation Science, who is also the Project Director for the CCGP, the Associate Director will have responsibilities in these broad areas: (1) communicate and coordinate with multiple committees and research teams; (2) promote collaboration among groups; (3) manage project reports, data archiving and production of deliverables; and (4) conduct integrative research relevant to the project. The incumbent will work with the Scientific Executive and UC-Wide Advisory Committees, and will be responsible for the management of the project, including (i) helping with the design of the sampling, (ii) overseeing the submission of data, and (iii) ensuring that reports submitted by multiple research teams are timely and complete. While the primary responsibility is project management, the ideal candidate would also undertake one or more research projects that analyze and synthesize findings from multiple studies to address conservation issues.

The successful applicant should be a PhD scientist with project management experience and research expertise in data management, GIS, landscape statistics, bioinformatics, and/or genomics. The candidate must have experience managing and archiving multiple large, complex data sets, and a demonstrated ability to conduct and publish synthetic research on natural populations, write reports, communicate with research teams, adhere to timelines and deadlines, and communicate findings to the public, governmental and NGO agencies, and the broad scientific community. The candidate should also have excellent interpersonal skills, be able to interact effectively with persons of differing social, educational, economic and cultural backgrounds, and have the ability to pay attention to detail while keeping in mind the overall mission of the CCGP.

Applicants are encouraged to apply before 10 December 2019 but applications will continue to be reviewed until January 3, 2020 or the position is filled. Candidates should submit a C.V., cover letter, statement of administrative experience, and description of a research project or activity relevant to the goals of CCGP to https://recruit.apo.ucla.edu/JPF05116 The salary will be commensurate with qualifications and experience. Full-time (100% time) position, with a possible starting date as early as February 1, 2020

Applications will be reviewed by the CCGP Science Executive Committee. 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: UC Nondiscrimination and Affirmative Action Policy (http://policy.ucop.edu/-doc/4000376/NondiscrimAffirmAct).

Please direct questions to CCGP PI and Director Brad Shaffer (brad.shaffer@ucla.edu) or Co-Director Victoria Sork (vlsork@ucla.edu).

Brad Shaffer <brad.shaffer@ucla.edu>

UCambridge Genetics

University Lecturer in Genetics (equivalent assistant professor)

Applications are invited for a research-oriented, tenure-track University Lectureship. The post is available from 1 April 2020 or as soon as possible thereafter.

The Department of Genetics is a world-class research and teaching environment with particular strengths in quantitative approaches to genomics, epigenetics, population and evolutionary genetics, cell and developmental biology and has numerous links with other local institutions. We are searching for an outstanding scientist, with an excellent publication record, who is undertaking cutting edge and fundable research in any field of contemporary genetics relating to or complementing our existing research programmes (http://www.gen.cam.ac.uk/-research-groups/research-by-subject).

Details: https://www.jobs.cam.ac.uk/job/23756/ “F. Jiggins” <fmj1001@cam.ac.uk>

UCLondon Independent Fellowships

Excellence Fellowships in Genetics, Evolution and Ecology

University College London

UCL’s Department of Genetics, Evolution and Environment (GEE) is looking to recruit promising early-career researchers. GEE is a world class Department with a broad research portfolio. We are aiming to strengthen research in the general areas of evolution and ecology and are particularly encouraging applicants in the following broad areas: - Biodiversity and ecology - Evolution, adaptation and origins of eukaryotic complexity - Computational and statistical genetics - Evolution and mechanisms of ageing and age-related diseases - Ecological genetics of disease

Recruitment opportunities are available through the UCL Excellence Fellowship scheme run by the School of Life and Medical Sciences (deadline 25 January 2020) and through externally funded Fellowship schemes

(ERC, Royal Society, NERC, BBSRC, Wellcome Trust). The UCL Excellence Fellowship offers salary and research funding, as well as generous financial supplements for individuals bringing externally funded fellowships to UCL: https://www.ucl.ac.uk/school-life-medical-sciences/research/ucl-excellence-fellowships Candidates should get in touch with fellowship contacts Dr Seirian Sumner (s.sumner@ucl.ac.uk) or Dr Max Reuter (m.reuter@ucl.ac.uk). Initial expressions of interest should include a CV, a short paragraph about the proposed research and the name of a GEE PI with related research interests who could act as sponsor for a fellowship. For applications to the UCL Excellence scheme, please contact us before 8 January 2020.

The Department has a track record of supporting fellowship applicants from initial application to securing subsequent permanent employment within the department. You can find more information about the department at https://www.ucl.ac.uk/biosciences/-departments/genetics-evolution-and-environment . A note for non-UK applicants: Fellowships are an integral part of the UK academic system. Externally funded grants covering salary and research expenses are open to non-UK applicants from a range of funding agencies. These awards allow early- and mid-career scientists to concentrate on their work unhindered by teaching and administrative loads.

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London Darwin Building Gower Street, London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: http://www.homepages.ucl.ac.uk/ ˜ ucbtmre/-Labsite/ Department: http://www.ucl.ac.uk/gee
“Reuter, Max” <m.reuter@ucl.ac.uk>

UKoblenz Landau GroundwaterPopGenetics

Biodiversity and population genetic structure of groundwater organisms

As part of a Federal Ministry of Education and Research (BMBF) funded network project to assess groundwater ecosystems and their function for drinking water quality the iES Landau, Institute for Environmental Sciences, University Koblenz-Landau, Campus Landau, Germany offers a doctoral research position (0,5 EGr. 13 TV-L). The position is fixed for 36 months, and the expected starting date is 1st March 2020.

Groundwater ecosystems represent a large, but hardly studied ecosystem which provides an essential ecosystem service: drinking water. Groundwater invertebrates play a central role for water quality and are suitable bioindicators for man-made environmental stress (i.e. global warming and toxic waste). Assessment of biodiversity patterns in crustacean communities (DNA metabarcoding) and population structures of selected species (DNA microsatellites) will be used to associate phylogeographic and population genetic data with environmental data.

Candidates should hold a diploma or MSc in a relevant topic such as ecology, evolution or similar. Fluent English talking and writing skills as well as solid background e.g. in population genetic and genomic techniques, multivariate statistical approaches or bioinformatics are required. A strong motivation to work in teams, to publish research articles, and to finish a PhD thesis within three years is needed.

It is the policy of the University Koblenz-Landau to increase the percentage of female PhD candidates. If equally qualified, preference will be given to female applicants. Disabled candidates are given priority, if equally qualified.

Please send your applications (1 pdf file, max 10 MB), with a 1-page letter of motivation, a reference letter from a mentor, degree certificates, a CV and a list of publications/presentations until 31 December 2019 via email to bewerbung@uni-koblenz-landau.de. Please make sure to mention your name and the reference number 131/2019 in the subject line of the email. For further details contact Prof. Dr. Klaus Schwenk (schwenk@uni-landau.de). We do not send an acknowledgment of receipt. You will receive information about the result of your candidature. Data destruction after the conclusion of the selection procedure is assured.

Prof.—Dr. Klaus Schwenk Molecular Ecology Institute of Environmental Sciences University of Koblenz-Landau Fortstraße 7 Building I, Room 5.01 76829 Landau in der Pfalz Germany Tel.: ++49 (0)6341 280 31170 E-Mail: schwenk@uni-landau.de homepage: www.molecol.uni-landau.de Klaus Schwenk <schwenk@uni-landau.de>

UMaryland ResAssist MarinePopGenetics

Faculty Research Assistant

The University of Maryland Center for Environmental Science (UMCES) is seeking applicants for a faculty research assistant at the Horn Point Laboratory (HPL) in the Plough Laboratory (https://www.umces.edu/-louis-plough)in Cambridge MD.

The position will be a full-time Faculty Research Assistant (BA or BS degree required) in support of grant-funded projects related to the population genetic analyses of estuarine and marine animals, particularly invertebrates (blue crabs, oysters, and zooplankton). Laboratory duties will include tissue preservation and DNA extraction, environmental DNA sampling, quantitative PCR and analysis, and preparation of genomic libraries for next-generation sequencing (NGS). The technician may also be involved in field work (local) collecting animals on small craft or from shore, and will assist with finfish care and shellfish culturing at HPL. Finally, the technician will be expected to assist in data organization/analysis and preparation of reports/manuscripts.

Field work may include light duty lifting (50 pounds), work on small boats (25 ft) and walking short distances between sample sites in lightly or heavily wooded areas.

Routine lab work may include the use of chemicals that require gloves, proper clothing, and eye protection.

Required skills include: laboratory experience in molecular genetics (e.g. PCR, agarose gel electrophoresis, DNA extraction; ideally in a research setting), handling of large datasets in spreadsheets, and familiarity/experience with bio statistical analysis using software such as R or similar. A willingness to be in the field for short periods of time (day trips) and to manage live cultures of larvae or fish is also required.

Ideal applicants will have some prior experience preparing next generation sequencing libraries and some familiarity with UNIX/Linux for command-line processing of genomic data sets. Some experience with animal culture or care (especially larval shellfish culture) is also a plus. Funding is currently available for two years with additional time possible dependent on future funding. Salary will be commensurate with experience and a comprehensive benefits package is available.

To apply, please visit: http://umces.peopleadmin.com/-postings/1359 To receive full consideration, apply by December 23nd, 2019.

UMCES is an AA/EOE institution. Individuals with disabilities, veterans, women, and minorities are encouraged to apply.

Thank you,

Addie C. Cropper Human Resources Associate II UMCES Horn Point Lab 410.221.8241

“Cropper, Addie” <acropper@umces.edu>

UMississippi GlobalChange

** Update: review of applications will begin November 25, 2019 **

The Department of Biology at the University of Mississippi is searching for a tenure-track Assistant Professor working on ecophysiological responses to global change. We seek candidates who use integrative approaches to understand the physiological mechanisms that underpin present-day or projected responses of invertebrates and/or vertebrates to environmental change in freshwater, marine, or terrestrial systems. Areas of research interest include but are not limited to climate change, land use change, urbanization, biological invasions, species interactions, or mechanisms of ecosystem resilience. Research should connect animal physiology to global change issues, and may integrate multiple biological, spatial and/or temporal scales. The successful candidate will be expected to develop an innovative, externally-funded research program, train graduate students, teach courses in their area of expertise, and contribute to teaching a core Introductory Physiology course. This positi on will complement and extend existing departmental strengths in symbiosis and species interactions, biodiversity and conservation biology, cell and molecular biology, or neuroscience and behavior (http://biology.olemiss.edu).

We have a vibrant, broad-based biology department that consists of 22 tenure-track and 13 instructional faculty members, and educates over 900 undergraduate biology majors and 38 graduate students (Ph.D. and M.S.). The University of Mississippi is a Carnegie-Designated R1 Highest Research University located near Memphis in Oxford, Mississippi, a beautiful college town known for its outstanding educational and cultural opportunities. The University of Mississippi has been repeatedly recognized by the Chronicle of Higher Education as a "Great College to Work For." The Department of Biology recognizes the importance of building a diverse faculty and welcomes applicants from groups underrepresented in science.

To apply, please visit our Online Employment Service at https://careers.olemiss.edu/. Applications should include: (1) cover letter outlining interest in and suitability for the position, (2) a curriculum vitae, (3) a statement of research interests and future plans (3 pages or less), (4) a statement of teaching interests, practices and philosophy (1 page), (5) a diversity statement addressing approaches to promoting inclusivity in research and training (1 page), (6) names and contact information for at least three references, and (7) reprints of up to three recent publications or submitted papers. Items 1-6 should be prepared as a single pdf and item 7 as a second pdf file.

The University of Mississippi complies with all applicable laws regarding equal opportunity and affirmative action and does not unlawfully discriminate against any employee or applicant for employment on the basis of race, color, gender, sex, sexual orientation, gender identity or expression, religion, national origin, age, disability, veteran status or genetic information.

Ryan Garrick Department of Biology 508 Shoemaker Hall University of Mississippi University, MS 38677-1848, USA

webpage: http://www.rcgarrick.org "rgarrick@olemiss.edu" <rgarrick@olemiss.edu>

UMississippi ResAssoc EvolutionMicrobialSymbiosis

Dear All,

I'Âm looking to hire a Research Associate for my group. Kindly forward to suitable candidates or apply yourself if you think you're a fit. Sincere apologies if you receive(d) this multiple times via cross-postings'K.

Best wishes, Erik Hom erik@olemiss.edu

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The Hom Lab at the University of Mississippi is seeking a dedicated, full-time Research Associate (RA) to assist with research and publications, the supervision and support of students, and overall lab management. The RA will primarily lead a NSF CAREER-funded project on experimentally co-evolving model fungal-algal mutualisms, but will also be given opportunities to be involved in several projects in our eclectic research portfolio (http://darwinsdaemon.com/research.php).

The successful candidate must be self-motivated and a self-starter, growth-minded, highly disciplined and organized, able to effectively multitask, and have an attestable record of productivity and working well with others. The candidate should have demonstrated experience working with microbes (fungi and algae are a plus) and be enthusiastic about learning/developing new techniques, approaches, and research areas. Experience in molecular genetics, next-gen sequencing/bioinformatics, and/or 3D-printing/device-tinkering are pluses. We envision strong candidates having a Ph.D. in biology (or related field) but welcome applications from candidates with a B.A./B.S./M.S. degree who have a substantial laboratory/research background. The expected commitment is for at least two years, with an initial one-year term with review, and the potential to renew for up to five years depending on annual performance.

Our lab is interested in understanding how biotic and abiotic factors dovetail to facilitate the formation, persistence, and evolution of species interactions, notably those that are symbiotic. We are particularly fond of studying associations involving fungi, algae, and cyanobacteria, and take a two-pronged approach towards understanding how microbes interact to form stable, functioning communities. In one approach, we create new ecosystems of interacting microbes (synthetic ecology) to test our predictive understanding of basic design principles in microbial ecology. In a complementary approach, we focus on dissecting, manipulating, and observing reduced microbial communities (polycultures) isolated from nature to infer fundamental rules. Our lab is passionate about STEM education and outreach to individuals and communities in underserved/disadvantaged contexts, while pushing forward an innovative and world-class research program.

The University of Mississippi is located in Oxford, MS, an idyllic and growing college town about 1 hr south of Memphis, TN. In addition to SEC sports, a famous tailgating culture at "The Grove," and a rich Southern culinary scene, Oxford is home to a vibrant music, arts, and literary community with strong historic ties to William Faulkner and The Blues. Ours is a very livable city with a small town feel for those who value work-life balance, community, and proximity to the countryside.

To formally apply, submit application materials here: https://is.gd/HomRA2020. Candidates should be prepared to upload: (1) a cover letter explaining specific interest in and fit for the position, (2) a detailed CV,

(3) names and contact information for at least 3 references, and (4) optional files to support their application (e.g., publication reprints). Compensation will depend on experience and will include health and retirement benefits. For informal questions/inquiries only, contact Erik Hom at: HomRA2020@gmail.com

Review of applications will begin immediately and continue until the position is filled. We seek to fill this position as soon as possible in early 2020 but are willing wait for the right candidate. We warmly invite women and others from diverse, non-majority backgrounds to apply'Xwe believe different perspectives are critical in our quest for creative excellence.

The University of Mississippi is an EOE/AA/Minorities/Females/Vet/Disability/Sexual Orientation/Gender Identity/Title VI/Title VII/Title IX/ADA/ADEA employer.

'X Erik F. Y. Hom Assistant Professor | Department of Biology Member | Center for Biodiversity & Conservation Research (http://cbcr.olemiss.edu) Director, ARISE@UM (arise.olemiss.edu) Treasurer, International Symbiosis Society (iss-symbiosis.org) University of Mississippi, University MS 38677-1848, USA http://darwinsdaemon.com "erik@olemiss.edu" <erik@olemiss.edu>

UMuenster EvolEcolAnimals

The Kurtz lab "Evolutionary Ecology of Animals", in the Institute for Evolution and Biodiversity at the University of Münster, Germany, invites applications for a

Postdoctoral Research Associate (salary level 13 TV-L, 100%)

The position will begin at the earliest possible date, and the initial contract will last for a period of three years. It is possible to extend the position for a further three years. The regular working time for a full (100%) position is currently 39 hours and 50 minutes per week. As a rule, vacancies can also be filled as part-time positions unless there are compelling reasons for not doing so in individual cases.

The successful applicant is expected to set up his/her own work group and independently raise third-party funding. The position is thus equivalent to an Assistant Professor (non-tenure track).

The job holder should work in the field of evolution and ecology of immune systems or host-parasite coevolution. Applicants should have an academic degree and a doctorate in biology. Experience with immunological, parasitological, molecular or genomic methods is an advantage.

The Kurtz lab addresses a variety of questions in the field of evolution of immune systems and host-parasite relationships. The research interests of the very international group range from experimental evolution and immunological/molecular processes to behavioral adaptation. In addition to flour beetles, sticklebacks and copepods also serve as host organisms. Experience with one of these organisms is advantageous but not absolutely necessary. In addition to conducting research, the successful applicant will also be involved in teaching in the fields of animal zoology and evolutionary ecology.

The University of Münster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. We also welcome applications from candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered.

Please send your application by 13 December 2019 with your curriculum vitae, list of publications, a brief description of your research interests and the contact details of three possible reviewers (as a single PDF file by email) to:

Prof Dr Joachim Kurtz Institut für Evolution und Biodiversität University of Münster Hüfferstr. 1 48149 Münster Germany Tel. +49 (0) 251 83 24 661 Email: joachim.kurtz@uni-muenster.de

"joachim.kurtz@uni-muenster.de" <joachim.kurtz@uni-muenster.de>

UNevada LasVegas MicrobialEnvironmentalGenomics

The University of Nevada, Las Vegas invites applications for a tenure-track or tenured position in Microbial Environmental Genomics, at the rank of Assistant/Associate/Full Professor in the School of Life Sciences, with primary responsibilities in research, teaching and service.

Role of the Position: The ideal candidate will apply genomics approaches (single-cell genomics, metagenomics, and/or functional genomics) to explore biodiversity and understand the roles of microorganisms in any natural environment. Research areas that complement current strengths in SoLS and other programs at UNLV are desirable. The successful candidate will hold a Ph.D. degree or equivalent in microbiology or a related field. Postdoctoral experience is preferred. Faculty members are expected to develop and maintain a vigorous, externally funded research program and teach at the undergraduate and graduate levels.

The successful candidate is expected to align with the research and teaching missions of SoLS and is expected to: 1) Design and sustain a high-impact research program that is extramurally funded and internationally recognized, and 2) Contribute to both graduate and undergraduate education through formal teaching and mentoring. Teaching strategies that are inclusive of UNLV's culturally rich environment are encouraged. The candidate is expected to mentor graduate students in the Ph.D. and/or Master's programs and to participate in service at the local, national, and international levels.

UNLV School of Life Sciences: UNLV SoLS (https://www.unlv.edu/lifesciences) maintains a highly active research environment with investigators working on microbiology, ecology and evolutionary biology, bioinformatics, integrative physiology, cellular and molecular biology, biomathematics, and biology education and assessment. The diverse group of microbiologists at UNLV currently have expertise in microbial genetics, physiology, pathogenesis, ecology, and environmental genomics. Research resources include a new animal care facility and the UNLV Confocal and Biological Imaging Core. Genomics resources, including next-generation DNA sequencing facilities, are available on campus through the Nevada Genomics Center and the Nevada Institute of Personalized Medicine (NIPM). NIPM recently received an NIH COBRE grant that provides opportunities to young faculty for pilot grants and collaboration for microbiome-related research. The UNLV National Supercomputing Institute provides high-performance computing to all UNLV faculty through the Cherry Creek Cluster and other supercomputers.

UNLV participates in the Established or Experimental Programs to Stimulate Competitive Research offered by many of the federal granting agencies (NSF, DOE, DOD, and NASA), and the NIH IDeA Network of Biomedical Research Excellence (INBRE) program. SoLS is also eligible for NIH Academic Research Enhancement Awards (NIH R15). Many SoLS faculty collaborate with other units in the College of Sciences, the Desert Research Institute, NIPM, and other units on campus.

Application Details: Applications should include a cover letter, a curriculum vitae, a statement of research interests and plans, a statement of teaching interests/philosophy, including how the candidate will support the learning success of the diverse UNLV student body, and contact information for three references, and should be addressed to Brian Hedlund, Search Committee Chair at brian.hedlund@unlv.edu. Additional information about the position is available at URL: https://www.unlv.edu/news-story/faculty-position-microbial-environmental-genomics .

Review of materials will begin January 15, 2020 and will continue until the position is filled. Applications should be submitted online at unlv.edu/jobs. For assistance with UNLV's online applicant portal, please contact Human Resources (702) 895-3504 or applicant.inquiry@unlv.edu. Other inquiries should be addressed to Dr. Brian Hedlund, Search Chair, at brian.hedlund@unlv.edu.

UNLV is ranked first in the country in the "Best Ethnic Diversity" category by U.S. News and World Report, and is a Title III and Title V Minority-Serving Institution (MSI), an Asian-American and Native-American, Pacific Islander-Serving Institution (AANAPISI), and Hispanic-Serving Institution (HSI). UNLV is an R1 institution (as classified by the Carnegie Classification of Institutions of Higher Education) and continues to invest heavily in research, driven by our Top-Tier Initiative. UNLV is the only major research university in the Mojave Desert and has great access to both desert and mountain environments for both research and recreation. UNLV is home to the only M.D.-granting medical school in Southern Nevada and the only dental school in Nevada, both of which play a critical role in the

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UNewHampshire QuantitativeBiology

The Department of Molecular, Cellular, and Biomedical Sciences (MCBS), College of Life Sciences and Agriculture (COLSA) at the University of New Hampshire

(UNH) invites applications for a full-time (9-month) tenure-track Assistant Professor of Quantitative Biology starting Fall 2020.

We seek an engaged new faculty member who demonstrates strong potential to develop an internationally recognized research program that leverages big data to address questions of fundamental importance in life sciences research and who will contribute passionately to our teaching mission.

Candidates working in fields including but not limited to Computational Biology, Computational Biochemistry, Epigenetics and Gene Regulation, Metabolomics, Statistical Genomics, Systems Biology, and others are encouraged to apply. We are particularly interested in candidates who conduct hypothesis-driven research utilizing evolutionary and/or comparative frameworks to advance novel algorithmic approaches for the analysis of large biological datasets.

The primary responsibilities of this position are to develop a high-impact, externally-funded research program in Quantitative Biology and to provide high-quality, vibrant instruction by developing and teaching courses that reach students at all levels of the curriculum including introductory courses in the candidate's discipline and graduate courses in the candidate's specialty. In addition, service to the department, college, and university is required.

The successful candidate will interface with any of several centers for excellence at the University of New Hampshire including the Research Computing Center, the Center of Integrated Biomedical and Bioengineering Research, the School of Marine Science and Ocean Engineering and the Hubbard Center for Genome Studies.

Graduate student training opportunities are provided through affiliation with any of the MCBS administered graduate programs including Microbiology, Genetics, Biochemistry, and Molecular & Evolutionary Systems Biology.

Review of applications will begin on January 15th, 2020 and will continue until the position is filled. We anticipate a start date of August 2020.

The following application materials are required: 1) a cover letter, 2) curriculum vitae 3) statement of teaching interests and philosophy (maximum two pages), 4) research statement (maximum four pages), 5) up to three representative publications and 6) contact information for 3 professional references.

We seek applicants with demonstrated commitment to diversity and inclusion.

For administrative questions related to application submission, please contact Paul Boisselle at paul.boisselle@unh.edu.

David Plachetzki david.plachetzki@unh.edu

David Plachetzki Assistant Professor Molecular, Evolutionary Systems Biology Graduate Program Coordinator Molecular, Cellular, & Biomedical Sciences University of New Hampshire Gregg Hall, 446 35 Colovos Rd. Durham NH 03824-2618 603-862-5144

david.plachetzki@unh.edu evodavo.org

David.Plachetzki@unh.edu

UppsalaU PlantBioinformatics

Dear all, we are happy to announce an exciting opening for a full-time permanent bioinformatics staff at NBIS/SciLifeLab, Uppsala University, Sweden. The National Bioinformatics Infrastructure Sweden at SciLifeLab (www.nbis.se, www.scilifelab.se) is a large, distributed national infrastructure in rapid development. For this position, we believe that you have experience of advanced analysis in areas such as resequencing and variant calling, population genomics, GWAS, and comparative genomics, with a keen interest in plant genomics and evolution.

Apply no later than December 13, 2019! https://www.uu.se/en/about-uu/join-us/details/-?positionId=301263 For questions, please contact Björn Nystedt, Bioinformatics Support manager bjorn.nystedt@scilifelab.se NBIS/SciLifeLab

Bjorn Nystedt, PhD Joint head of facility Bioinformatics Long-term Support (WABI) National Bioinformatics Infrastructure Sweden at SciLifeLab www.nbis.se, www.scilifelab.se/platforms/bioinformatics

BMC E10:3206, entrance C11 Husargatan 3, SE-752 37 Uppsala

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

När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ 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 Björn Nystedt <bjorn.nystedt@scilifelab.se>

USDA Maryland MolecularSystematists

Assistant Director of National Identification Services, APHIS, USDA. Successful candidate will manage a group of National Taxonomists and Molecular Systematists. https://www.usajobs.gov/GetJob/ViewDetails/-550346800 James A. Robertson, Ph.D Molecular Systematist National Identification Services USDA-APHIS-PPQ

10300 Baltimore Ave BARC-West, Bdg. 004, Rm. 112 Beltsville, MD 20705 USA Work: 240.549.3220 Website: www.ELYTRA.org James Robertson <erotylid@gmail.com>

UtahValleyU GenomicsBioinformatics

Faculty Tenure-Track Genomics/Bioinformatics

Position Category: Faculty - Tenure Track (FT)

Summary: The Department of Biology at Utah Valley University invites applications for an open rank tenure-track faculty position, to begin in August 2020. We seek an outstanding candidate with a background in Genomics/Bioinformatics. The successful candidate should have a strong commitment to undergraduate education and a research program amenable to undergraduate students. Candidates must have a doctorate degree, research background in Genomics/Bioinformatics or a related discipline, and a strong commitment to effective teaching utilizing evidence-based pedagogies. Teaching responsibilities include: courses in Genomics and/or Bioinformatics, additional biology courses, including courses within the successful applicant's area of expertise, or as needed by the department. The candidate will also help to develop curricula for a proposed Bioinformatics degree. The successful candidate is expected to establish an active research program that includes mentoring of undergraduates, leading to peer-reviewed publications. Additional responsibilities include working collaboratively with faculty, staff, and students to promote successful growth of the department and serving on department, college, and university committees as fitting a tenure-track position.

Utah Valley University is the largest public university in the state of Utah with over 40,000 undergraduate students and offers a dual-mission model that combines the rigor and richness of a first-rate teaching university with the openness and vocational programs of a community college. UVU is located in Orem, Utah at the foot of the beautiful Wasatch Mountains about 40 miles south of Salt Lake City. Utah Valley University is an Affirmative Action/Equal Opportunity/ Equal Access employer.

Required Qualifications: Graduation from an accredited institution with a doctorate in Genomics/Bioinformatics or related biological discipline required. Evidence of experience teaching genomics/Bioinformatics or related courses to undergraduate students.

ABD applications will be considered if doctorate verification is received by March 30, 2020.

Knowledge, Skills and Abilities: Demonstrable knowledge of the theory and practice of Genomics/Bioinformatics, and research methods in the field of Genomics/Bioinformatics. A record of incorporating evidence-based pedagogy, such as active learning techniques, and innovative use of instructional technology in the classroom. A record of curriculum development, effective verbal and written communication, and the ability to work collaboratively with faculty, staff, and students. The ability, desire, and skills to mentor undergraduate student research.

Preferred Qualifications: Strong knowledge of active learning pedagogies and an established record of incorporation of those techniques in the classroom (especially in general biology and molecular biology courses). Experience or strategies for teaching at open-enrollment institutions. Experience in and/or commitment to hybrid and online instruction. Publication record and/or work experience that indicates successful use of Genomics/Bioinformatics methods. Evidence of mentorship of undergraduates.

Physical Requirements: As necessary to conduct classroom teaching and supervision of undergraduate students.

Benefits Summary: UVU offers an excellent benefits package which includes a generous leave policy, 12 paid holidays, affordable medical and dental insurance options, life and AD&D insurance, tuition waiver (undergraduate resident) for employee and dependents and substantial employer contribution to a retirement plan.

FLSA:Exempt

Pay Range:DOQ

Advertisement Number:FAC59518 Biology Faculty Open Date:11/07/2019 Review Start Date:12/07/2019 Close Date: Open Until Filled:Yes

Special Instructions to Applicant:Please list a minimum of three references. References may be contacted at some point during the screening and selection process for a letter of recommendation.

To apply, visit:https://www.uvu.jobs/postings/16353 Employment decisions are made on the basis of an applicants qualifications and ability to perform the job without regard to race, color, religion, national origin, sex, sexual orientation, gender identity, gender expression, age (40 and over), disability, veteran status, pregnancy, childbirth, or pregnancy-related conditions, genetic information, or other bases protected by applicable federal, state, or local law.

T. Heath Ogden, Ph.D. Department of Biology, SB 242P Utah Valley University Orem, Utah 84058 E-mail:heath.ogden@uvu.edu Phone: (801) 863-6909 Fax: (801) 863-8064

“T. Heath Ogden” <Heath.Ogden@uvu.edu>

UTyumen 4 EvolutionaryBiology

Professors (open rank) in Biology at the School of Advanced Studies, University of Tyumen

The School of Advanced Studies (SAS, https://sas.utmn.ru/en/) is recruiting 4 professors in environmental biology, evolutionary biology and neuroscience, as well as other disciplines

SAS is a new and rapidly growing institution at the University of Tyumen (Siberia), supported by the Russian academic excellence project (https://5top100.ru/en/). SAS is an interdisciplinary research center and educational institution (BA/MA), it operates in English and currently employs 25 faculty from 11 countries (https://sas.utmn.ru/en/people-en/), most of whom received their PhDs from universities top-ranked globally.

The distinctive feature of SAS is the organization of research around multidisciplinary team projects (https://sas.utmn.ru/en/research-projects-en). We are interested in scholars committed to both research and teaching, who believe in the power of complex conversations across disciplinary boundaries

Jobs at SAS provide a rare chance to develop one’s own research in the framework of a multidisciplinary team project, and also to contribute to shaping an innovative new institution. While scholars wishing to pursue all kinds of topics are encouraged to apply, we are particularly interested in the following research directions, within which more concrete team projects can be designed:

1)——— Multilevel evolution and the possibilities and limitations of applying evolutionary theory and ’the logic of chance’ to social, economic, and cultural structures in their historical development.—

2)——— Ethical and societal implications of genome technologies and neuroscience, such as genetic engineering, resurrection of extinct species, and direct manipulation of cognition and emotion in the brain, including in new media.

3)——— Arctic cities in the changing environment, ’glocalization’ of the impact of environmental and technological changes on the economy, everyday urban experience, culture and society.

4)——— Implications of changing economic dominance of Global South vs. Global North, East vs. West, etc. for the economic, technological, social and national divides in the multipolar world. The possibilities of the creation of communities across these divides, including by means of storytelling and visual media.

5)——— The challenges posed by AI decision-making, machine creativity and technological objects becoming social subjects.

As SAS has the ambition to be part of an international network of multi- and interdisciplinary teaching and research centers, an international search committee will supervise the hiring process:-————— Alexei Grinbaum, Institut de Recherche sur les Lois Fondamentales de l’Univers, CEA/Saclay (philosophy of science),-————— Arne Dietrich, American University of Beirut (psychology and neuroscience), -————— Barbara Igel, Moscow School of Management SKOLKOVO (economics),-————— James P. Gibbs, SUNY College of Environmental Science and Forestry (environmental studies),-————— Svetlana Borinskaya, Vavilov Institute of General Genetics, RAS (genetics, evolutionary biology), -————— Kevin M. F. Platt, University of Pennsylvania (cultural history), -————— Lev Manovich, City University of New York (media studies),-————— Machiel Keestra, Institute for Interdisciplinary Studies, University of Amsterdam (interdisciplinary studies),-————— Victor Vakhshtain, The Moscow School of Social and Economic Sciences (sociology).

Preliminary interviews will be conducted by Skype. Short-listed candidates will have the opportunity to team up through virtual contact in order to formulate draft multidisciplinary team projects. They will continue working on the project proposals during the project design session (https://sas.utmn.ru/en/project-design-sessions-en/) to be held at SAS in March 2020 where these projects will be assessed by the committee.

Successful candidates will be offered 3-year renewable contracts to pursue these projects and teach in the SAS BA life sciences major and the core curriculum (https://sas.utmn.ru/en/education-en/) SAS biologists can also work with X-Bio Institute for Environmental and Agricultural Biology (https://www.utmn.ru/en/-x-bio/institute/), use the institute's lab facilities and collaborate with X-Bio's permanent and visiting scholars from around the world. SAS faculty receive

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UWisconsin Madison EvolutionaryBiology

Assistant or Associate Professor of Evolutionary Biology, University of Wisconsin-Madison

The Department of Integrative Biology at the University of Wisconsin-Madison is accepting applications for an Assistant Professor (tenure-track) position, or Associate level for exceptional candidates, beginning in August 2020. We seek a candidate to develop an internationally-recognized research program in Evolutionary Biology. We are particularly interested in candidates who can address fundamental questions in evolutionary biology using data-rich genomics, computational, statistical, and/or mathematical approaches. Potential areas of expertise might include, but are not limited to, population genetics, population genomics, molecular evolution, physiological genomics, phylogenomics, functional genomics, computational genomics, conservation genomics, evo-devo, and eco-evolutionary genomics. Exceptional candidates outside these areas will also be considered. The candidate's research program may focus on any taxon or domain of life.

A Ph.D. in biology or related field and postdoc experience in evolutionary biology or related field is required prior to the start of the appointment. Expectations of the successful candidate include excellence in research and graduate training, engagement in collaborative research, establishment of an extramurally funded research program, University and professional service, public outreach, and skilled teaching at undergraduate and graduate levels. Our goal is to hire an outstanding and collaborative individual with broad research interests and promise for intellectual growth.

The position is based in the Department of Integrative Biology, which has 19 regular faculty members and 62 graduate students, drawn from multiple interdepartmental graduate programs on campus. The department brings together faculty and research programs that span a wide range of interests, including behavioral neuroscience, developmental and cellular neuroscience, cell biology, developmental biology, animal behavior, ecology and evolution. The department offers a stimulating research environment as well as opportunities for collaborative research in other departments. Located at the nexus of four beautiful lakes, Madison, the state capital, consistently ranks among the top American cities for its quality of life. Additional information regarding the Department of Integrative Biology is available at http://integrativebiology.wisc.edu.

Additionally, the University of Wisconsin has an active and vibrant research community with ~37 biology departments and several biological research institutes. Faculty members conducting research in Evolutionary Biology across campus are listed here: http://www.evolution.wisc.edu/ . Interested candidates can apply for Job (PVL100601) here: https://jobs.hr.wisc.edu/en-us/job/502884/assistant-or-associate-professor-of-evolutionary-biology To ensure consideration, applications should be received by December 1, 2019.

Diversity is a source of strength, creativity, and innovation. UW-Madison aims to fulfill its public mission by creating a welcoming and inclusive community for people from every background. Candidates from underrepresented groups are especially encouraged to apply.

Feel free to contact Carol Lee directly if any questions arise.

Carol Eunmi Lee, Ph.D. Professor Department of Integrative Biology

430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

Carol Eunmi Lee <carollee@wisc.edu>

WestTexasAMU TeachingEvolution

Tenure-track Assistant Professor of Biology West Texas A&M University Canyon, Texas West Texas A&M University, a Member of The Texas A&M University System located in Canyon, Texas, invites applications for a tenure-track Assistant Professor position in Biology (60% teaching, 35% research, 5% service) with an emphasis in genetics. This full time (9 month) position at West Texas A&M University will include responsibilities in teaching (9 ACH/semester), research, and service supportive of the biology, wildlife biology, environmental science, and Biology Education programs. Candidates with expertise in the application of modern molecular methods (e.g. genomics, bioinformatics) to the study of natural populations (e.g. population genetics/genomics, evolutionary biology, or wildlife biology) are encouraged to apply. Teaching duties will include existing or new courses within the successful candidate's area of expertise at the undergraduate and graduate levels, particularly related to areas of genetics and evolution. The successful candidate is expected to conduct research in some area of genetics, evolution, or wildlife biology and be amendable to collaboration with other faculty on relevant, genetics oriented projects; attract and secure extramural funding, publish in genuine peer reviewed journals, attend professional meetings, provide academic advisement to undergraduate and graduate students, engage students in research, and develop and deliver effective educational programs to the community.

Primary responsibilities include:

- Teaching selected undergraduate and graduate courses, such as Genetics, Conservation Genetics, Molecular Cytogenetics, and General Biology with the possibility of developing new courses based on candidate's experience and expertise.

- Developing a dynamic research program by attracting new grants and opportunities that would allow undergraduate and graduate student participation.

- Conducting professional service for the institution, academic field, and community.

- Recruiting students for the undergraduate and graduate programs in Life, Earth, & Environmental Sciences

- Advising students on matters of degree plans, course scheduling, and other academic matters Necessary Qualifications:

- An earned Ph.D. in Biology or related area from an accredited institution. ABD will not be considered.

- Demonstrated experience and excellence in teaching related to the courses listed above.

- Willingness to teach 9 adjusted contact hours (ACH) per semester.

- Competency in research related to genetics, as evidenced by publications (full citations) in genuine peer-reviewed journals.

- Demonstrated experience in seeking/obtaining extramural funding (including documentation of awards and amounts).

- Excellent quantitative, computer, written, and oral communication skills. Preferred Qualifications:

- Familiarity with the diversity of modern genetic techniques/methodology.

- Demonstrated ability and skills in leadership, mentoring, and building teamwork.

- Experience in developing collaborative research with other scientists, research centers and/or agencies and organizations.

Special Instructions: Review of applications will begin Dec. 1, 2019 and continue until the position is filled. Position is available beginning in the fall semester of 2020. Salary and benefits are competitive and commensurate with qualifications and experience. Interested applicants may apply at jobs.wtamu.edu.

Please attach all documents in the attachment box at the bottom of the "My Experience" page before continuing through the application. Although the attachment box is labeled "CV/Resume," more than one document may be included. All revisions must be made prior to application submission. If you need assistance with downloading documents, please contact WTAMU Human Resources at hr@wtamu.edu.

Equal Opportunity/Affirmative Action/Veterans/Disability Employer committed to diversity.

Texas law requires all males age 18 through 25 to be properly registered with the Selective Service System. All positions are security-sensitive.

Applicants are subject to a criminal history investigation, and employment is contingent upon the institution'Âs verification of credentials and/or other information required by the institution'Âs procedures, including the completion of the criminal history check.

"Johnson, James B." <jbjohnson@wtamu.edu>

Yale-NUS College Evolution

Yale-NUS College in Singapore invites applications for the Wong Ngit Liong Professorship in Science

Position Description:

Yale-NUS College is a liberal arts and sciences college with approximately 1000 students and 110 full-time faculty. The College is a collaboration between Yale University and the National University of Singapore. Yale-NUS students are intellectually outstanding, with an acceptance rate of less than 7%, and internationally diverse, representing over seventy countries. They go through a unique and rigorous Common Curriculum in the sciences, social sciences and humanities that combines Western and Eastern traditions with contemporary skills.

The College invites applications for a visiting (1-3 years duration) or full-time (tenured) endowed professorship position in science. Application by established academics with an international reputation in any scientific discipline are encouraged. Preference may be given to those who show clear potential for collaborative interaction with existing faculty or are engaged in interdisciplinary inquiry. A demonstrated commitment to pedagogical excellence and innovation is also required. Relevant career experience in a liberal arts and sciences environment would be advantageous.

Applicants should have a relevant PhD and demonstrate an outstanding research and teaching track record in their field.

The incoming faculty member would join a committed team dedicated to the development and teaching of majors in Environmental Studies, Life Sciences, Mathematical, Computational and Statistical Sciences, and Physical Science (https://www.yale-nus.edu.sg/curriculum/majors/).

The appointee would also be expected to engage with our flagship Common Curriculum (see http://www.yale-nus.edu.sg/curriculum/common-curriculum).

The appointee will be expected to begin duties in time for the start of the 2021-2022 academic year (i.e. from July 2021) or sooner.

Faculty receive internationally competitive salaries and start-up grants as well as a yearly travel and research allowance, and are able to access additional funding from Yale-NUS, the National University of Singapore and Singapore's Ministry of Education. Most faculty qualify for highly subsidized faculty housing. Yale-NUS College is located in Singapore, a multicultural city of six million at the heart of a vibrant region.

Application Procedure

Applications should consist of the following: a cover letter explaining why the position at Yale-NUS is of interest; a full curriculum vitae, including a complete list of publications; statements on research interests, teaching experience and teaching philosophy, including how these might fit with the College's particular mission and curriculum; names and contact information of three academic referees.

Applications should be submitted via https://academicjobsonline.org/ajo/YaleNUS . Review of applications begins January 1st 2020 and will continue until the position is filled.

Only shortlisted candidates will be notified.

https://www.nature.com/naturecareers/job/wong-ngit-liong-professorship-in-science-yalenus-college-709881
philip.m.johns@gmail.com

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AMNH NewYork Women STEM fellowship

Dear Colleagues,

The BridgeUP: STEM program at the AMNH is excited to announce that the application for the Helen Fellowship is open. This fellowship is a one-year residency for post-baccalaureate, self-identifying females, to devote time immersed in computational scientific research and educational outreach at the AMNH. This fellowship is an initiative at the AMNH dedicated to increasing the diversity of the talent pipeline by providing underrepresented students access to the skills and tools required for the 21st Century.

To learn more about the fellowship and the application process, visit https://www.amnh.org/learn-teach/-higher-education/helen-fellowship . A colorful PDF flyer can be downloaded at this website.

Who is eligible to apply? The fellowship is intended for recent college graduates with a conferred bachelor's or master's degree in computer science, natural sciences, applied mathematics, computational science, or other relevant majors prior to the fellowship start date in September.

What are the benefits? Fellows will receive an annual salary of $70,000 plus generous benefits. Funding is also available for research, travel and equipment expenses.

How do I apply? The online application is now open and is due by midnight of January 19, 2020. To learn more about application requirements, visit https://www.amnh.org/learn-teach/higher-education/helen-fellowship . With Regards,

The BridgeUP: STEM Team

Email: bridgeupstem@amnh.org

Louise Crowley <crowley@amnh.org>

ArnoldArboretum HarvardU funding

Research Funding opportunities at the Arnold Arboretum of Harvard University

The Arnold Arboretum of Harvard University promotes and supports research consistent with its mission to discover and disseminate knowledge of the plant kingdom. To foster both independent and collaborative work, the Arboretum offers fellowships and awards to students, post-doctoral researchers, and professionals of the biological sciences including evolution, ecology, development, and genetics. Applicants are encouraged to define and develop paths of inquiry using the Arboretum's resources, including its world-renowned living collection, herbarium, plant records, library and archives, greenhouse and laboratories, and the expertise of its staff.

There is currently one fellowship, eight awards, and an internship program. Applicants must submit a research proposal online by Feb 1. Please see the website for the specific requirements of each award.

http://www.arboretum.harvard.edu/research/-fellowships/ Available opportunities:

DaRin Butz Research Internship Program of the Arnold Arboretum of Harvard University Ashton Award for Student Research Cunin / Sigal Research Award Deland Award for Student Research Shiu-Ying Hu Student/Postdoctoral Exchange Award Putnam Fellowship in Plant Science Arnold Arboretum Genomics Initiative and Sequencing Award Jewett Prize Sargent Award for Visiting Scholars Sinnott Award

Application Deadline: Feb 1 annually

– Faye Rosin, PhD Director of Research Facilitation

Arnold Arboretum of Harvard University 1300 Centre St Roslindale, MA 02131

phone: (617) 384-5095 fax: (617) 384-6596

frosin@oeb.harvard.edu http://arboretum.harvard.edu/ "Rosin, Faye M" <frosin@oeb.harvard.edu>

CallForProposalsToHostSMBE2023 DeadlineNov30

Subject: Call for Proposals to Host SMBE 2023 - Deadline 30 November 2019

Dear SMBE Members:

Want to meet like-minded colleagues from all over the world?

Wish you could have an international conference in your field closer to home?

SMBE is looking for a local host for its 2023 international meeting. Informal expressions of interest should be from a prospective local organizing committee of scientists headed by an SMBE member, and should reach SMBE President-Elect Marta Wayne by 30 November 2019. Full proposals will need to be submitted using the SMBE template by 30 April 2020. Please email your proposal to Smbe.contact@gmail.com.

For details of meeting organization, please see the SMBE Conference Guidelines (https://www.smbe.org/smbe/-MEETINGS/ConferenceGuidelines.aspx and specifically Appendix 2 which outlines the format of proposals).

The primary role of the local organizing committee will be to plan the scientific programme. All other aspects of the organization will be done in association with SMBE representatives and a professional conference organizer appointed by SMBE.

SMBE rotates its meetings geographically to encourage international participation. For 2023, we are particularly requesting proposals from North America. The next three years' meetings will be in Quebec, Canada (2020), Auckland, NZ (2021) and Ferrera, Italy (2022).

Please note that SMBE is not interested in proposals from professional conference organizers.

Looking forward to hearing from you.

Sincerely,

Marta Wayne

President-Elect, SMBE

Smbe.contact@gmail.com

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

ESEB Call MaynardSmith Hewitt Awards

John Maynard Smith Prize 2020: Call for Nominations

Every year the European Society for Evolutionary Biology (ESEB) distinguishes an outstanding young evolutionary biologist with a prize named after John Maynard Smith (1920 - 2004), eminent scientist, great mentor, author of many books on evolution, and a former President of ESEB.

Nomination:

The prize is open to any field of evolutionary biology. The candidates for the 2020 prize must have begun their PhD study after January 1, 2013. In addition, nomineeswill be considered who are more than 7 years from the start of their PhD if they have had career breakstaken for family, caring or health reasons; the nature of the reason must be given. The nomination of the candidate may be by a colleague or self-nominated. The nominations should be sent as a single PDF file to Ute Moniatte at the ESEB office <office@eseb.org>. The nomination should include a brief justification, the candidate's CV and list of publications (indicating three most significant papers), a short description of future research plans (about 1-2 pages), and a letter from the candidate approving the nomination. A letter of reference from another colleague (or two in case of self-nomination) should be sent directly to Ute Moniatte.

Nominations and letters of support should arrive no later than Friday,**January 17, 2020. Please take care to limit the size of attachments (total < 10 MB) in any one email.

The nomination committee, chaired by the ESEB Vice President Sara Magalhāes, will evaluate the nominations and inform the winner approximately by the end of February 2020.

The prize winner is expected to attend the ESEB congress in August 2021 in Prague, Czech Republic, where he or she will deliver the 2020 John Maynard Smith Lecture. The Society will cover registration, accommodation, and travel expenses (economy fare). The JMS Prize comes with a monetary prize of 2500 euro , the invitation to write a review for the Journal of Evolutionary Biology, and the possibility of a Junior Fellowship of 6 months at the Institute of Advanced Study (Wissenschaftskolleg) in Berlin, Germany. For more information on the Institute of Advanced Study see www.wiko-berlin.de/en/ . Previous winners of the JMS Prize are listed on the ESEB web site: www.eseb.org Sincerely, Sara Magalhāes ESEB Vice-President

Ute Moniatte ESEB Office Manager – Email: office@eseb.org European Society of Evolutionary Biology - eseb.org

ESEB <office@eseb.org>

Godfrey Hewitt Mobility Award 2020 'V Call for Applications

Godfrey Hewitt (1940-2013) was President of the European Society for Evolutionary Biology (ESEB) from 1999-2001. He was exceptionally influential in evolutionary biology both through his research and through his mentoring of young scientists. He was also a great believer in seeing organisms in their environment firsthand and in exchanges of ideas between labs. Therefore, ESEB annually offers mobility grants for young scientists in his name.

Closing date: Friday, 17 January 2020.

*Eligibility: *

The award is open to PhD students or postdoctoral scientists who are, at the closing date for applications, within 6 years of the start date of their PhD and ESEB members. In addition, applicants will be considered who are more than 6 years from the start of their PhD if they have had career breaks, worked part-time, or for other reasons have not worked continuously. Applicants who have previously received a Godfrey Hewitt mobility award are not eligible. The maximum single award will be 2000 Euros. It must be used to support fieldwork or a period of research at a lab that you have not previously visited. There is no restriction on the country of residence or nationality of the applicant. A report will be required by 30 April 2021, by which time the funds must have been used.

*Application procedure: *

Your application should be sent as a single PDF file to Ute Moniatte at the ESEB office, office@eseb.org. It should include your name, current status and institution, your PhD start date, your ESEB membership number, a description of the work to be carried out (maximum 500 words), an outline budget with brief justification (maximum 100 words) and a signed statement from your PhD supervisor or postdoctoral adviser (maximum 100 words) explaining why the work cannot be funded from your home institution or your proposed host institution.

Applications will be considered by a committee chaired by Mike Ritchie. The aim will be to announce decisions before the end of March 2020. In previous rounds, success rates have been between 20 and 40%.

The committee will consider the following key criteria:

1.The value of the proposed mobility in terms of its expected output and impact on the applicant'Âs career. The committee prefers projects that are:

— / —

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

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NSF EnvironmentalBiology VirtualOffice

Check out our blog at DEBrief: https://debblog.nsfbio.com/ Virtual Office Hours on December 9th: Register Here

The National Science Foundation's Division of Environmental Biology (DEB) will begin to hold monthly Virtual Office Hours to discuss a variety of topics and provide an opportunity to have a questions & answer period on the second Monday of every month.

The FIRST Virtual Office Hour, on December 9th from 1pm-2pm EST, will provide an introduction to DEB and present on the no-deadline solicitation (NSF 20-502). Representatives from each of the four clusters will be available to introduce their program, followed by a brief discussion on the no-deadline process. There will then be an open question and answer period - questions can be on any NSF/DEB topic.

Use the registration link below to set up your participation in our DEB Virtual Office Hour. https://nsf2.webex.com/nsf2/onstage/g.php?MTID=e8df6e3273f17115492cac899eedb556a Upcoming DEB Virtual Office Hours will be communicated through DEBrief (https://debblog.nsfbio.com/), so sign up for blog notifications for reminders. Also, follow us on the NSF Biology Twitter account (@NSF_BIO) where they will be announced. For any of the events you are unable to attend, we will be posting a recap of our presentations on our blog.

Upcoming Office Hours and Topics: December 9: Intro to DEB/Submission and Review Process January 13: Integration Institutes February 10: Rules of Life vs. Understanding Rules of Life March 9: RAPID/EAGER/workshops April 13: OPUS May 11: CAREERs June 8: BIO Postdoc Program

"Lewis, Megan" <meglewis@nsf.gov>

Practical Exercises

Hello Evoldir community

I teach an introductory course on ecology for first year undergraduates. I assume it follows a typical standard format: two hours per week, mostly lectures, some compulsory reading (mostly "Ecology" by Begon et al.). In between, we also offer short practical parts, where the students have the opportunity to experience some fundamental topics in ecology by themselves. Now, it is quite challenging to offer a practical experience to 200 students in 2 hours and I was wondering whether you are willing to share your ideas. In my opinion, such intermezzi are a great way to spark motivation and to repeat the theory from the previous lesson.

However, good exercises are often only suitable for small groups, require a lot of preparation, etc. I am looking for the exact opposite: Ideally, the exercises require little preparation, are happening outdoor, are minimally destructive for the environment, cover central topics of ecology, allow testing a hypothesis within two hours, are more or less season-independent, and can be done with minimal tutoring (using an app?). It is difficult to check all these boxes, but you get the gist.

If you have a great idea for such an exercise, it would be great if you could share it. Here are two of ours (we are looking for a great third one!):

Measuring biodiversity In groups of 24 students (teams of 4), they learn how to assess plant species diversity in randomly chosen quadrants. This gives the opportunity to discuss things such as: how to chose a location randomly, how to quantify heuristically the proportion of every species in the quadrant, how to calculate a diversity index. By doing this on a gradient from the edge of a forest to the center, they can also verify whether there is a change in diversity and you can discuss the reasons for this (e.g. intermediate disturbance hypothesis). Per group, this takes about 2 hours and with the help of assistants, we can offer ten of these exercises in one week. Later, you can also combine all results and carry out some simple statistics to test a hypothesis.

Stage-structured matrix models This exercise is taken from the great book "Spreadsheet Exercises in Ecology and Evolution" by Donovan and Welden. I converted it into an online-course with some documents to download and work on and some videos that explain what to do. This allows the students to work independently at home. The following week, I offer a lesson to ask questions and clarify things. The downside: it is not a real hands-on experience, as the student sits in front of the computer.

I am happy to share them, by the way, but I have to warn that they are in german.

All the best

Dominik

Dr Dominik Refardt Zurich University of Applied Sciences ZHAW Institute of Natural Resource Sciences IUNR Grüental Campus CH-8820 Wädenswil Switzerland

"Refardt Dominik (refa)" <refa@zhaw.ch>

SiberianJayProject FieldAssist

Expenses paid field assistant positions to assist in social observations and bird ringing of Siberian jays in Swedish Lapland

For the field season spring 2020 (29.2-29.3.2020), we are looking for two highly motivated, expenses paid field volunteer to join our field project (main responsible Dr. Michael Griesser). The study site is located near Arvidsjaur, Swedish Lapland. An overview over our work can be found here: https://www.youtube.com/watch?v=-JaH6wjAYAiE Our current project investigates social interactions of Siberian jays. The work of the field volunteers will be to help with a population census, behavioural observations, catching and colour-ringing birds, blood sampling, and data management. This work will give insight into a long-term study system and will be carried out in managed and pristine boreal forests.

Observe that we can access the study site only on X-country skis, requiring a basic knowledge of X-country or down-hill skiing. Moreover, field work can be physically demanding at times, with temperatures falling below -25C at times.

The team will vary in size depending on the weeks, but at least two other people will be present during the whole field season.

Qualifications: (1) Basic skiing experience (X-country or downhill) (2) Preferably bird ringing and mist-netting experience (3) Previous field experience (4) Ability to work in small teams and sociable personality (5) Driving license (6) Fluent in English

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

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

Applications received until 15 Dec 2019 will be given full consideration.

Michael Griesser <michael.griesser@gmail.com>

SMBE conference CallForProposalsToHost2023

Dear SMBE Members:

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Wish you could have an international conference in your field closer to home?

SMBE is looking for a local host for its 2023 international meeting. Informal expressions of interest should be from a prospective local organizing committee of scientists headed by an SMBE member, and should reach SMBE President-Elect Marta Wayne by 30 November 2019. Full proposals will need to be submitted using the SMBE template by 30 April 2020. Please email your proposal to Smbe.contact@gmail.com.

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SMBE rotates its meetings geographically to encourage international participation. For 2023, we are particularly requesting proposals from North and South America. The next three years' meetings will be in Quebec, Canada (2020), Auckland, NZ (2021) and Ferrera, Italy (2022).

Please note that SMBE is not interested in proposals from professional conference organizers.

Looking forward to hearing from you.

Sincerely,

Marta Wayne President-Elect, SMBE

Smbe.contact@gmail.com

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

SocietySystematicBiologists CouncilStudentRepPosition

Are you a graduate student systematist? Do you also want to give a voice to students on the Society of Systematic Biologists council? Submit an application to run for SSB council. Send the application to ssbstudentcouncilreps@gmail.com by December 1, 2019 with the subject SSB Student Rep. The nomination application should be a single PDF document (SSBStudentRep_LastName.pdf) containing the students CV (1 page) and a short paragraph for voters (maximum 150 words) describing their background and why they are a good candidate to represent students on SSBs council.

Any student member is allowed to nominate themselves or other students, and faculty are also strongly encouraged to nominate students. Ballots to vote for the graduate student representative will be sent out to student members of SSB in December 2019.

KINSEY M. BROCK Ph.D. Candidate Quantitative & Systems Biology School of Natural Sciences University of California, Merced

Kinsey Brock <kbrock@ucmerced.edu>

SouthAfrica Volunteers StripedMouseProject

Volunteers needed from Dec 2019 / January 2020 onwards

Minimum stay 2 months

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work related to animal behavior, evolution, eco-physiology, and ecology before starting an MSc or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, solitary living, and social flexibility in the striped mouse and the bush Karoo rat. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As these species are diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 AM), and stops its activity with dusk (7 PM). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40Â^{o}C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of volunteer field assistants: Trapping, marking and radio-tracking of small mammals; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements and how we measure metabolic rate. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1750 (around 110 Euro) must be paid for accommodation at the research station. Students must buy their own food in Springbok. Including extras (going out for dinner; shopping), you should expect costs of about 500 Euros or 600 US$ per month.

German students can apply for a grant from the Deutsche Akademischer Auslandsdienst (DAAD, www.daad.de). Here, commonly travel grants of 300 Euro are given to students. Students from other countries are encouraged to seek funding from their home institutions / home country. Students get an invitation letter which they can use to apply for funding in their home country.

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: We are looking for volunteers to start in December 2019 as well as beginning of 2020. Volunteers are expected to stay for a minimum of 2-3 months, though longer periods are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to succulent.karooo.research.station@kabelbw.de.

More information under

http://www.stripedmouse.com/documents/-GeneralInformationResearchStationJan2018.pdf

http://stripedmouse.com/site1_3_5.htm Dr. Carsten Schradin

Director of the Succulent Karoo Research Station (South African non-profit organization), Goegap Nature Reserve, PO Box 541, 8240 Springbok, South Africa

http://www.stripedmouse.com

Description: Logo_June 2014

Director Succulent Karoo Research Station <succulent.karoo.research.station@kabelbw.de>

StudentResearchFunding ForLepidoptera

Students (graduate or undergraduate) who are studying Lepidoptera are encouraged to apply for the Ron

Leuschner Memorial Fund for Research on the Lepidoptera - deadline January 15, 2020. The application is on the awards page for the Society https://www.lepsoc.org/content/awards. Contact Shannon Murphy (email address on the application) if you have any questions!

< https://www.lepsoc.org/content/awards?fbclid=IwAR269zYzDme6UjsWlSB0iKVwYtaGGcGzkdcrCP4_77KXRoKoRlLvgZLKKQ >

Bruce Walsh Professor, Ecology and Evolutionary Biology Professor, Public Health Professor, BIO5 Institute Professor, Plant Sciences Adjunct Professor, Animal and Comparative Biomedical Sciences Adjunct Professor, Molecular and Cellular Biology Member, Graduate Committees on Applied Math, Insect Sciences, Genetics, Statistics University of Arizona

Evolution and Selection of Quantitative Traits (Oxford 2018) https://global.oup.com/academic/product/evolution-and-selection-of-quantitative-traits-9780198830870 https://www.amazon.com/gp/product/0198830874 Genetics and Analysis of Quantitative Traits (Sinauer <Oxford> 1998) https://global.oup.com/academic/product/genetics-and-analysis-of-quantitative-traits-9780878934812 https://www.amazon.com/Genetics-Analysis-Quantitative-Traits-Michael/dp/0878934812 Goggle Scholar https://scholar.google.com/citations?user=7iQEFwIAAAAJ&hl=en&oi=ao "Walsh, Bruce - (jbwalsh)" <jbwalsh@email.arizona.edu>

UParis Saclay Internship BirdBehavior

Internship opportunity (5 months) : Daily foraging routines in common garden birds using birdfeeders - is the proverbial ≪early bird≫ living in the garden?

UMR 8079 Ecologie, Systématique, Evolution (ESE), Université Paris-Saclay, Bât 362 Orsay in collaboration with CESCO, MNHN

Carmen Bessa-Gomes (UMR 8079 ESE) François Chiron (UMR 8079 ESE) Romain Lorrillière (UMR 7204 CESCO) Nicolas Deguines (UMR 7204 CESCO)

Timing of feeding and daily foraging routines have been the object of research in the past, particularly in the field of optimal foraging. Daily foraging routines will influence energy budgets. Hence, albeit the proverbial advantage of the "early" bird, past research has highlighted that under cold temperatures individuals may delay the beginning of their foraging journey, limiting the metabolic costs of foraging under cold temperatures. Daily routines also depend of intraspecific interactions and subdominant individuals have been shown to have longer foraging hours in relation to dominant individuals. While an early start can reduce competition, it may increase predation risk, diminishing overall survival. Research on daily foraging routines has often been made in controlled feeding apparatus focusing on target species or functional groups. Hence, the role of interspecific interactions other that predation have received scant attention. Such approaches limit our understanding of the impact of such interactions, particularly competition. We propose to further such understanding by examining the question of daily foraging routines at the community level using bird feeders for garden birds.

Here we propose to examine the question of daily foraging routines at the community level using bird feeders for garden birds. We propose to test the following hypothesis:

"Territorial species favour an early/dusk feeding pattern relatively to species likely to participate in winter foraging flocks"

Other than being present at close proximity to the resource, territorial individuals are likely to benefit from their familiarity with the local environment. We propose that they should reduce the cost of interspecific competition by feeding before/after the presence hours of winter foraging flocks.

We propose to test our hypothesis using the citizen science scheme BirdLab. BirdLab is the first citizen science scheme that couples a serious game and bird observation on a smartphone. It aims at gathering information about foraging social behaviours of birds during winter, using a standardized protocol. Data provided are species abundance and interactions at feeders. The participants set up two identical feeders 1-2 meters apart and filled with sunflower seeds. They can record up to 27 species among the most common and easily identified ones at bird-feeders. A user-friendly app (available for tablet and smartphone on Android and iOS) represents the two feeders, as well as icons of the 27 species. During exactly five minutes, the participant will drag and drop these icons between the feeders to mimic bird movements they see. Hence, timing of bird arrivals, departures and switch between feeders are recorded in real time. Participants can repeat this 5 minutes protocol any time they want during winter season (from November 15th to March 31th). After five winters (since the 15th November 2014), ca. 33,000 5 minutes sessions have been performed covering the whole France and

2,264 participants sent data at least once.

The student will be based at the ESE lab in Orsay, but there will be regular monthly meetings with all researchers working on the project. The student will receive a monthly stipend of 600 euro .

Starting date : February 2020

Requirements: * Bachelors degree in a relevant field of study (ecology, biology, environmental sciences) * Good skills in data management and analysis * Skill in R

How to apply : Send your motivation letter and CV to Carmen Bessa Gomes (carmen.bessa-gomes@u-psud.fr) prior to December 10, 2019.

Carmen Bessa-Gomes <carmen.bessa-gomes@u-psud.fr>

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AarhusU Denmark MutationRateEvolution

We seek a motivated and independent candidate for a 2-year postdoc position available at the Department of Molecular Medicine (MOMA), Aarhus University. The position is available from February 1st, 2020 or as soon as possible thereafter.

The postdoc will work on an exciting project concerning the evolution of germline mutation processes in humans. This can include comparisons with datasets of human somatic mutations or germline mutations from other species. Depending on your interests, focus can be on methods development, large-scale data analysis, or both.

We are looking for a highly motivated applicant that have or are about to obtain a PhD in a relevant subject, which could be bioinformatics, population genetics, molecular evolution, statistical genetics or a similar subject.

Application deadline is December 8th.

For details see: https://www.nature.com/naturecareers/job/readvertisement-postdoc-in-bioinformatics-aarhus-university-au-711741 "besenbacher@clin.au.dk" <besenbacher@clin.au.dk>

AMNH NewYork BioinformaticsComputationalBiology

American Museum of Natural History Postdoctoral Fellowships in Bioinformatics and Computational Biology

The American Museum of Natural History seeks highly qualified applicants for two postdoctoral positions for its Gerstner Postdoctoral Scholars program in Bioinformatics and Computational Biology. The 2019-20 application cycle includes a special opportunity for applicants who want to pursue comparative biology research relevant to human health or biomedicine.

Successful applicants will pursue independent and collaborative computational research in integrative studies of genomics, spatial bioinformatics or biodiversity informatics, alongside faculty and other researchers interested in phylogenetics, phylogeography, evolutionary, and high- throughput phenomic/phenotypic studies. Gerstner Scholars in Bioinformatics & Computational Biology (GSB&CB) also will contribute to the design, development and implementation of new algorithms and other bioinformatics tools that are customized for Museum research and address emerging big data issues in phylogenetic and comparative biology analyses. In association with their professional development and contributions to the Museum, a portion of each Scholars' efforts will include teaching and workshops (with the https://www.amnh.org/our-research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/gerstner-scholars-program/gerstner-scholars-in-bioinformatics-computational-biology and https://www.amnh.org/our-research/sackler-institute-for-comparative-genomics) and assistance to Museum scientists and students with their bioinformatics and computational biology research.

The initial appointment will be for one year, potentially renewable for one to two additional years based on performance, and includes a highly competitive salary and generous benefits.

Requirements: Applicants must have a PhD in Biological Sciences, Bioinformatics, Computational Biology, Computer Science, Molecular Biology, Genomics, or a related discipline, with experience in the bioinformatics of large biological data sets. Proficiency in Python, Perl, and/or R is required, and familiarity with those and other languages, such as C++/C, or Java, is desirable. Candidates should have documented skills in genome informatics, such as sequence processing, de novo and reference guided assembly, read mapping, gene annotation and discovery, and/or processing phenomic, transcriptomic, or phylogenomic datasets. Candidates should have extensive research experience with a solid publication record, ideally with some experience in phylogenetic methods, and excellent interpersonal, writing and problem-solving skills.

Applicants are encouraged to contact potential research mentors/collaborators in advance to develop a research statement (see https://www.amnh.org/our-research/richard-gilder-graduate-school/faculty-searchhttps://www.amnh.org/our-research/richard-gilder-graduate-school/faculty-search or https://www.amnh.org/our-research/richard-gilder-graduate-school/faculty-search). This program encourages applications from scholars with research interests that may have broad implications for such themes as advancing our understanding of the evolution and diversity of species and the "tree of life," genomics, and/or human and medical research. Further information on the Gerstner Scholars program and prior Scholars are at https://www.amnh.org/our-research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/gerstner-scholars-program/gerstner-scholars-in-bioinformatics-computational-biology and https://www.amnh.org/our-research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/gerstner-scholars-program/gerstner-bioinformatics-and-computational-biology-scholar-profiles . For more information and how to apply please click the link below:

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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

Amsterdam 2 MolecularUrbanEvolution

For the ERC-funded project CITISENSE we are searching for a post-doc who will be in charge of unravelling the genomic architecture underlying urban adaptation. In the project we aim to understand whether and how tÂÂ^{2}ngara frogs have evolved in response to urbanization and whether observed phenotypic differences are related to genomic differences. Our study system in Panama consists of multiple paired urban and forest frog populations which we would like to screen for genetic divergence and signs of selective sweeps. Furthermore, we have started a breeding program that will allow us to link acoustic phenotypes to genotypes.

Your duties

* develop and execute new line of research within the project * publish results in scientific journals Requirements

* a PhD degree with an interest in ecology and evolution * strong background in genomics * experience with molecular techniques. Expertise in next-generation sequencing, RADseq or programming is a plus * excellent ability to communicate in both written and spoken English * good social skills, ability to work independently and strong scientific motivation * APPLICATION * Are you interested in this position? See for more details and how to apply here <https://workingat.vu.nl/ad/post-doc-positie-2-on-molecular- urban-evolution/itdg7c> * * Please only apply via the application button found on this page <https://workingat.vu.nl/ad/post-doc-positie-2-on-molecular- urban- evolution/itdg7c> and upload your curriculum vitae and cover letter until 15 December 2019. The job interviews are planned for January 2020, when possible please take them into account when applying for the position. * * * Vacancy questions If you have any questions regarding this vacancy or the project description, you may contact:

Name: Wouter Halfwerk Position: Assistent Professor E-mail: w.h.halfwerk@vu.nl Telephone: +31(0)20-5987046

For the ERC-funded project CITISENSE we are searching for a post-doc who will assess urban evolution by comparing real and artificial phenotypes. In the project we aim to understand whether and how male tÂÂ^{2}ngara frogs have adapted their acoustic sexual signals to urban sensory conditions such as anthropogenic noise and artificial light. We would like to run an experimental evolution experiment under urban and forest field conditions, by making use of a system of evolvable artificial acoustic phenotypes. You will be in charge of developing and employing automated setups that will allow us to carry out interactive playbacks in the tropical rainforest of Panama.

Your duties

* develop and apply novel field techniques within the project'Âs scope * publish results in scientific journals Requirements

* a PhD degree in the field of ecology and evolution * experience with behavioral experiments in the lab or the field * expert skills in signal analyses/acoustics, and/or, engineering/programming * excellent ability to communicate in both written and spoken English * good social skills, ability to work independently and strong scientific motivation

APPLICATION Are you interested in this position? See for more details and how to apply here < https://workingat.vu.nl/ad/post-doctoral-research-position-on-urban-evolution/nh4gql >

Please only apply via the application button found on this page < https://workingat.vu.nl/ad/post-doctoral-research-position-on-urban-evolution/nh4gql > and upload your curriculum vitae and cover letter until 15 December 2019. The job interviews are planned for January 2020, when possible please take them into account when applying for the position.

Vacancy questions If you have any questions regarding this vacancy or the project description, you may contact:

Name: Wouter Halfwerk Position: Assistent Professor E-mail: w.h.halfwerk@vu.nl Telephone: +31(0)20-5987046

"Halfwerk, W.H." <w.h.halfwerk@vu.nl>

ArnoldArboretum HarvardU PlantEvolution

Katharine H. Putnam Fellowships in Plant Science The Arnold Arboretum of Harvard University invites applicants for research fellowships in plant science. Putnam Fellowships offer excellent opportunities for advanced research and study using the Arboretum's living collections of woody plants. Scientists with a PhD and who have identified an independent research project that would utilize the Arboretum's living collections are encouraged to apply. The living collection, numbering some 15,000 plants, in over 2,200 species, is distinguished as one of the most thoroughly documented collections of temperate woody plants in the world. Taxonomic diversity and breadth within the collection are noteworthy, and the floras of China, Japan, and Korea are particularly well represented.

Deadline: Feb 1

Eligibility: Proposals are sought from early-career individuals with a PhD in plant biology, evolution, plant genetics, plant ecology, horticulture, or related discipline. Applicants should be well positioned to conduct original, independent research and to publish their findings in peer-reviewed publications.

Fellowship Details: Putnam Fellows are full-time employees of Harvard University during their tenure, with stipends of up to $48,000 per year depending on the duration of the fellowship, and are eligible for health insurance benefits. Modest support is available for research expenses and travel costs. The fellowship is typically awarded for 2 years, pending a satisfactory progress report at the end of the first year. Putnam Fellows are expected to be in full-time residence at the Arboretum and are provided office and research space. The Putnam Fellowship is an independent post-doctoral position. As an independent scholar, Putnam Fellows have access to shared laboratories, resources, and interactions with fellow scientists, students and staff. It is not necessary to have a specific faculty host.

More information: https://arboretum.harvard.edu/-research/fellowships/ – Faye Rosin, PhD Director of Research Facilitation Arnold Arboretum of Harvard University 1300 Centre St Roslindale, MA 02131

phone: (617) 384-5095 fax: (617) 384-6596

frosin@oeb.harvard.edu http://arboretum.harvard.edu/ "Rosin, Faye M" <frosin@oeb.harvard.edu>

AuburnU PDF PhD InvertEvolGenomics

Invertebrate Evolutionary Genomics - postdoc and student positions

Strong applicants are being sought for a Ph.D. Student(s) and a Postdoctoral fellow to work on an US National Science Foundation funded project on population genomics of Antarctic marine invertebrate taxa. The research will use RAD-tag based SNP approaches, as well as complete genome sequencing, to explore various phylogeographic hypotheses in the Southern Ocean.

Additionally, a Ph.D graduate student is sought to help with phylogeny and life history evolution in trematode blood flukes.

For all positions, a strong backgrounds organismal biology and bioinformatics is desired.

Postdoctoral candidates will start in early 2020. Those interested should send CV and brief (1 paragraph) statement of interest to ken@auburn.edu

Potential student candidates should contact ken@auburn.edu and copy Kirby Norrell, kln0009@auburn.edu, the Department of Biological Science Graduate Program professional assistant.

Ken Halanych Auburn University

https://scholar.google.com/citations?user=-

T9MulP4AAAAJ&hl=en&oi=ao http://-metazoan.auburn.edu/halanych/lab/projects.html
Kenneth M. Halanych Schneller Chair, Alumni Professor Curator of Marine Invertebrates Biological Sciences Department Life Sciences Bld. 101 Auburn University Auburn, AL 36849

http://metazoan.auburn.edu/halanych/lab/index.html Phone: (334)-844-3222 e-mail: ken@auburn.edu

Editor-In-Chief The Biological Bulletin http://-www.journals.uchicago.edu/toc/bbl/current Kenneth Halanych <ken@auburn.edu>

Berlin 2 AdaptiveBehaviour

As a joint project of Max Wolf and Jens Krause, we are looking for two postdocs working with us at uncovering the behavioural rules underlying the development of adaptive behaviour. This project is embedded in the Science of Intelligence Cluster in Berlin (https://www.scienceofintelligence.de/) which will provide an extremely stimulating research environment.

We are looking for one experimental person working with fish (Amazon molly) and one theoretician developing mathematical and/or computer simulations models. The positions are for three years, application deadline is 29.11.2019, project start should be between April 2020 and October 2020. Details on the project, the two positions and the application process can be found on:

https://www.scienceofintelligence.de/call-for-applications/open-positions/ Projects “Mapping behavioral-experiential trajectories...” and “Algorithmic models of exploration behavior”.

For further questions please get in touch with Max Wolf (m.wolf(at)igb-berlin.de)

Max Wolf <m.wolf@igb-berlin.de>

BOKU Vienna DiseaseEvolution

University of Natural Resources and Life Sciences, Vienna (BOKU)

Department of Forest and Soil Sciences,

Postdoctoral Research Fellow

Full-time (40 h/week)

Fixed-term contract (3 years)

A Postdoctoral position is available at the Institute of Forest Entomology, Forest Pathology and Forest Protection, Department of Forest and Soil Sciences, at BOKU Vienna in the lab of Christian Stauffer.

The project aims to unravel factors influencing phytoplasma transmission by plant-sucking insects. Phytoplasmas are bacterial pathogens that cause hundreds of plant diseases affecting many important vegetables and fruit crops, thus being responsible for high yield losses worldwide. These pathogens reside in the plant’s phloem and transmission among plants is mainly mediated by phloem-sucking insects. Apple proliferation is a disease caused by the phytoplasma Candidatus Phytoplasma mali. While several phloem feeders occur on apple, only a small number is able to acquire and transmit phytoplasmas. We aim to unravel different phytoplasma transmission pathways in different insect vectors using a population genetic approach.

We are looking for an enthusiastic candidate with a strong background in next-generation sequencing and bioinformatic analyses. The candidate will be responsible to investigate factors affecting transmission efficiency of Phytoplasma mali by the two main vectors Cacopsylla picta and Cacopsylla melanoneura. Specifically, s/he will perform population genetic analyses of the insects, its microbiome and phytoplasma strains.

The following activities are planned:

- Insect sampling
- Genome sequencing of different insect-vector species and populations
- Genome sequencing of phytoplasma strains

The project is in close collaboration with Hannes Schuler (Free University of Bozen-Bolzano), Katrin Janik (Research Centre Laimburg), Rosemarie Tedeschi (University of Turin) and Omar Rota-Stabelli (Fondazione Edmund Mach). The salary is according to the standard personnel costs of the FWF https://www.fwf.ac.at/-en/research-funding/personnel-costs/ . General requirements for the position: We ask a PhD degree in Plant Sciences, Biotechnology, Biology or Evolution with a multidisciplinary profile. The candidate should have excellent communication skills and should be fluent in English. German skills, although helpful, are not essential.

The project is expected to start in February 2020, but the starting date is negotiable.

Please send applications tochristian.stauffer@boku.ac.at until 30. November 2019 includingtwo reference letters,CV, a list of publications, and a cover letter expressing motivation. Please indicate FIGHToplasma as subject of the mail.

Christian Stauffer <christian.stauffer@boku.ac.at>

Bolzano Italy 2 InsectPhytoplasmaGenomics

Two Postdoc positions are being offered at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler. The project is funded for three years by the Austrian Science Fund (FWF) and the Province of Bolzano and aims to study different factors that are influencing the transmission of phytoplasmas by psyllid species.

Phytoplasmas are bacterial pathogens that cause hundreds of plant diseases affecting many important vegetables and fruit crops, thus being responsible for high yield losses worldwide. These pathogens reside in the plant's phloem and transmission among plants is mainly mediated by phloem-sucking insects. Apple proliferation is a disease caused by the phytoplasma 'Candidatus Phytoplasma mali'. While several phloem feeders occur on apple, only a small number is able to acquire and transmit phytoplasmas. We aim to unravel phytoplasma transmission pathways in different insect vectors using a population genetic approach.

We are looking for enthusiastic candidates with a strong background in next-generation sequencing and bioinformatic analyses as well as experience in performing ecological studies. The successful applicants will be responsible to study factors affecting transmission efficiency of Phytoplasma mali by the two main vectors Cacopsylla picta and Cacopsylla melanoneura. Specifically, s/he will perform population genetic analyses of the insects, its microbiome and phytoplasma strains. Moreover, in vivo phytoplasma transmission trials will be performed to determine the key factors influencing the acquisition and transmission of phytoplasma.

The project is in close collaboration with Christian Stauffer (Boku, Vienna), Katrin Janik (Research Centre Laimburg), Rosemarie Tedeschi (University of Turin) and Omar Rota-Stabelli (Fondazione Edmund Mach).

The Free University of Bozen-Bolzano is located in one of the most fascinating European regions, at the crossroads between the German-speaking and Italian cultures. Its trilingualism in teaching and research, its high level of internationalisation as well as an ideal study environment guaranteed by its excellent facilities are some of the reasons why unibz regularly reaches top positions in national and international rankings.

General requirements for the position: We ask a PhD degree in Plant Sciences, Biotechnology, Biology or Evolution with a multidisciplinary profile. The candidate should have excellent communication skills and should be fluent in English.

The project is expected to start in February 2020, but the starting date is negotiable. Application deadline is 16.12.2019 (post mark)

For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler hannes.schuler@unibz.it. Since the application process is pretty rigorous, I highly recommend to contact me before applying to the positions.

All documents for the application procedure can be found at: https://www.unibz.it/en/home/position-calls/positions-for-academic-staff/4415-general-and-applied-entomology-dr-schuler-pos-1?group= https://www.unibz.it/en/home/position-calls/positions-for-academic-staff/4416-allgemeine-und-angewandte-entomologie-dr-schuler-pos-2?group= Dr. Hannes Schuler Faculty of Science and Technology Free University of Bozen-Bolzano Universitätsplatz 5 I-39100 Bozen Tel: +39 0471 017648 http://hschuler.people.unibz.it Hannes.Schuler@unibz.it

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Brazil ForestAdaptation

Come work with us in a postdoc involving Brazilian dry and humid forests, genomics and adaptation in a project involving fantastic Brazilian and US collaborators at Unicamp, Usp, Ufscar, Unifesp, Harvard, Cornell, AMNH, OSU and VSU!

Please see additional details here: http://www.fapesp.br/oportunidades/adaptacao_na_diagnonal_seca_brasileira_ligando_genomas_e_fenotipos/3319/?fbclid=IwAR0AhopxBOV0iihO5orzSPDhGz0ag-Mi5Rvg2GdXqZLxNyaYDD1OsJ3IGw4 Summary

This post-doc fellowship focus on exploring genomes and phenotypes of birds and cacti from the so-called Dry Diagonal area in South America. The selected candidate will work at the Federal University of Sāo Paulo in Diadema (Sāo Paulo State, Brazil) where he/she will develop a research project linked to the Dry Diagonal Dimensions Project, which is conducted jointly by the Biology Institute of the University of Campinas (UNICAMP, Brazil) and Harvard University (US) - such collaboration is under the aegis of an agreement between the São Paulo Research Foundation (FAPESP) and National Science Foundation (NSF) through their respective programs BIOTA and Dimensions of Diversity.

Adaptation is a central process in evolution, and ecologically diverse groups of species offer opportunities to study adaptive evolution in many levels of biological organization. The Dry Diagonal Dimensions Project will use different types of data in order to understand how adaptation contributes to phenotypic, genomic, and phylogenetic diversification in dry vegetation and neighboring humid forests. Species from neotropical birds to cacti offer exciting examples of groups of closely related species occupying dry/open and humid forest, including cases involving species from Caatinga, Cerrado, Amazonia, and Atlantic Forest biomes. Those species complexes offer opportunities to explore the genomics of adaptation. Recent advances in sequencing technology facilitate the task of interrogating hundreds - or even thousands - of loci potentially related to phenotypic variation using both genomes and transcriptomes.

The selected researcher will:

- Collect and process samples of birds and cacti, and occasionally trait data; - Perform sequence capture of candidate genes and sequence complete genomes and transcriptomes; - Perform bioinformatics, genome and trait evolution analyses; - Write scientific reports and manuscripts.

This opportunity is open to candidates of any nationalities. The selected candidate will receive a FAPESP's Post-Doctoral fellowship in the amount of R$ 7,373.10 monthly and a research contingency fund, equivalent to 15% of the annual value of the fellowship which should be spent in items directly related to the research activity.

Dr. Fábio Raposo do Amaral Professor Adjunto Universidade Federal de São Paulo http://www.amarallabunifesp.wix.com/labsite

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CarnegieStanford QuantEvolutionaryGenetics

Postdoc position in Quantitative Evolutionary Genetics Carnegie Institution for Science, Stanford, CA 94305, USA Moi Exposito-Alonso Lab - www.moisesexpositoalonso.org Annual salary $62,700 Flexible starting date Accepting applications until filled

Description We aim to recruit a highly motivated and creative person with strong training in quantitative or population genetics / evolutionary biology / bioinformatics / computer science.

We seek to study the impacts of climate change on the genetic diversity and evolutionary potential of plant species. Specifically, we aim to experimentally quantify the mode and tempo of genetic adaptation to climate, find genetic loci involved in past adaptations, and model evolving populations using population genetic theory and computational approaches.

The core projects for this position include the analysis of next-generation sequencing data to track the evolution of experimental populations subject to different climates (GrENE-net.org), and the development and testing of realistic population genetic models of evolutionary rescue. This position involves conducting research independently, working with large genomic and experimental datasets, being involved in collaborative projects, preparing publications, and presenting research in scientific meetings.

The lab has links to the center of Computational Evolutionary and Human Genetics (http://CEHG.stanford.edu/). The ideal candidate would become an active member of this community and would strengthen collaborative connections with grad students, postdocs, and faculty members of CEHG, Biology, and Genetics.

*Position details and requirements*This is a full-time position with a competitive annual salary of $62,700 and benefits. The lab is located at the Carnegie Institution on Stanford campus. Carnegie Postdocs have access to Stanford facilities. Stanford campus is a vibrant community embedded in the San Francisco Bay area, with opportunities for extensive social and scientific interactions. The initial position will be for one year with potential renewal of up to three years depending on performance.

Required qualifications for this position are a doctoral degree in population genetics, evolutionary biology, ecology, bioinformatics, computer sciences, or statistics, fluency in a major programming language, a track record of research productivity and independence, and willingness to work closely with collaborators and lab members.

*Additional information:*The Department of Plant Biology of the Carnegie Institution is located on the campus of Stanford University. Formerly known as the Carnegie Institution of Washington, the Carnegie Institution for Science is a U.S.-based non-profit, private endowment. Andrew Carnegie founded the Carnegie Institution of Washington in 1902 as an organization for scientific discovery to serve as a home to exceptional individuals - men and women - with imagination and extraordinary dedication capable of working at the cutting edge of their fields. Today, Carnegie scientists work in six scientific departments on the west and east Coasts and at the Las Camapanas Observatory in Chile. Carnegie investigators are leaders in the fields of plant biology, developmental biology, Earth and planetary sciences, astronomy, and global ecology. The Department of Plant Biology and Department of Global Ecology have state-of-the-art facilities for molecular genetic studies of plants and computer resources. To learn more about the Department of Plant Biology and Global Ecology, visit https://dpb.carnegiescience.edu https://dge.carnegiescience.edu.

Carnegie is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, religion, color, national origin, sex, sexual orientation, gender identity, age, veteran status, disability or any other protected status in accordance with applicable laws.

Contact Informal inquiries about this position can be made by emailing Moises (Moi) Exposito-Alonso at moisesexpositoalonso@gmail.com.

To be formally considered, please include (1) a cover letter, (2) CV, and (3) three referees that I can ask for letters of recommendation.

Moisés Expósito Alonso <mexpositoalonso@carnegiescience.edu>

CornellU FisheriesAdaptationGenomics

The laboratory of Nina Overgaard Therkildsen at Cornell University (https://www.therkildsenlab.com/) is looking for a highly motivated postdoc to uncover genome-wide patterns of variation in American shad across its distribution range and develop cost-effective genomic screening tools to aid conservation efforts and fisheries management. The American shad (Alosa sapidissima) is an anadromous fish native to the east coast of North America. It has for centuries been one of the region's most important and commercially valuable fisheries species - so much that it in the US has been called "the fish that fed the nation's founders". More recently, however, the species has faced population extirpations across its range and despite extensive restoration efforts, abundances are at historic lows in many areas. Conservation planning efforts would substantially benefit from a better understanding of the population structure and degree of local adaptation in American shad and an ability to assign ocean-going adults back to their river of origin.

Earlier microsatellite work detected only weak genetic differention across the species range, but shad are distributed across very heterogeneous environments and divergent selection may have driven highly elevated levels of differentiation in localized genomic regions associated with local adaptation, a pattern now seen in many other fish species. The goal of this project is to conduct genome-wide scans to identify genomic regions that show maximal differences in allele frequencies across both small and large spatial scales, and based on these develop powerful genetic assignment tools for inferring where shad caught as bycatch in ocean fisheries originate from. A better understanding of the natal origin of shad caught in different types of fisheries and different areas can help target interventions to activities that impact the most vulnerable stocks.

The project will be carried out in close collaboration with the New York Department of Environmental Conservation and being based on low-coverage whole genome sequencing of >400 individuals, it will provide an exciting opportunity to leverage novel high-resolution genomic techniques to address practical management needs in a high-profile species while at the same time exploring more basic questions about the forces that drive genome-wide patterns of variation in high gene flow systems. Exhibiting a remarkable variation in reproductive strategy and other phenotypic traits across its range, and recently having successfully colonized the entire west coast of North America after being introduced to California in the late 1800s, the American shad has tremendous, but yet unexplored, promise as a model to study how species adapt to new conditions - an issue of urgent importance in our rapidly changing world. The postdoc will be encouraged to pursue and integrate both the applied and more fundamental lines of inquiry based on their interests.

Qualifications: Candidates should have completed or be within 1-3 months of completing a PhD in evolutionary genomics, molecular ecology, bioinformatics or a related field. We are looking for a creative and talented scientist who is a team player with a good publication record and excellent organizational and communication skills. The successful candidate must have a strong computational/bioinformatics background and previous experience with analyzing large population genomics data sets. Experience working in the Unix environment is essential and familiarity with one or several programming languages is highly desirable. Molecular lab experience and past experience with conservation/fisheries applications would also be a plus.

Interested candidates should send their CV, a description of their motivation and research interests and contact information for three references to Nina Overgaard Therkildsen (nt246@cornell.edu). We are committed to increasing diversity in STEM and especially encourage applications from underrepresented minorities. Review of applications will begin immediately and continue until the position is filled. Pre-application inquiries are welcome. The start date is January 1 2020, or as soon as possible thereafter, and the position is initially for one year, with possibility of renewal for up to two years, depending on performance.

The position will be based in the Department of Natural Resources at Cornell University. Our lab is part of the larger campus-wide Cornell Center for Comparative and Population Genomics (http://3cpg.cornell.edu) whose mission includes fostering research, education, and outreach in comparative and population genetics, and which brings together a vibrant and interactive group of over 350 faculty, postdocs, graduate students and staff who share a commitment to comparative and evolutionary genomic approach to the study of living systems.

CRGBarcelona ModelingCancerEvolution

Postdoctoral researcher position in the group “Evolutionary Processes Modeling” at the Centre for Genomic Regulation (CRG), Barcelona, Spain

Application portal and more information here: https://-recruitment.crg.eu/content/jobs/position/postdoctoral-researcher-position-group-%E2%80%9Cevolutionary-processes-modeling The Institute

The Centre for Genomic Regulation (CRG) is an international research institute based in Barcelona, Spain, with more than 400 scientists from 44 countries. The CRG shares principles of an interdisciplinary and creative scientific team that is supported by high-end and innovative technologies and a flexible and efficient administration.

In 2013, the CRG received the ’HR Excellence in Research’ logo from the European Commission. This is in recognition of the institute’s commitment to developing an HR Strategy for Researchers designed to bring the practices and procedures in line with the principles of the European Charter for Researchers and the Code of Conduct for the Recruitment of Researchers.

The Group

Cancer is a genetic disease, subject to population genetics forces like mutation, selection and stochasticity. Our lab has recently demonstrated that coding sequences of cancer tumors not only exhibit positively selected mutations that drive cancer (www.biorxiv.org/content/-10.1101/485292v1), but that there exist genes that the tumor cannot afford to lose to the mutational pressure (www.nature.com/articles/ng.3987). In addition to genes, we have also identified cancer driver loci in the non-coding part of the genome (www.nature.com/-articles/s41467-017-00100-x). Both coding and non-coding selection can act to promote cancer defense mechanisms against therapy, which can be unveiled through the analysis of time-sequence data of cell-free DNA and of patient survival data.

Our lab is particularly interested in how the evolution and survival of cancer cell populations relies on mutation influx and in the selection inference from allele frequency information. To this end, we develop mathematical and computational approaches to estimate mutation rates and selection. We use whole-exome sequencing and whole-genome data repositories to analyze selection on coding and non-coding sequences. In addition, we analyze cell-free DNA from tumors and their temporal evolution in response to therapy. Estimates of the strength of selection in cancer allow for a prioritization of genes and non-coding regions by their disease relevance, with the ultimate goal of promoting therapeutic advances.

The Evolutionary Processes Modeling lab was established in October 2018 and is part of the "Bioinformatics and Genomics" program at the CRG in Barcelona, Spain. Further information can be found at www.crg.eu/en/-programmes-groups/weghorn-lab . The Role

We are looking for a postdoctoral researcher to join the "Evolutionary Processes Modeling" group to help elucidate cancer evolutionary dynamics using population genetics predictions and statistical modeling, together with computational analysis of recently published and unpublished cancer sequencing data.

Whom would we like to hire?

- PhD degree in population genetics, physics, statistics, genetics, bioinformatics, computer science or a related discipline. - Familiarity with principles of population genetics and statistical analysis. - Experience with computational analysis of sequencing and other biological datasets. - Fluency in English. - You are highly motivated and eager to work on evolutionary and biological problems through the use and development of theoretical and computational approaches.

The Offer

- Contract duration: 1 year (with possibility of extension). - Estimated annual gross salary: Salary is commensurate with qualifications and consistent with our pay scales. - Target start date: Immediately.

We provide a highly stimulating environment with state-of-the-art infrastructure and unique professional career development opportunities. We offer and promote a diverse and inclusive environment and welcome applicants regardless of ageWarning: base64 decoder saw premature EOF! , disability, gender, nationality, race, religion or sexual orientation.

Application Procedure

Applications should be addressed to Dr. Donate Weghorn and include:

1. A letter of motivation. 2. A complete CV, including a list of publications. 3. A brief statement of research interests. 4. Contact details (or reference letters) of at least two referees.

Applications should be submitted online via the CRG Careers website

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Czech Brno FishEvo

POSTDOCTORAL RESEARCH POSITION FOR 12-24 MONTHS, FURTHER EXTENSION NEGOTIABLE

TOPIC: Fish Evolutionary Ecology

REICHARD LAB(reichardlab.eu)

Institute of Vertebrate Biology, Czech Academy Of Sciences, Brno

One full-time postdoctoral position for 2 years is available at the Institute of Vertebrate Biology, Czech Academy of Sciences, located in Brno, Czech Republic. Position may start when filled (since 1 January 2020 or later); all applications submitted until 15 December 2019 will be fully considered. Selected candidates will be interviewed by Skype. Further extension negotiable.

The position is intended for experimental or laboratory work on brood parasitism, primarily on the cuckoo catfish and their cichlids hosts and/or bitterling fishes and their mussel hosts. We expect applications from candidates with a background in ecology and evolution, ideally with a previous track record of working with fish models. For experimental work, access to well-equipped fish breeding facility and outdoor system of separate tanks is granted.

Alternative focus is on work in the molecular ecology lab (phylogenomics, MHC analysis, ddRAD sequencing) using data from experiments and field collections. There is a level of flexibility in research topic but within the constraints of the current work in the lab.

QUALIFICATIONS - PhD in Biology

SALARY - 40 000 CZK, c. 1650 EUR per month (well above average for Czech living expenses)

APPLICATION PROCEDURE

For formal applications, please submit a CV and explain your previous work and motivation to apply for this position in your Cover Letter (1 page is sufficient). Email your application to reichard@ivb.cz

For informal enquires and more details, feel free to email reichard@ivb.cz

Ifremer France EvolutionaryBiology

(Windows NT 6.1; WOW64; rv:52.0) Gecko/20100101 Thunderbird/52.9.1

Dear colleagues

Please find below a link towards the announcement of the launch of Ifremer's new postdoctoral fellowship programme:

https://wwz.ifremer.fr/en/Research-Technology/Scientific-strategy/Join-Ifremer-for-your-Post-Doc This programme invites applicants originating from research labs from outside France to build their own reserach project in collaboration with a hosting Ifremer research Unit.

More detailed information can be found on the website.

Please, do not hesitate to spread the word within your institutes and networks as well as among potentially interested young researchers.

Best regards

Bruno Ernande.

– Bruno ERNANDE Cadre de recherche, Unité HMMN / Research scientist, HMMN Research Unit Référent écologie halieutique, Direction Scientifique / Fisheries ecology adviser, Science Directorate IFREMER, 150 quai Gambetta, BP 699, 62321 Boulogne-sur-Mer, France Tel: +33(0)321995685 / Secretariat: +33(0)321995600 / Fax: +33(0)321995601 http://wwz.ifremer.fr/manchemerdunord http://annuaire.ifremer.fr/cv/16861/

Bruno ERNANDE <Bruno.Ernande@ifremer.fr>

ISTAustria EvolutionaryGenomics

A postdoctoral position in population and evolutionary genomics is available in the Vicoso group at the Institute of Science and Technology, Austria. The general focus of the lab is the evolution of sex chromosomes, which we investigate using a combination of experimental and computational approaches. Questions that motivate our research include: why do some Y/W chromosomes degenerate while other remain homomorphic? What forces drive some species to acquire global dosage compensation, while others only compensate specific genes? What are the frequency and molecular dynamics of sex-chromosome turnover?

The successful applicant will work on an ERC-funded project investigating the influence of sex-specific selection on genome evolution. This will entail a combination of comparative genomics and population genetics in sexual and asexual species of the brine shrimp Artemia.

Applicants should have obtained, or anticipate obtaining by the start date, a PhD in biology, genetics, bioinformatics, or a related field. A strong background in one or more the following areas is highly desired: - population genetics - comparative genomics - molecular evolution - bioinformatics The initial appointment is for two years, with the possibility of extension and a minimum salary of 49,070 Euros per year (gross).

IST Austria (www.ist.ac.at) is a young and vibrant institute dedicated to basic research, with a strong focus on evolutionary biology (other EB groups include those of Nick Barton, Sylvia Cremer and Fedya Kondrashov) and ties to several evolutionary groups in the area (www.univie.ac.at/evolvienna/). We are located on the outskirts of Vienna, and the official language of the institute is English.

To apply, send a short summary of research interests, a CV, up to three relevant publications/manuscripts, and the names and contact information for three references to Beatriz Vicoso (bvicoso@ist.ac.at). The review of applications will start on December 15st and continue until the position is filled. The start date is flexible, but early 2020 would be preferable.

More information on the lab is available at: http://pub.ist.ac.at/˜bvicoso/index.html bvicoso@ist.ac.at

KBS MichiganStateU GenomicMechanismsOfAdaptation

Postdoctoral position in evolutionary biology available immediately in the Conner lab < http://jeffreykconner.com/ > at Michigan State University's Kellogg Biological Station. The lab studies mechanisms of adaptation by integrating genetics, genomics, ecology and evolution in the field, greenhouse, and growth chamber, using wild radish and Arabidopsis as model organisms. Research focuses on floral and agricultural weed adaptations as well as fitness effects of duplicate genes. Substantial publication and grant-writing opportunities are available using abundant existing data and resources. Bioinformatic expertise required to analyze existing and new sequence data, including creation of the first reference genome for the radish genus Raphanus. Experience with, or a strong interest in, field and greenhouse research also necessary. This is a one-year position, salary $50,000 with a possibility of extension based on performance and funding. Contact Jeff Conner (connerj@msu.edu) with questions; apply here < https://careers.msu.edu/en-us/job/502697/research-associatefixed-term >. The Conner Lab, Kellogg Biological Station, and Michigan State University are all committed to fostering a diverse, equitable, and inclusive environment. Jeff Conner W.K. Kellogg Biological Station Michigan State University 3700 East Gull Lake Drive, Hickory Corners, MI 49060 e-mail: connerj@msu.edu @JeffreyKConner

“connerj@msu.edu” <connerj@msu.edu>

Lausanne Switzerland 2 TheoreticalEvolutionaryBiology

Dear colleagues,

I am pleased to announce openings for two postdoc positions funded by an ERC Starting Grant in my new group at EPFL (Ecole Polytechnique Federale de Lausanne, Switzerland). Both positions will be initially for 1 year, with the possibility of renewal. Start dates are March 1st, 2020 or later.

1- Post-doctoral researcher in statistical physics / stochastic processes applied to evolutionary biology. Topic: Characterizing the exploration of rugged fitness landscapes by subdivided populations. Full information: https://recruiting.epfl.ch/Vacancies/1175/-Description/2 2- Post-doctoral researcher in computational biology, working on protein sequence data. Topic: Sequence-function relationship in proteins. Full information: https://recruiting.epfl.ch/Vacancies/1173/-Description/2 Best regards, Anne-Florence Bitbol

Anne-Florence Bitbol <anne-florence.bitbol@epfl.ch>

MARE CIBIO Portugal eDNA CompareGenomics

We are looking for a postdoctoral researcher to work at the interface between environmental DNA and comparative genomics of freshwater fish. This position has an expected duration of 24 months, starting January 1, 2020, and will be based at the Research Center MARE (University of Lisbon) and CIBIO (University of Porto). There will be plenty of opportunities to interact with scientists locally, and also internationally (Indiana State University and the Norwegian Sequencing Centre).

For more information on the project, contract details and application procedures, please visit: http://-www.eracareers.pt/opportunities/index.aspx?task=-global&jobId=121727 and feel free to email me.

Hugo.Gante@indstate.edu

MonashU EvolutionaryBiologist

Postdoctoral Position: Ecologist /Evolutionary Biologist

Professor Dustin Marshall is seeking an experienced Ecologist / Evolutionary Biologist, who specialises in microalgal biology and who has a strong empirical background, to explore the ways in which size affects the structure and function of marine phytoplankton. This position will be with the Centre for Geometric Biology (www.cgb.org.au) within the School of Biological Sciences at Monash University.

As the successful candidate, you will be expected to maintain our evolved lines of the microalgae Dunaliella and use these evolved microalgae to undertake experiments that test ecological and evolutionary theories. You will also have a strong quantitative background and have a demonstrated track record in producing high quality publications.

The Centre for Geometric Biology is developing and testing a new theory for how and why organisms grow. Our particular focus is on how the net flux of energy (the energy acquired through food, photosynthesis, or chemosynthesis minus the energy lost to metabolism) changes with size, whether it be cell size or total body size. We are using a range of approaches and systems to test these predictions. For example we work on yeast, bacteria, phytoplankton and animals. We use artificial selection, experimental evolution, ecological experiments, comparative analyses and theoretical models, as well as different types of bioenergetics measurements to explore a wide range of specific questions about organismal growth.

For more information about the Centre please visit our website https://cgb.org.au/ To apply please go to: http://careers.pageuppeople.com/513/cw/en/job/-599806/research-fellow-centre-for-geometric-biology Enquiries

Dustin Marshall, Professor, School of Biological Sciences, +61 3 9902 4449

– Dr. Liz Morris Administration Manager Centre for Geometric Biology School of Biological Sciences Monash University Clayton, Vic 3800 Australia Mob: +61 3 404 069 210 Email: Liz.Morris@monash.edu

liz.morris@monash.edu

NNRL Bethesda VisionEvolution

We are seeking a postdoctoral fellow with a background in evolutionary biology and bioinformatic expertise to join us in the Neurobiology Neurodegeneration & Repair Laboratory (NNRL) at the National Institutes of Health in Bethesda, MD.

The primary goal of our research in the NNRL is to develop novel therapies for retinal and macular degeneration by identifying the cellular pathways and regulatory networks underlying photoreceptor development, aging, and disease. The postdoc we are looking for will join a nascent group within the NNRL applying an evolutionary framework to a pan-chordata dataset to answer fundamental questions relating to retinal development and function. This is an opportunity to conduct evolutionary analyses in an environment with a wealth of resources.

Applicants should have received a PhD or MD/PhD in genetics, evolution, developmental biology, molecular biology, bioinformatics, or a similar field. Successful candidates will display a strong motivation to conduct scientific research, experience in bioinformatic analysis and use of a high-performance computing cluster, molecular laboratory experience, a solid publication record, and excellent communication and interpersonal skills.

The postdoc will be located within the National Eye Institute at the National Institutes of Health. The campus is located in Bethesda, MD–easy public transportation access from Washington, DC. The position is for 2-3 years, and includes health benefits. Annual stipend will be commensurate with experience and training.

For more information, please visit the NNRL website here: https://nei.nih.gov/research/research-labs-and-branches/neurobiology-neurodegeneration-repair-laboratory As well as the Retinal Development, Genetics and Therapy section website here: https://-/nei.nih.gov/research/research-labs-and-branches/-neurobiology-neurodegeneration-repair-laboratory/-retinal-development-genetics-and-therapy-section Interested applicants should submit a cover letter with a description of career goals, cv with publications, and the contact information for 3 references to Dr. Anand Swaroop at swaroopa_at_nei.nih.gov

“White, Noor (NIH/NEI) [F]” <noor.white@nih.gov>

OpenU TelAviv EvolutionaryGenomics

Our group at the Open University, Tel Aviv, Israel, invites applications for a postdoc position in Evolutionary Genomics.

Our group research interests are focused on Evolutionary signatures of genome instability. In our research we use computational approach the study the abundance and significant of naturally occurring organelle-to-nucleus gene transfers.

Candidate qualifications: (1) Highly motivated person with a PhD degree in Molecular Evolution, Bioinformatics or related fields (2) Proficiency in computer programming (preferable - PERL/Python). (3) Any of following expertise is an advantage: phylogenomics, genomics, biostatistics. (3) Good oral and written communication skills (English is required). (4) Skills and motivation to communicate and interact with other scientists.

The appointment is for one year initially, with the possibility of renewal of an additional year, based on satisfactory performance and funding.

Informal inquiries are welcome please contact einatco@openu.ac.il with questions.

Applicants should send curriculum vitae with a list of publications, a motivation statement and contact addresses of at least two referees to Dr. Einat Hazkani-Covo (einatco@openu.ac.il).

Dr. Einat Hazkani-Covo, Department of Natural and Life Sciences The Open University of Israel http://www.openu.ac.il/Personal_sites/einat-hazkani-covo/ Einat Hazkani-Covo <einatco@openu.ac.il>

ParisCollegedeFrance CoevolutionAntibioticResistance

A postdoctoral position in evolutionary mathematical/computational biology is available to work on project “Deciphering evolutionary trajectories to characterize emergence and dissemination of multidrug resistant Escherichia coli” in collaboration with the three following research groups located in Paris

SMILE group (Collège de France): Guillaume Achaz & Amaury Lambert http://www.lpma-paris.fr/smile GEM group (Institut Pasteur): Eduardo Rocha https://research.pasteur.fr/en/team/microbial-evolutionary-genomics/ ERRA group (Institut Pasteur): Philippe Glaser https://research.pasteur.fr/en/team/microbial-evolutionary-genomics/ The project aims at understanding the most likely evolutionary path(s) – sequence(s) of mutations– that lead to the emergence of antibiotic resistance in E. coli. The recruited postdoctoral fellow will be in charge of methodological developments, more specifically the set-up and implementation of a statistically robust and sound phylogenetic co-evolution framework to decipher relationship between mutations and antibiotic resistance, following previous works of the SMILE group (Behdenna et al, Syst Biol, 2016 ; Behdenna et al., in prep)

We are looking for a highly motivated post-doc with interest in co-evolution, phylogeny and probabilistic models. Applicants should have good background in evolutionary theory/molecular evolution as well as solid mathematical and computational skills. C programming would be welcome. Excellent written, verbal, and interpersonal skills are desired. Speaking French is not mandatory.

The project is funded by Inception and is led by the Institut Pasteur (i.e. GEM and ERRA groups) in collaboration with the Collège de France (i.e. SMILE group), two of the French most competitive research centers, both located in downtown Paris. The position is initially for one year, renewable once. It will be hosted at Collège de France.

Salary will be commensurate with experience and will range from 25 to 30 K euro /yr (free of charge but before income tax) - schools and healthcare in France are cheap when not free.

Starting date is as soon as January 2020, but some flexibility can be arranged. Review of applications starts immediately and will continue until position is filled.

Questions should be sent to Guillaume ACHAZ <guillaume.achaz@college-de-france.fr>

To apply please submit i) a cover letter summarizing research interests and expertise; ii) a CV; iii) a list of publications; and iv) names and contact information of two references, all in a single pdf document sent to both:

Guillaume Achaz <guillaume.achaz@college-de-france.fr> Amaury Lambert <amaury.lambert@college-de-france.fr>

Guillaume Achaz - Homo sapiens http://bioinfo.mnhn.fr/abi/people/achaz/ - Je connais une planète oÃ^1 il y a un Monsieur cramoisi. Il n’a jamais respiré une fleur. Il n’a jamais regardé une étoile. Il n’a jamais aimé personne. Il n’a jamais rien fait d’autre que des additions. Et toute la journée il répète comme toi: “Je suis un homme sérieux! Je suis un homme sérieux!” et ça le fait gonfler d’orgueil. Mais ce n’est pas un homme, c’est un champignon! - Un quoi? - Un champignon! Le petit prince était maintenant tout pâle de colère. - Il y a des millions d’années que les fleurs fabriquent des épines. Il y a des millions d’années que les moutons mangent quand même les fleurs. Et ce n’est pas sérieux de chercher à comprendre pourquoi elles se donnent tant de mal pour se fabriquer des épines qui ne servent jamais à rien? Ce n’est pas important la guerre des moutons et des fleurs? Ce n’est pas sérieux et plus important que les additions d’un gros Monsieur rouge? Et si je connais, moi, une fleur unique au monde, qui n’existe nulle part, sauf dans ma planète, et qu’un petit mouton peut anéantir d’un seul coup, comme ça, un matin, sans se rendre compte de ce qu’il fait, ce n’est pas important ça?

Guillaume Achaz <guillaume.achaz@mnhn.fr>

Paris France BacterialEvolutionInTheGut

Postdoc position: Modeling evolution of bacteria in the gut (Sorbonne Université, Paris, France)

Context and project: The gut harbors a complex microbiota whose impact on our health is currently being discovered. In particular, it can constitute a reservoir of antibiotic resistance, both in humans and in farm animals. Indeed, 99% of the bacteria we carry are in our gut. When we take an antibiotic treatment, it can promote the evolution of antibiotic resistance in these bacteria. It is therefore crucial to understand how microbial evolution unfolds in the gut. In particular, the gut is not a well-mixed environment, and the transport of bacteria and their resulting spatial population structure likely has a strong impact on their evolution. We aim to progress towards a better understanding of bacterial evolution in the gut by developing models of microbial evolution on graphs, and by taking into account gut flow and gradients, e.g. of nutrients or drugs. The recruited postdoc will construct theoretical models of structured populations, combining analytical calculations and numerical simulations.

Practical information: The postdoc position is funded for one year and should start in January 2020 at the latest. The recruited postdoc will be co-advised by Claude Loverdo and Anne-Florence Bitbol. The project will be performed in the theory group of Laboratoire Jean Perrin (http://www.labos.upmc.fr/ljp), a dynamical and strongly interdisciplinary scientific environment, where all researchers work at the interface between physics and biology. Laboratoire Jean Perrin is hosted by Sorbonne Université, on the Jussieu campus, right at the center of Paris.

How to apply: The candidate should have a PhD (or have it completed before the start of the position) in a relevant field, and a strong experience in modeling. To apply, please send a CV and a cover letter describing your interests and previous work to claude.loverdo@sorbonne-universite.fr and anne-florence.bitbol@sorbonne-universite.fr

Claude Loverdo <claude.loverdo@upmc.fr>

Paris SudU FungalEvolutionaryGenomics

Post-doc in evolutionary genomics of fungal sex chromosomes in Paris Sud, France

The Giraud lab in Paris Sud University, France is searching for a postdoc with experience in evolutionary genomics and bioinformatics to join us on a project funded by an ERC advanced grant on the evolution of sex chromosomes in fungi. We have shown that chromosomes involved in sexual compatibility in fungi lacking male and female functions can display stepwise suppression of recombination beyond mating-compatibility genes (Branco et al. PNAS 2017, Branco et al. Nat Com 2018). The post-doc fellow will use high-quality genome assemblies for studying the patterns of recombination suppression in sex chromosomes in various fungi and for identifying the evolutionary causes for stepwise recombination suppression. Applicants should possess demonstrated experience in research topics related to evolutionary genomics, bioinformatics and genome evolution. Applicants should have excellent bioinformatics skills related to large genomic datasets, as well as knowledge in evolution, selection, population and comparative genomics. Further desirable attributes include knowledge of and interest in orthology relationships, phylogenomics, genome-wide synteny, and gene prediction. Great emphasis will be placed on personal qualities such as creativity, motivation and ability to work in a team. Candidates should also have a good ability to conduct independent research, take initiative, ask pertinent scientific questions, and work collaboratively. Female scientists are especially encouraged to apply. The Department of Ecology, Systematics and Evolution in Paris Sud University has about 130 employees and is active within research areas focused on ecology and evolution, providing an excellent scientific environment. It also offers state-of-the-art infrastructure, includingplant and fungus growth facilities as well as equipment for molecular biology and bioinformatics. The Paris Sud University benefits both from the proximity of Paris and from a nice environment outside Paris. The initial appointment will be for one year, with the possibility for renewal for up to three years. The salary is depending on experience. The starting date is negotiable, but can be as soon as early 2020. If interested, please contact Tatiana Giraud tatiana.giraud@u-psud.fr. Provide a CV and a brief statement of research interests and qualifications, and arrange to have two letters of recommendation sent. Applications should be submitted through the website: http://bit.ly/33GaMRD Tatiana Giraud

Departement Genetique et Ecologie Evolutives Laboratoire Ecologie, Systématique et Evolution UMR 8079 CNRS-UPS-AgroParisTech Bâtiment 360 360 rue du Doyen André Guignier Université Paris-Sud 91400 Orsay France

phone: +33 1 69 15 56 69 + 33 6 34 64 45 14 fax: +33 1 69 15 46 97

English: https://www.ese.u-psud.fr/en/team-members/tatiana-giraud/ Francais: https://www.ese.u-psud.fr/personnel/tatiana-giraud/ http://www.ese.u-psud.fr/ Tatiana Giraud <tatiana.giraud@u-psud.fr>

PurdueU PlantEvolutionaryGenetics

Postdoctoral position in plant ecological and evolutionary genetics at Purdue University

The Oakley lab at Purdue University is looking for a postdoctoral scholar. Research topics in the lab encompass many aspects of plant ecological and evolutionary genetics and genomics, but our primary focus is the genetic basis of local adaptation, and locally adaptive traits. We use a combination of field experiments in native habitats and experiments in controlled growth chambers to investigate the links between sequence polymorphism, ecologically important phenotypes, and ultimately, fitness in contrasting environments. The foundation for this work is a decade-long dataset of reciprocal transplant experiments, trait measurements, and site level measures of climate variables. Additional research in the lab is focused on the evolutionary ecology and genetic basis of heterosis and outbreeding depression. Development of new research directions building on these themes, and/or developing new approaches to our existing long-term dataset, is strongly encouraged. There is a vibrant community of interdisciplinary plant biologists at Purdue (https://ag.purdue.edu/cpb/faculty/), providing ample opportunity for interaction and new collaborations.

Research activities may include (but are not limited to): Overseeing growth chamber experiments that simulate native climatic conditions in order to estimate lifetime fitness, freezing tolerance, and other traits, and likely incorporating RNAseq data; data analysis and manuscript preparation from these experiments; field work in beautiful locations in Italy and Sweden (3-4 trips per year for about a week each); overseeing ongoing development of new genetic resources for mapping loci of interest; and the potential for development of mutant lines (using CRISPR-CAS9) to functionally validate candidate genes. A PhD in biology or related discipline is required, and a strong foundation in R, and at least a basic familiarity with bioinformatic analysis on a cluster is strongly preferred. The ideal candidate will have a broad skill set, having some combination of wet lab, bioinformatic, and experimental biology experience. Preference will be given to candidates with a strong background in evolutionary biology. This is initially a one-year appointment, with the possibility of an extension of another year dependent on funding and performance. The start date is no later than April 1, 2020.

Applicants should send (as a single PDF attachment): CV, a letter summarizing research interests, accomplishments, and fit to the lab and project, and the names and contact information for two professional references. Review of applications will begin December 9, 2019 and will continue until a suitable candidate is found.

Chris Oakley oakleyc@purdue.edu https://-dev.btny.purdue.edu/labs/oakley/ "Oakley, Christopher G" <oakleyc@purdue.edu>

RutgersU GlobalChangePopulationGenomics

Postdoc in population genomics and global change at Rutgers University

A three-year postdoctoral position is available in the Global Change Ecology & Evolution Lab at Rutgers University. The postdoc will join a NSF PIRE-funded project to study micro-evolutionary responses to a century of habitat degradation and intensive exploitation in Southeast Asia. The project is using DNA sequencing from a unique historical collection of coastal marine fishes in the Philippines from the R/V Albatross expedition (1907-1909), complemented with modern re-collections of the same species and locations. The postdoc will join a team of researchers that includes Kent Carpenter and Dan Barshis (Old Dominion University), Chris Bird (Texas A&M), Beth Polidoro (Arizona State), Robin Waples (NOAA), Jeff Williams (Smithsonian), Angel Alcala (Silliman U.), and others.

The postdoc will lead analyses of multiple population genomic datasets through time, including changes in diversity and signatures of selection, compare impacts and changes across species, and conduct trait-based analyses to understand characteristics of populations more or less prone to genetic bottlenecks. The postdoc will also contribute to summer population genomic workshops in the Philippines. Extensive opportunities for collaboration across the multi-institutional team, across Rutgers, and in the region are available, including within the Rutgers Genome Cooperative, the Institute of Earth, Ocean, and Atmospheric Sciences, and the Genetics Department. The postdoc will have the opportunity to mentor undergraduate and graduate students.

The position is ideally suited to quantitative researchers with a strong background in population genomics, bioinformatics, data science, and global change. No experience in marine biology required, though experience with population genomic modeling, Approximate Bayesian Computation, database management, and/or hierarchical modeling is a plus. Applicants with evidence of creativity, productivity, strong oral and written communication abilities, and enthusiasm are especially encouraged to apply, particularly those that bring a new perspective, new ideas, or a new skillset to the team. A promising record of publication is valued. The successful applicant will be an independent, motivated problem solver who communicates well and enjoys working in a collaborative setting.

Position details The postdoc start dates are flexible, with preferred dates between May and October 2020. Salary starts at $50,000 per year and includes health insurance, retirement, tax savings plans, and other benefits. Funding for conferences and a computer are available. This is a one-year appointment with the expectation that it will be renewed twice (three years total), contingent upon satisfactory performance. Applicants must have a PhD at the time of employment.

Application process Review of applications will begin on December 16, 2019 and will continue on a rolling basis. Interested candidates should email to malin.pinsky@rutgers.edu: 1) a oneÂ'page cover letter that describes their interest in the position and their relevant background, 2) a CV, and 3) the names and contact information for three scientists familiar with their work.

Rutgers, The State University of New Jersey Rutgers is situated in New Jersey at a crossroads of American innovation, commerce, and culture and with a history entwined with that of the nation. Chartered in 1766, the university is the only one in the United States that is, at once, a colonial college, a land-grant institution, and a state university. Located within an easy drive of New York City, there are nonetheless an exceptionally wide array of marine, freshwater, and terrestrial ecosystems nearby, from the continental shelf and estuaries to barrier islands, coastal plains, the piedmont, Precambrian highlands, and ridge and valley geological provinces. Ecology & evolution at Rutgers consists of approximately 60 faculty and 50 graduate students pursuing research and training in conservation biology, ecosystem ecology, evolutionary biology, marine biology, microbial ecology, population and community ecology, population genetics, and restoration ecology.

Malin Pinsky Associate Professor Global Change Ecology & Evolution Lab Department of Ecology, Evolution, and Natural Resources Institute of Earth, Ocean, and Atmospheric Sciences Rutgers University New Brunswick, NJ 08901 USA

http://pinsky.marine.rutgers.edu malin.pinsky@rutgers.edu

Malin Pinsky <malin.pinsky@gmail.com>

SanFranciscoStateU ForensicPopulationGenetics

An NIJ-funded post-doc position is available to quantify the accuracy of specialized forensic genetic technologies, particularly

low-template DNA mixture analysis and genealogical searching. Thus, the postdoc will gain experience in the areas of statistical genetics and pedigree-based IBD analysis. Depending on the interests of the postdoc and practical constraints, these projects may include collaborations with population geneticists Graham Coop at UC Davis, Doc Edge at USC, bioethicist Malia Fullerton at UW, law professor Erin Murphy at NYU, and collaborative work with a very large personal genomics data set. The position is initially for one year, with strong possibility of extension depending on performance and funding.

The postdoc will be situated in the joint Pennings-Rohlfs-Roy lab space at San Francisco State University. The lab space also houses another postdoc or two, a few PhD students from other universities, and a number of masters students and undergraduates. The postdoc will be well-positioned to mentor some of these diverse students. The postdoc will also have teaching opportunities, but not requirements. In general, the lab welcomes innovative clear communication, and examination of social justice questions related to our work.

This is an ideal opportunity for a scientist who is 1) looking to do population/statistical genetics research with a social impact, 2) interested in working with a diverse population of brilliant, tenacious, and creative students, and 3) excited to live in the SF Bay Area.

Interested scientists can email me rrohlfs@sfsu.edu with a 1-2 page cover letter, CV, a paper (or draft) you've written, and names and email addresses for three references. I will start looking at applications on 1 December.

Rori Rohlfs (she/her) Assistant Professor Department of Biology San Francisco State University Ohlone territory

https://rohlfslab.weebly.com/ Rori Rohlfs <rrohlfs@sfsu.edu>

SangerInst UK 4 SeniorBioinformatician

Postdoc: Senior Bioinformatician in Chromosome Evolution at Tree of Life, Sanger Institute, UK

The Blaxter lab is looking for an enthusiastic bioinformatician to explore the evolution of chromosomes and chromosome structure across the tree of life.

Tree of Life (https://www.sanger.ac.uk/science/programmes/tree-of-life) is a new research programme at the Wellcome Sanger Institute that is exploring the evolutionary biology of genomes from across the Eukaryota to understand pattern and process in the generation of diversity. We are assembling thousands of high quality genomes, chromosomally-resolved wherever possible, of protists, fungi, plants and animals. We are building an analysis group to work on diverse aspects of the evolution of genomes, their contents and structure, and their presentation to the wider world.

While organisms and genes evolve rapidly, karyotypes are relatively stable, such that many genes have been linked on the same chromosome for hundreds of millions of years. Chromosomes also have internal structures that persist through deep time. With the Tree of Life chromosomal assemblies you will ask what maintains karyotypes and chromosome structures through time, and how conserved synteny affects linked gene coevolution.

This is one of four positions available in Mark Blaxters lab in the Tree of Life programme at Sanger.

See https://tinyurl.com/ToL-Blaxter-Bioinfx2019 for full details and to apply online.

For informal enquiries please email mark.blaxter@sanger.ac.uk General The post is at the WSI Senior Bioinformatician grade, and is for 3 years in the first instance, with strong prospects for extension. The post is suitable for career bioinformaticians and postdoctoral candidates. The post holder will work closely with other researchers in the growing Tree of Life programme. Within the underpinning need to deliver to overall goals, the post will have independence in defining research focus and in establishing key collaborations.

The Wellcome Sanger Institute is a world leading genomics research centre. We undertake large-scale research that forms the foundations of knowledge in biology and medicine. Positions include an attractive benefits package. We appreciate the importance of achieving work-life balance and support this with family and career-friendly policies. We hold an Athena SWAN Bronze Award, will consider all individuals without discrimination and are committed to creating an inclusive environment for all employees, where everyone can thrive.

– The Wellcome Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

Postdoc: Senior Bioinformatician in Genome Databasing at Tree of Life, Sanger Institute, UK

The Blaxter lab is looking for an enthusiastic bioinformatician/curator to support research communities in genome database analysis of their target species across the tree of life.

Tree of Life (https://www.sanger.ac.uk/science/programmes/tree-of-life) is a new research programme at the Wellcome Sanger Institute that is exploring the evolutionary biology of genomes from across the Eukaryota to understand pattern and process in the generation of diversity. We are assembling thousands of high quality genomes, chromosomally-resolved wherever possible, of protists, fungi, plants and animals. We are building an analysis group to work on diverse aspects of the evolution of genomes, their contents and structure, and their presentation to the wider world.

We are delivering interactive genome databases to diverse research communities through GenomeHubs (https://genomehubs.org). We are seeking a curator/developer who will support these communities in installing and maintaining instances of GenomeHubs, train users (including generating online training materials), and collaborate in the development of new functionality. The position is (part) funded by the BBSRC.

This is one of four positions available in Mark Blaxters lab in the Tree of Life programme at Sanger.

See https://tinyurl.com/ToL-Blaxter-Bioinfx2019 for full details and to apply online.

For informal enquiries please email mark.blaxter@sanger.ac.uk General The post is at the WSI Senior Bioinformatician grade, and is for 3 years in the first instance, with strong prospects for extension. The post is suitable for career bioinformaticians and postdoctoral candidates. The post holder will work closely with other researchers in the growing Tree of Life programme. Within the underpinning need to deliver to

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SaoCarlosFederalU MammalianDiversity

Dear Colleagues,

I would appreciate your help for announcing a Postdoc position for Mammal Inventory and Ecology at Sāo Carlos Federal University, Brazil as follows.

PD fellowship opportunity: Mammal diversity in the fragmented landscape of northeastern Atlantic Forest, Brazil

The Laboratory of Animal Diversity (LDA), Department of Biology, Sāo Carlos Federal University, here represented by Dr. Ana Paula Carmignotto, participates in the FAPESP Thematic Project “Evaluation, recovering and conservation of the endangered fauna of the Pernambuco Endemism Center (CEP)”, which is coordinated by Dr. Luis Fabio Silveira (MZUSP, Sāo Paulo), and offers a postdoctoral fellowship for a foreign or Brazilian candidate, who has completed a PhD in Life Sciences (Zoology, Ecology or Biology) no more than six years before the start of the scholarship.

The Project “Mammal diversity in the fragmented landscape of northeastern Atlantic Forest, Brazil” aims to: 1- estimate the diversity (richness, abundance, functional and phylogenetic diversity) of mammals in forest remnants from northeastern Atlantic Forest in Brazil; 2- investigate the relationship between landscape characteristics and habitat quality with mammal diversity (functional and phylogenetic); and 3- estimate the abundance, and patterns of activity and occupancy of mammals in the forest remnants. This opportunity is open to highly qualified Brazilians and foreigners. The applicants may present a CV that attest their knowledge on landscape ecology (GIS); statistics (R); occupancy models; and survey, identification and preservation of mammals (including the small mammals). Also, applicants must be available to live abroad, in Sāo Paulo and Alagoas states, Brazil; stay 12 months in a foreign research institution; have a license to drive; be able to read, write and speak English and write scientific papers; offer classes for graduate students; aid in the guidance of graduate and undergraduate students; present experience and availability for field work (in the first 2 years), held at forest remnants of northeastern Atlantic Forest (Alagoas state, Brazil); experience in camera trapping; and with data analyses and small mammal ecology; and be familiar with bibliographic search tools. The selected candidate will be involved in the planning and execution of the research activities mentioned in this notice and may present ability to plan and conduct experiments independently.

*Contract period and start of work: *The scholarship lasts 36 months (research in Brazil) and an additional 12 months (research outside the country - upon approval from FAPESP). The forecast is to begin in February 2020.

Values and conditions:

1. Monthly income (free of taxes) of R$ 7,373.10 (Brazilian currency), plus 15% of the annual value for expenses related to research (Technical Reserve);

2. Financial support for travel and installation expenses may be requested for selected applicants and the merits will be analyzed by FAPESP upon acceptance of the concession;

3. The candidate must have completed a PhD no more than six years before the start of the scholarship;

4. The scholarship requires full dedication to the research project (except under the conditions described in resolution PR 13/2009 of July 15, 2009);

5. The grantee may not have any formal or informal employment, nor receive, during the period of the fellowship, a scholarship from another entity, salary or remuneration derived from the exercise of activities of any nature;

6. For the implementation of the scholarship the selected candidate must present all documentation required by FAPESP;

For more details, go to: *http://www.fapesp.br/270 < http://www.fapesp.br/270 >*

*How to apply: *The submission deadline is December 20, 2019. Registration exclusively by email (apcarmig@gmail.com). Include the subject "Post-doctoral ARCA project", followed by your name, and send the following files in PDF format:

1. An English text with a maximum of 3 pages explaining your motivations to work on this project, showing previous experience in the project expertise;

2. Summarized CV (maximum 3 pages), including published papers attesting the capacity to carry out the project;

3. Two letters of recommendation from researchers who should send them directly to the email above;

4. A PD research project considering the aims mentioned in this notice, following FAPESP terms (see *http://www.fapesp.br/270 < http://www.fapesp.br/270 >)*.

*Selection: *The selection will be made based on the candidate's CV (experience in the research area of the project and quality of the publications) and in the letters of motivation and recommendation. Applicants may be invited to a personal or via Skype interview. The

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SaoPauloFederalU BirdAndCactiGenomics

The Amaral Lab at the Department of Ecology and Evolutionary Biology, Federal University of São Paulo has an open post-doc opportunity.

This post-doc fellowship focus on exploring genomes and phenotypes of birds and cacti from the so-called Dry Diagonal area in South America. The selected candidate will work at the Federal University of São Paulo in Diadema (São Paulo State, Brazil) where he/she will develop a research project linked to the Dry Diagonal Dimensions Project, which is conducted jointly by the Biology Institute of the University of Campinas (UNICAMP, Brazil) and Harvard University (US), among other Brazilian (UFSCAR and USP) and US (Cornell, OSU, VSU, AMNH) institutions. Such collaboration is under the aegis of an agreement between the São Paulo Research Foundation (FAPESP) and National Science Foundation (NSF) through their respective programs BIOTA and Dimensions of Diversity.

Adaptation is a central process in evolution, and ecologically diverse groups of species offer opportunities to study adaptive evolution in many levels of biological organization. The Dry Diagonal Dimensions Project will use different types of data in order to understand how adaptation contributes to phenotypic, genomic, and phylogenetic diversification in dry vegetation and neighboring humid forests. Species of Neotropical birds and cacti offer exciting opportunities to explore the genomics of adaptation, as they represent examples of closely related species occupying dry/open and humid forest in areas as Caatinga, Cerrado, Amazonia, and Atlantic Forest biomes. Recent advances in sequencing technology facilitate the task of interrogating hundreds - or even thousands - of loci potentially related to phenotypic variation using both genomes and transcriptomes.

The selected researcher will:

- Collect and process samples of birds and cacti, and occasionally trait data; - Perform sequence capture of candidate genes and sequence complete genomes and transcriptomes; - Perform bioinformatics, genome and trait evolution analyses; - Write scientific reports and manuscripts.

This opportunity is open to candidates of any nationality. The selected candidate will receive a FAPESP's Post-Doctoral fellowship in the amount of R$ 7,373.10 monthly and a research contingency fund, equivalent to 15% of the annual value of the fellowship which should be spent in items directly related to the research activity.

Applications or questions should be sent to amarallab.unifesp@gmail.com. Interested applicants should send a letter of intent, CV and contact information of two references up to December 15th 24h00 GMT.

Fabio Raposo do Amaral Adjunct Professor, Federal University of São Paulo http://www.amarallabunifesp.wix.com/labsite "Fabio R. Amaral" <fabioraposo@gmail.com>

SGN Frankfurt EvolutionaryGenomics

Job offer ref. # 12-19012

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

The Senckenberg Gesellschaft für Naturforschung and the LOEWE-TBG invite applications for a PostDoc Position (m/f/d) Evolutionary genomics of marine animals (full time, 100 %)

Your tasks:

§Comparative genomic analysis of transposable elements in non-model organisms, especially nemerteans

§Evolutionary inference of transposable elements to study their dynamics, phylogeny, and/or mode of transmission

Your profile:

§PhD in biology, bioinformatics or related subjects

§Experience with genome assembly and scripting

§Interest in mobile genetic elements

§Experience and solid understanding as well as exceptional interest in comparative genomics and evolutionary biology research

§Teamwork oriented and excellent communication skills in both written and spoken English

§Can work independently and meet deadlines

What is awaiting you?

§An interesting task in a dynamic team of researchers in an international research group and joining the new LOEWE excellence centre with its 20 new research groups.

§Access to unpublished genomes from exotic animal phyla

§The opportunity to habilitate at Goethe University or get teaching experience

§The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics

Salary and benefits are according to a full time public service position in Germany (TV-H E13). The contract should start as soon as possible and will initially be limited to December 31th, 2021. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung. Equally qualified handicapped applicants will be given preference.

Please send your application, mentioning the reference of this job offer (ref. #12-19011) before December 08th, 2019 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your certification to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

For more information please contact Prof. Dr. Axel Janke (axel.janke@senckenberg.de).

Mit freundlichen Grüßen / Best Regards

Jessica Helm Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß ç 22 BGB) Senckenberganlage 25

60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG)

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting) - 1564 di-Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1445

Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof.

Dr. Katrin Böhning-Gaese, Prof. Dr. Karsten Wesche

Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Mitglied der Leibniz-Gemeinschaft

Vernetzen Sie sich mit uns: www.senckenberg.de/socialmedia Jessica Helm <jessica.helm@senckenberg.de>

SLU Sweden PlantRootMicrobiome

??Two year postdoctorial position in evolutionary biology at SLU Alnarp, Sweden - plant interactions with antagonists and the root microbiome

Project description

We seek a motivated postdoctoral researcher who will work on a new project investigating selection of plant defence against antagonists in wild Solanum in relation to the composition of the root microbiome in different habitats. An exciting new development in studies of plant and animal immunity indicates that microbial composition in the animal gut, or the phylo- or rhizosphere of plants, is a strong contributing factor to good health. It has been suggested that microorganisms present on plants may act as an outer, first layer of immune defence against infection by pathogenic microbes. To gain a more general understanding of evolution of plant health, we need to conduct studies in natural populations taking into account selective forces generated by microbial communities and their interactions with plants.

The project also has important applied aspects for future development of sustainable plant protection strategies. The project will be performed in close connection with integrated plant protection in cultivated potato against the important potato diseases early and late blight.

Organisation

This position is based in the Integrated Plant Protection unit at the Department of Plant Protection Biology at the Swedish University of Agricultural Sciences (SLU, Alnarp, Sweden). Our department, is an interdisciplinary constellation, encompassing Chemical Ecology, Resistance Biology and Integrated Plant Protection research units, providing excellent opportunities for strong research collaboration within and outside the departmental area. Research efforts at the department are directed towards both fundamental and applied research. Applied plant protection research is carried out in collaboration with industry and focuses primarily on the development of environmentally sustainable pest and disease control strategies for agriculture and horticulture, both in Sweden and internationally.

Qualifications

The candidate should hold a PhD degree in biology or equivalent. Previous experiences from research in evolutionary biology, molecular biology, interactions between plants and their antagonists, bioinformatic analyses of microbiome data or quantification of selection differentials are merits. Candidates should be fluent in spoken and written English. The candidate must be capable of independent planning, execution and evaluation of experiments. As a person you are enthusiastic and responsible, and have excellent collaborate skills. Personal skills are therefore an important part of the evaluation. Applicants that hold a driving license will be evaluated favorably.

As postdoctoral appointments are career-developing positions for junior researchers, we are primarily looking for candidates with a doctoral degree that is three years old at most.

Closing date 6th of December, 2019.

For more information and how to apply, see https://www.slu.se/en/about-slu/jobs-vacancies/ Questions can also be sent to Ãsa Lankinen, asa.lankinen@slu.se.

— När du skickar e-post till SLU sÃ¥ innebär detta att SLU behandlar dina personuppgifter. För att läsa mer om hur detta gÃ¥r till, klicka här < https://www.slu.se/om-slu/kontakta-slu/personuppgifter/ > E-mailing SLU will result in SLU processing your personal data. For more information on how this is done, click here < https://www.slu.se/en/about-slu/contact-slu/personal-data/ >

Ãsa Lankinen <Asa.Lankinen@slu.se>

SouthAfrica ReproductiveCompetitionAndSociality

Please poste the following for me on evoldir. Thanks! Carsten

Postdoc Project: Reproductive Competition and Sociality

(Seasonal Unpredictability and Social Flexibility)

We are looking for a highly motivated postdoc to join the striped mouse project www.stripedmouse.com and our group at the University of the Witwatersrand (Johannesburg) to study the influence of the degree of reproductive competition on sociality. The postdoc is expected to apply for a 2 years postdoctorial fellowship at the University of the Witwatersrand (Johannesburg, South Africa) with us and to spend most of the time at the Succulent Karoo Research Station, conducting field work, analysing and publishing long-term field data.

Application deadline is next week, with skype interviews taking place Thursday the 21st and Friday the 22nd November.

The call has just been published and deadline for application is already the 6th of December, the decision being expected to be made before Christmas 2019, onset of the project in the first halve of 2020. We have an existing research proposal for the project outlined below, so the successful applicant would be able to submit her / his proposal by the 6th of December if she / he can work the last week of November on it.

Project: For the project, a long-term dataset on social organisation of striped mice will be available for analyses (from 2003 to present) and further data collection will extend to 2021. Sociality (% of solitary versus group-living striped mice) will be studied in relation to population density and the intensity of reproductive competition, which is (i) very high during the spring breeding season when all females breed, (ii) absent during most summer dry seasons, (iii) low during summers with unexpected rains when few females breed (6 out of 17 summers in the current data set).

Questions and predictions: We expect that reduced reproductive competition during summer breeding will lead to more social instability in spring compared to summer, i.e. groups to be more stable in summer. We will also study which factors differ between females that breed during the summer vs. females that don't. Finally, the impact of rare summer breeding on population dynamics will be studied.

Key requirements: Strong statistical skills. Good understanding of social evolution. Strong CV with 3 publications from the PhD and at least 1 publication per year from postdoc studies, some of them in high ranking journals (impact factor >3). Willingness to spend considerable time in the field in South Africa. Ability to analyse data and to write manuscripts while being field based.

What you will learn: Strong field skills. The postdoc will spend considerable time in the field (at least 1.5 of the 2 years). It is expected that the postdoc will prepare and start analysing the database while being based at the Succulent Karoo Research Station in South Africa www.stripedmouse.com . Key references:

Schradin, C. 2013. Intraspecific variation in social organization by genetic variation, developmental plasticity, social flexibility or entirely extrinsic factors. Philosophical Transactions of the Royal Society B-Biological Sciences, 368, doi:10.1098/rstb.2012.0346.

Schradin, C., Hayes, L. D., Pillay, N. & Bertelsmeier, C. 2018. The evolution of intraspecific variation in social organization. Ethology, 124, 527-536.

Schradin, C., Konig, B. & Pillay, N. 2010. Reproductive competition favours solitary living while ecological constraints impose group-living in African striped mice. Journal of Animal Ecology, 79, 515-521.

Schradin, C., Lindholm, A. K., Johannesen, J., Schoepf, I., Yuen, C.-H., Konig, B. & Pillay, N. 2012. Social flexibility and social evolution in mammals: a case study of the African striped mouse (Rhabdomys pumilio). Molecular Ecology, 21, 541-553.

How to apply: In a single PDF, send a letter of motivation, your academic CV, and contact details of a minimum of 2 referees to Carsen Schradin, carsten.schradin@iphc.cnrs.fr and Neville Pillay, neville.pillay@wits.ac.za. Send your application as soon as possible, as interview will take place the 21st of November!

More information:

www.stripedmouse.com http://www.iphc.cnrs.fr/-Carsten-Schradin-.html https://www.researchgate.net/-profile/Neville_Pillay .

Director Succulent Karoo Research station
<succulent.karoo.research.station@kabelbw.de>

TempleU InvasionGenetics

POSTDOC POSITION: Invasion genetics, Temple University, Philadelphia, USA

The Integrative Ecology Lab (iEcoLab) at Temple University is seeking creative and productive applicants for a postdoctoral researcher to lead research into the invasion genetics of the invasive spotted lanternfly (Lycorma delicatula) pest. The spotted lanternfly is an invasive Asian planthopper that was first introduced to the US just outside of Philadelphia, Pennsylvania in 2014, and has since spread to five nearby states. In addition to natural dispersal, human-assisted dispersal occurs during all lanternfly life stages: adults and nymphs hitchhike on cars and it can spread long distances in the egg stage because it lays eggs on mobile outdoor objects like recreational vehicles and landscaping materials. It feeds on over 70 plant species, sometimes at very high densities, including economically important species like maples, apples, hops, and grapes. Invaded vineyards have lost entire crops, affecting wine production. We are just beginning to understand its ecology and potential to cause economic and ecological impacts, but there is still more to learn. You can be at the forefront of cross-disciplinary research on this emerging invasion.

The postdoctoral researcher will be mentored by Jocelyn Behm (https://www.iecolab.org/jocelyn-e-behm/) and will be part of a larger collaborative team of postdocs, graduate students, and faculty at Temple University studying and modeling spotted lanternfly spread and impacts from the labs of Matt Helmus (Biology) and Benjamin Seibold (Math) (for a brief overview of the project see: https://www.iecolab.org/projects/spotted-lanternfly/).— The postdoc will also interact with a USDA-funded multi-university team of cross-disciplinary scientists and public stakeholders and will regularly attend working groups and meetings on this invasive pest.— The anticipated start date for the invasion genetics postdoc position is early 2020. The position is for one year, with the possibility for renewal upon satisfactory performance and funding. Salary is commensurate with experience and benefits are included.

The role of the invasion genetics postdoc will be to develop research using microsatellites and/ or whole genome sequencing to explore the relative contributions of human-assisted versus natural dispersal to spotted lanternfly spread, as well as elucidate dispersal corridors and pathways in its invaded range. There will also be opportunities for the postdoc to develop and pursue additional research questions based on their interests.

Qualifications: A PhD in Biology, Ecology, Evolution, Genetics or other related field Expertise in landscape genetic and/or landscape genomic lab and statistical methods A competitive publication record appropriate for career stage Well-organized and able to work both independently and in a team setting

Applications should be emailed to Jocelyn Behm (jebehm@temple.edu). Please send as a single PDF: Cover letter outlining qualifications, experience and why you are interested in the position Curriculum vitae including links to authored publications Name, phone number, and email addresses of three references

Review of applications will begin November 22 and will continue until the position is filled.

iEcolLab is in a new LEED-Gold certified building in historic Philadelphia. iEcoLab is part of the Center for Biodiversity, which provides state-of-the-art biodiversity research facilities along with support staff with expertise in media development, GIS technology, high-performance computing, and genetics. Temple University, founded in 1884, is a public R1 university with a diverse student body of ca. 40,000 students. It is the sixth-largest provider of graduate school education in the U.S., is within the top 4% of research institutions in the U.S. and is in the top ten of the fastest gainers in ranking by the U.S. News & World Report Best Colleges.

Philadelphia is the birthplace of the United States. It is filled with numerous attractions (e.g., Philadelphia Museum of Art, Philadelphia Zoo, Academy of Natural Sciences), amazing food, and it is a quick train ride to New York City and Washington DC. Philadelphia is nestled within an extensive national/state trail and park system and is very close to Valley Forge National Park, the Pocono Mountains, the unique Pine Barren ecosystem, and beaches of the Atlantic shore.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community. iEcoLab believes the crisis in biological diversity can only be addressed by scientists from diverse backgrounds and with diverse viewpoints. iEcoLab strongly encourages applicants from diverse backgrounds.

Jocelyn E. Behm, Ph.D.

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UCalifornia LosAngeles Conservation

Postdoc: UCLA_La Kretz_Center_for_California_Conservation_Science

The UCLA La Kretz Center for California Conservation Science < http://www.environment.ucla.edu/lakretz/ > invites applications for its 2020 Postdoctoral Fellowship in California Conservation Science. We seek a postdoctoral scholar who conducts innovative biological research to work with the La Kretz Center and partner agencies to achieve outcomes that will direct and lead California conservation efforts. Candidates may work in any discipline that provides the scientific underpinnings for the preservation, protection, management, or restoration of at-risk species, environments, or ecological communities in California. Our current research directions include:

(i) conservation science at the urban/wildland interface, particularly biological invaders at the urban/wildland interface, behavioral attributes of introduced species, and the ecological and evolutionary effects of urbanization; (ii) urban biodiversity, ecosystems, and ecosystem services with an emphasis on comparative assessments of urban biodiversity (phylogenetic, richness, and genetic diversity are key areas), evaluations of ecosystem services in the urban environment, and ecosystem ecology including carbon and/or nitrogen management and soil and water conservation; and (iii) California conservation science that leverages networks of protected areas to answer questions about speciation, adaptive evolution, and species delimitation or uses these lands to understand the impact(s) of disturbance on species ecology, conservation, or behavior.

The successful applicant will be expected to collaborate with partner agencies and UCLA faculty to help deliver applied conservation outcomes. Thus, we seek Fellows whose research overlaps with a minimum of (1) UCLA faculty member who is a La Kretz affiliate < https://www.ioes.ucla.edu/lakretz/people/?ioesrole=3Daffiliates > and (1) agency partner in California (see below). Applicants should identify in their cover letter potential faculty and agency mentors to collaborate with on their proposed project; ideally those mentors will have already been identified. The Fellow is expected to work closely with their UCLA faculty mentor and agency partner(s) to produce the most impactful research possible. Our current list of possible agency partners includes:

- The Nature Conservancy: Sophie Parker (sophie_parker@tnc.org): restoration; urban conservation; invasive species - LA Natural History Museum: Jann Vendetti (jvendett@nhm.org): mollusk ecology and evolution; species natural history - U.S. Geological Survey: Robert Fisher (rfisher@usgs.gov): applied conservation; biodiversity; ecology and evolution - US Bureau of Land Management: Mike Westphal (mwestpha@blm.gov): applied conservation, climate change - US Fish and Wildlife Service: Cat Darst (cat_darst@fws.gov): endangered species management) - Nature Communities Coalition of Orange County: Danny Fry (dfry@occonservation.org): protection and recovery of sensitive species in Orange County

National Park Service: Katy Delaney (katy_delaney@nps.gov): amphibian and avian ecology, evolution, and conservation; Seth Riley (seth_riley@nps.gov): mammalian ecology, evolution, and conservation Department of Defense: Robert Lovich (robert.lovich@navy.mil): conservation on DoD lands

The La Kretz Fellowship is for two years, subject to review after the first year. The start date is on or about September 2020. The position offers full benefits, an annual research fund of $5,000, and an additional travel allowance of $1000 per year. Candidates who have recently completed their Ph.D. or will have completed it by August 2020 are encouraged to apply.

To apply, please send applications to lakretz@ioes.ucla.edu as a single PDF file that includes (i) a cover letter, (ii) your CV, (iii) a research and management accomplishments statement (max 2 pages), (iv) a project proposal that includes potential La Kretz affiliates and agency partners, (max 2-pages, including references), and (v) two of your relevant publications. We also ask that you have (vi) two letters of reference sent, one of which must be from your Ph.D. advisor. Please arrange to have reference letters emailed to the same address with the subject line “La Kretz Postdoc letter for (your last name)”. The deadline for completed applications is January 19, 2019. Please e-mail questions to Brad Shaffer, Director of the La Kretz Center at brad.shaffer@ucla.edu.

“garyb@g.ucla.edu” <garyb@g.ucla.edu>

UCalifornia LosAngeles MicrobiomeEvolution

Postdoc:UCLA.MicrobiomeEvolution

Postdoctoral research position atUCLAon the evolutionary dynamics of the microbiome.

A postdoctoral research position is available in the lab of Dr. Nandita Garud in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles. We are broadly interested in understanding the evolutionary dynamics of natural populations with a current focus on microbiomes. The lab develops statistical and computational methods to gain insight into evolutionary processes from population genomic data.

The successful candidate will have substantial input in the specific nature of their research project. However, the project should broadly fit within the lab's goals of learning about adaptation in natural populations and evolutionary dynamics in the microbiome.

Additional information can be found at:http://garud.eeb.ucla.edu The Ecology and Evolutionary Biology department atUCLAoffers a cutting-edge research environment with many opportunities for collaboration. The lab is affiliatiated with the Microbiome Center atUCLAand the Institute for Quantitative and Computational Biology atUCLA.

The position is available for 1 year and may be continued for additional years contingent on successful progress and available funding. Salary will be competitive. The University of California offers a competitive benefits package including medical, dental, vision, life insurance, accidental death and dismemberment insurance, and short and long term disability insurance.

Candidates should have a Ph.D. in biology, genetics, computer science, bioinformatics, statistics, computational biology, or a related field. A background in population genetics/evolutionary genomics is preferred. As this is a computational position, proficiency in programming in R, Perl, or Python, and shell scripting is essential. Preference will be given to candidates with a strong publication record, evidence of substantial research productivity, and ability to successfully communicate scientific information.

Review of applications will begin immediately and will continue until the position is filled.

Interested candidates should send a CV, short (1-2 pages) description of research interests and ideas for possible projects, and contact information for 3 references to Dr. Nandita Garud at ngarud@ucla.edu.

The University of California is an equal opportunity/affirmative action employer.

Nandita Garud <nandita.garud@gmail.com>

UCDavis QuantBioEducationResearch

My lab is currently recruiting apostdoctoral fellowwho isinterested in improving how on-line content and associated courses are delivered.

We're looking for someone with STEM training and experience with data analysis and educational research. While the successful candidate doesn't need to be an AI expert - collaborators at MIT and Edinburgh have that covered - a demonstrated ability to analyze data computationally is a big plus.

If you have questions about the position please email me directly at:mtfacciotti@ucdavis.edu.

The full position description can be found below: NATIONAL SCIENCE FOUNDATION FUNDED CONTENT DEVELOPMENT AND EDUCATIONAL DATA MINING POSTDOCTORAL POSITION

Location: UC Davis Genome Center Description: We seek a skilled, creative, and motivated postdoctoral scholar with an interest in building the knowledge and computational tools that can help change how students interact with online content. The successful candidate will work with the project Principal Investigator (PI) Marc Facciotti and co-PIs to design, execute and report on experiments that will test: how the design of online content and its delivery impact student affect and engagement while interacting with content; how different strategies for interventions during student/content interaction can influence student affect and engagement; how knowledge of student interaction with content can influence instructor behavior; and how each of these variables impacts student learning and inclusion.

This project applies artificial intelligence and machine learning approaches to build newunderstandings of how to engineer student engagement with online content to enhance learning. Tools derived from this project will improve students' and instructors' experiences with online content, increase the value of online content delivery, and contribute to the personalization of online resources.

Depending on the candidate's strengths and interests, duties may also include: analysis of multidimensional data and modeling, taking part in online tool creation, grant-writing, writing reviews and/or perspectives, presenting findings at conferences, development of improved course pedagogy and content, networking with and extending the use of knowledge gained and tools constructed with collaborators beyond the home institution, and coordination of multi-university studies through the SEISMIC consortium. Interaction and collaboration with members of the broader scholarship of teaching and learning community (both at and beyond UCD) is encouraged and will be facilitated by the senior investigators.

Qualifications:

The applicant must have a Ph.D. in biology, mathematics, physics, chemistry, statistics, computer science, engineering, evolution, environmental sciences, psychology, or related fields, including science education. Experience with scholarship of teaching and learning, especially in undergraduate STEM disciplines is preferred. It is also preferred that the candidate have experience with quantitative techniques and approaches, including programming and data analysis, and have experience with and knowledge of modern online educational technologies. We are looking for a highly self-motivated, eager to learn, and excited to teach individual. The candidate should have an interest in improving undergrad STEM education, particularly with online learning. The candidate should have excellent communication skills, both verbal and written, be comfortable collaborating with faculty in both the natural and computer sciences, and be able to work independently under minimal supervision.

How To Apply:

Applicants should submit Curriculum Vitae, including list of publications, a Letter of Interest, Statement of Research, Statement of Contributions to Diversity, Equity, and Inclusion, and contact information for three references to Prof. Facciotti atmtfacciotti@ucdavis.edu. Questions: Please direct questions to Marc Facciotti:mtfacciotti@ucdavis.edu

The University of California, Davis commits to inclusion excellence by advancing equity, diversity and inclusion in all that we do. We are an Affirmative Action/Equal Opportunity employer, and particularly encourage applications from members of historically underrepresented racial/ethnic groups, women, individuals with disabilities, veterans, LGBTQ community members, and others who demonstrate the ability to help us achieve our vision of a diverse and inclusive community. Under Federal law, the University of California may employ only individuals who are legally able to work in the United States as established by providing documents as specified in the Immigration Reform and Control Act of 1986. Certain UC Davis positions funded by federal contracts or sub-contracts require the selected candidate to pass an E-Verify check. More information is availablehttp://www.uscis.gov/e-verify. UC Davis is a smoke &

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UCopenhagen ComparativeAntGenomes

A three-year postdoc position is available at the Department of Biology, University of Copenhagen, working on comparative genomic analyses for 100 ant genomes.

Project description

The Global Ant Genomics Consortium (http://antgenomics.dk/) aims to sequence high—quality reference genomes for ca. 200 ant species covering the major diversity of—Formicidae family. We expect to finish the first 100 genomes by 1st May 2020 and—will start organizing the first pilot comparative genomics analyses. All the genomes—have been assembled with PacBio long reads and HiC sequencing, thus will be in—near chromosome level. This project will perform the comparative genomics—analyses with the first 100 ant genomes to reconstruct ant phylogeny and to reveal—the genomic changes associated with the evolution of ant social structure, behavior,—and lineage-specialized adaptation.

General job description

Independently carry out the comparative genomics analyses Coordinate analyses together with other collaborators Limited participation in teaching and dissemination activities of the Centre

Required qualifications

A PhD degree within computational biology, ecology and evolution, genomics or related fields Highly experienced on comparative genomics and transcriptomics A convincing publication track record An active interest in insects or ant evolution Fluent spoken and written English Excellent communication skill and ability to work in teams Have experience in working independently and coordinating with other teams

Inquiries about the position can be made to Professor Guojie Zhang; email—guojie.zhang@bio.ku.dk . —

Application procedure

Your online application must be submitted in English by clicking 'Apply now' below.

Furthermore, your application must include the following documents/attachments -—all in PDF format:

- Motivated letter of application (max. one page). -

CV incl. education, work/research experience, language skills and other skills relevant for the position. - A certified/signed copy of a) PhD certificate and b) Master of Science certificate. If the PhD is not completed, a written statement from the supervisor will do. - List of publications. - Contacts of three referees know yourself

The deadline for applications is at 31st December 2019, 23:59 GMT+1

After the expiry of the deadline for applications, the authorized recruitment manager—selects applicants for assessment on the advice of the Interview Committee.

You can—read more—information from https://candidate.hr-manager.net/ApplicationInit.aspx/?cid=1307&departmentId=18965&ProjectId=150713 Guojie Zhang <guojie.zhang@bio.ku.dk>

UMaryland EvolutionaryandQuantitativeGenomics Nov

The Fritz lab is seeking a post-doc to study the evolutionary and quantitative genomic basis of traits involved in insect adaptation to transgenic crops in the landscape. The job posting can be found at: http://www.meganfritzlab.com/uploads/1/0/0/9/100940634/position_announcement_-_fritz_post_doc_nov_2019.doc_1_.pdf Megan Fritz

Assistant Professor of Entomology University of Maryland 4291 Field House Dr. Plant Sciences Bldg. Rm. 3126 College Park, MD 20742 Office Phone: 301-405-3945 Website: www.meganfritzlab.com Twitter Handle: @MosquitoDoc

Megan Lindsay Fritz <mfritz13@umd.edu>

UMassachusetts Boston ComputationalPhylogenetics

A postdoctoral position is available in the lab of Dr. Liam Revell at the University of Massachusetts Boston.

The postdoc has a maximum duration of 2 years & is to work on the NSF project entitled 'ABI Development: Computational infrastructure for phylogenetic analysis in the R environment.' Proposals for a remote postdoc will be considered equally, although postdocs working remotely should plan to spend at least 1-2 months/year in Boston (specifics to be negotiated).

More details about the position as well as a link to apply can be found on the UMass-Boston HR site: http://employmentopportunities.umb.edu/boston/en-us/job/503625/post-doctoral-research-fellow .Questions should be directed to lab PI Liam Revell (liam.revell@umb.edu).

Liam J. Revell Associate Professor, University of Massachusetts Boston Profesor Asistente, Universidad Católica de la Ssma Concepción web: http://faculty.umb.edu/liam.revell/, http://www.phytools.org

Academic Director UMass Boston Chile Abroad (starting 2019): https://www.umb.edu/academics/caps/international/biology_chile Liam Revell <Liam.Revell@umb.edu>

UMinnesota EcologicalSpeciation

Postdoctoral Position in Ecological Speciation at the University of Minnesota, Twin Cities

We are seeking a postdoc to work on an NSF-funded project on ecological speciation in plants. The project is particularly focused on the contribution of mating system evolution to the evolution of reproductive isolation and character displacement between incipient species of Clarkia xantiana, an annual plant with a long history of research in evolutionary biology. The project is a collaboration among two labs at the U. of Minnesota: Dave Moeller (moellerlab.wordpress.com) and Yaniv Brandvain (brandvainlab.wordpress.com). The project integrates field experiments, population genomics, and mathematical modeling.

We are particularly interested in candidates with expertise in ecological genetics, evolutionary ecology, and population genetics, along with potential interest in developing skills in genomic analysis. Some of the major goals of the project are to (1) examine the role of natural selection in the evolution of reproductive character displacement using a combination of mathematical models and field experiments, (2) quantify the ecological and genetic costs of hybrid formation using field experiments and genomic analysis, and (3) assess the consequences of pre- and post-zygotic isolating mechanisms for genome-wide patterns of introgression. As a part of the broader project, we are sequencing and assembling the genome of C. xantiana.

Initial appointment will be for one year with competitive salary ($48,426) and full benefits. Renewal for 1-2 more years is possible, pending excellent performance and mutual agreement. The start date is flexible. To apply, please assemble (i) a one page cover letter that highlights how your research interests and skills fit with this project, (ii) a CV, and (iii) names and contact information for three professional references. Materials should be submitted online at https://humanresources.umn.edu/jobs (Click on the tab in the center of the page that corresponds to their situation; Search Job ID# 334054). Review of materials will begin November 15, 2019, but candidates will be considered upon submission until the position is filled. Please also contact moeller@umn.edu if you are interested in being considered or learning more.

The Twin Cities campus of the U. of Minnesota is home to an exciting and diverse set of scientists, expertise, and resources, particularly within the Departments of Plant and Microbial Biology (cbs.umn.edu/plantbio), Ecology, Evolution & Behavior (cbs.umn.edu/eeb), and the U. of Minnesota Genomics Center (genomics.umn.edu), the Minnesota Supercomputing Institute (msi.umn.edu), and the Bell Museum of Natural History (bellmuseum.umn.edu). The campus is located in the heart of the Minneapolis-Saint Paul metropolitan area, which is rich in cultural attractions, has an extensive park system, lies close to a diverse array of natural areas, and is consistently ranked as one of the best places to live in the U.S.

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, veteran status, or sexual orientation.

David A. Moeller Associate Professor Plant & Microbial Biology University of Minnesota moellerlab.wordpress.com

"moeller@umn.edu" <moeller@umn.edu>

UMuenster 4PhD PDFs MolecularEvolution

Four Positions (PhD and Postdoc) in Molecular and Genome Evolution are available at the Bornberglab.org:

1) PhD: ORIGINS AND ADAPTATION OF NOVEL HUMAN GENES, including introgressed genes from Neanderthals and de novo emerged genes. This 75%FTE PhD project is part of the EvoPad graduate school and will start on April 1st. For further details see: https://www.uni- muenster.de/EvoPAD/ For related literature see: https://www.ncbi.nlm.nih.gov/pubmed/30201962 , https://www.ncbi.nlm.nih.gov/pubmed/29802682 2) PhD/Postdoc: HOW DID SOCIALITY ARISE IN INSECTS? This project will study the premises of how eusociality arose via the multiple emergences of sub-sociality in various cockroaches using genomic and transcriptomic resources. This project can be seen as a "prequel" to our successful research on the evolution of "true" eusociality in termites: https://www.ncbi.nlm.nih.gov/pubmed/29403074 https://www.ncbi.nlm.nih.gov/pubmed/24845553 Starting date is quite flexible and the project may be conducted either by a PhD student (75% FTE, 3 years) or a postdoc (100% FTE ca. 2.5 years). French language skills are an advantage (though not a must) since the project will be in close collaboration with the Natural History Museum in Paris (PIs Dr Frederic Legendre and Philip Grandcolas).

3) Postdoc: THE HALLMARKS OF AGEING IN SOCIAL INSECTS and how the tradeoff between ageing and fertility has been uniquely overcome in reproductives (queens, kings) of social insects. This project will include analysis of genomic and transcriptomic and other data from several insect lineages and aims at deciphering commonalities and specificities between e.g. ants and termites, bees and flies. The project is part of a "Forschergruppe" Solong, FOR 2281 which includes 8 groups from across Germany, Switzerland and the Netherlands. Excellent communication skills and proven ability to handle multiple collaborations are an advantage.

4) PhD: PROTEIN EVOLUTION – THEORY AND/OR DATA ANALYSIS (50% FTE initially): This project will cover one of two project areas, either: (i) the theory of how functional proteins or RNA can evolve from random sequences and which role epistatic inter-

actions play during this process or (ii) the modular evolution of proteins by domain re-arrangements – evolutionary analysis and software development.

Details on both project areas can be found on: bornberglab.org/researches, further details are still flexible and can be tuned to the post-holder's requirements. Either way, a background on simulations, modelling and the essences of biophysics as well as good programming skills are essential. Example publications: https://www.ncbi.nlm.nih.gov/pubmed/10485887 https://www.ncbi.nlm.nih.gov/pubmed/22927372 https://www.ncbi.nlm.nih.gov/pubmed/29802682 https://www.ncbi.nlm.nih.gov/pubmed/24222210 https://www.ncbi.nlm.nih.gov/pubmed/22016574 All projects require prior skills in programming and/or data analysis.

MSc position with the option for some financial support (depending on extra tasks to be carried out) are available in all project areas.

Projects 1 - 3, 5 are suitable for candidates with a background in biology, biochemistry or bioinformatics, projects 3 and 4 are suitable for applicants with a background in a more theoretical field such as bioinformatics, biochemistry, physics or applied mathematics and some experience with handling biological questions.

Projects 2 and 3 will be co-supervised by Dr Mark Harrison, project 4ii by Dr Carsten Kemena.

See also bornberglab.org/positions

Erich Bornberg-Bauer PhD, Prof. of Molecular Evolution + Genomeinformatics Institute for Evolution and Biodiversity, Huefferstrasse 1 D-48149 Germany Westfalian Wilhelms University Muenster, bornberglab.org ebb.admin@wwu.de Phone / Fax / Direct Line: +49 (0) 251 83 21630 / 24668 / 21011

"E. Bornberg" <ebb@uni-muenster.de>

UOulu Finland ForestEvolutionaryGenomics

https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&lang=en&id=-00008137&jc=1 Postdoctoral Researcher, Ecology and Genetics

The University of Oulu is one of the biggest and most multidisciplinary universities in Finland. We are an international science community working in close cooperation with research institutes, companies, and the public sector. Together we form a globally significant research hub, relentlessly pushing the boundaries of known for a more sustainable and intelligent future.

The Department of Ecology and Genetics has strong expertise and tradition in plant population genetics. Current research topics include population and evolutionary genomics of forest trees, quantitative genetics, biodiversity genomics, conservation genetics and molecular evolution. We offer a scientific environment that is enthusiastic about plant evolutionary genetics, a possibility to develop your genomics and bioinformatics skills and initiate international collaboration. The postdoctoral researcher will be part of Pyhäjärvi Lab working on various aspects of Scots pine genetics, evolutionary genomics of haploid and diploid life cycle states, patterns of gene expression, developing genomic tools for various forest tree species and applying genomic selection for trees. Pyhäjärvi Lab (oulu.fi/pyhajarvilab) collaborates closely with other European forest geneticists via the Horizon 2020 projects GenTree and B4EST.

The applicant should have a doctoral degree, recorded scientific expertise and interest in population, evolutionary and quantitative genomics. Experience in bioinformatics and gene expression analysis is an advantage. The successful applicant will contribute to evolutionary focused combined analysis of gene expression and nucleotide diversity data of Scots pine and analysing the performance and data from recently developed SNP chips for multiple European tree species in B4EST project (http://b4est.eu/) in collaboration with French National Institute for Agricultural Research (INRA). The exact duties will depend on the persons skills and interests. The duties also include a small amount of teaching and supervising students.

The salary will be based on the level 5 of the demand level chart for teaching and research staff of Finnish universities. In addition, a salary component based on personal work performance will be paid (maximum of 50 % of the job-specific component). The successful candidate will receive the benefits provided by the University of Oulu to university employees, including free occupational health care services, and obtain access to high-quality public affordable childcare services.

Applications and further information

Apply online latest on Friday, 29 November 2019 at 23:59 (Finnish local time). Please include the following attachments in your application:

- CV according to guideline of the Finnish Board on Research Integrity (https://www.tenk.fi/en/template-researchers- curriculum-vitae) - list of publications according to the guidelines of the Academy of Finland (https://www.aka.fi/en/funding/apply-for-funding/az-index-of- application-guidelines/list-of-publications/) - contact details of at least two referees - a motivation letter (max 1 page) The position is filled for 24 months as of 1 January 2020 or as soon as possible thereafter. A trial period of 6 months is applied in the position.

Further details are available from Academy Research Fellow Tanja Pyhäjärvi, tanja.pyhajarvi[at]oulu.fi.

https://rekry.saima.fi/certiahome/open_job_view.html?did=5600&lang=en&id=00008137&jc=1 About Oulu and Finland

Finland is one of the most livable countries in the world, with a high quality of life, equality, safety and excellent education system. The City of Oulu is Northern Finland's largest city, with a population of over 200,000. Located in the Gulf of Bothnia in the Oulu River delta, the city has good access from anywhere (one hour flight from Helsinki). Oulu is a very easy-going and family friendly community with plenty of cultural activities as well as opportunities for exploring the beautiful, northern nature. As the world's northernmost tech hub, Oulu has a highly educated and innovative workforce and the University has a strong role in the community. Oulu is a marvelous place to live, work and enjoy a vibrant academic community. Welcome to the home of science with Arctic Attitude!

tanja.pyhajarvi@oulu.fi

UPaulSabatier PangolinConservation

Subject: Postdoctoral position – Université Paul Sabatier, Toulouse, France

Pangolins are scaly Afro-Asian mammals that suffer from an unprecedented rise in the amplitude of their illegal trafficking. A postdoctoral position is available at the Laboratoire Evolution et Diversité Biologique (EDB; http://edb.cnrs.fr/) to trace the dynamics of pangolin trade networks in Africa through population genomics. The successful candidate will mostly explore the contribution of RAD-Seq data to the geographical tracing of traded pangolins from local to regional scales.

We are seeking a researcher with a high interest in conservation genomics and wildlife forensics. Experience in population genomic analysis on RAD-seq data is required. Experience in SNP calling from other types of genomic data (full genomes, gene capture) and in traditional population genetics would be a plus.

The successful candidate will work with Drs Philippe Gaubert (http://www.edb.cnrs.fr/annuaire/philippe-gaubert/) and Pablo Tedesco (http://edb.cnrs.fr/annuaire/pablo_a-tedesco/), in a highly motivating, multi-disciplinary team including 4 PhDs and one Engineer (https://philippe-gaubert.eu/projets/pangogo1/).

EDB is located within the campus of Université Paul Sabatier (UPS), one of the top research establishments in France. Toulouse is France's second largest university town, with 120,000 students, and benefits from an enjoyable situation at the foot of the Pyrenees, between the Mediterranean and the Atlantic coasts.

The position and lab work are fully supported by an ANR - Agence Nationale de la Recherche research grant (http://www.agence-nationale-recherche.fr/Project-ANR-17-CE02-0001). The position is for 1 year and a half. Gross monthly salary is 2324,26 euros.

Applicants should send their CV (2 pages max.) and a Statement of Interest including academic referents to Philippe Gaubert (philippe.gaubert@univ-tlse3.fr). Application deadline is 15th December 2019. Starting date is 1st March 2020.

Philippe Gaubert <philippe.gaubert@univ-tlse3.fr>

UPennsylvania HumanGenomics

Postdoctoral fellowship in human genomics University of Pennsylvania, Perelman School of Medicine

A postdoctoral position is available in the labs of Christopher Brown and Jennifer Philips-Cremins in the Genetics Department at the University of Pennsylvania. Research will be focused the genetics and engineering of human genome 3D structure. Successful applicants will have the opportunity to design their own projects relating to the genetics of gene expression regulation, eQTLs, chromatin structure, and genome engineering. The fellow will also have the opportunity to work as a part of large collaborative and consortium scale projects involving both labs.

Candidates with expertise in experimental or computational biology will be considered, but the ideal candidate will have significant wet and dry experience. Applicants must have an MD, PhD, or equivalent degree in genetics/genomics, bioengineering, evolutionary biology, computational biology, or a related discipline. Candidates with backgrounds in statistics, computer science, physics, or other quantitative fields will be considered if they have experience with biological data. Experience with next-generation sequencing techniques and data, Hi-C, ChIP and related functional genomics techniques, and/or scientific programming are desired.

Applications (including CV, statement of research interests, and references) and informal inquiries should be emailed to Christopher Brown (chrbro@pennmedicine.upenn.edu) and Jennifer Philips-Cremins (jcremins@seas.upenn.edu). Applications will be considered as they are received; positions are available now.

Christopher Brown Associate Professor Department of Genetics University of Pennsylvania 538 Clinical Research Bldg 415 Curie Blvd Philadelphia, PA, 19104 chrbro@pennmedicine.upenn.edu T: (215) 746-4049

Christopher Brown <casey6r0wn@gmail.com>

UppsalaU AvianMalaria

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our mission is to pursue top-quality research and education and to interact constructively with society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has 44.000 students, 7.100 employees and a turnover of SEK 7 billion.

A position as a researcher in avian malaria is available at the Department of Ecology and Genetics, animal ecology.

The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see www.ieg.uu.se . Project description: Vector borne diseases are a major threat to human, domesticated and wildlife populations. Many vectors are bloodsucking insects that rely on olfactory cues for finding their meal. These olfactory cues can be manipulated by the pathogen to ensure transmission. We will use avian malaria to study the chemical ecology of vector borne pathogen transmission. First, we will investigate how particular malaria strains and the birds' MHC genes determine odour profiles. Second, we will use a combination of blood-feeding behavioural tests and RNAseq to reveal the genetic basis to variation in vector responses to host odour profiles. We predict that specific avian malaria strains affect their vectors such that they avoid hosts with MHC genes that would allow the host to defend themselves. Our results will also lead to predictions of specific combinations of genotype frequencies of hosts, pathogens and vectors that promote pathogen transfer resulting in more infected individuals in the population.These predictions will be tested using data from geographically separated populations. We also predict that the pathogen strains that are most efficiently transmitted between hosts also are the most virulent ones. Our findings will be relevant in the general context of predicting and preventing the spread of vector borne pathogens. Our results will in particular contribute to improved general guidelines for predictions of the likelihood and consequences of pathogen range expansion.

Duties: Analyze and publish already available data, perform experiments in the field and contribute to the future development of the project.

Qualifications required: A doctoral degree, or a foreign degree equivalent to a doctoral degree, in ecology and/or evolution. Previous experiences with analyses of genomic data are required. Candidates must be able to express themselves fluently in spoken as well as written English. In ranking eligible candidates special importance will be given to scientific skills.

Qualifications desired: Earlier experiences of field work on birds are desired.

Application: The application should include 1) a letter of intent describing yourself, your research interests and why you want this position, 2) your CV, 3) a short description of your education, 4) a copy of your doctoral degree and course grades, 5) the names and contact information to at least two reference persons (e-mail address and phone no.), 6) a copy of your master thesis and 7) publications produced. The application should be written in English.

Uppsala University strives to be an inclusive workplace that promotes equal opportunities and attracts qualified candidates who can contribute to the University's excellence and diversity. We welcome applications from all sections of the community and from people of all backgrounds.

Salary: Individual salary.

Starting date: 2020-01-01, or as agreed.

Type of employment: The position is a temporary position until 2020-12-31.

Scope of employment: 100 %

For further information about the position please contact: Professor, Anna Qvarnström, anna.qvarnstrom@ebc.uu.se, +46 18 471 64 06.

Please submit your application by 6 December 2019, UFV-PA 2019/3840.

Please do not send offers of recruitment or advertising services. Applications must be submitted as described in this advertisement.

Placement: Department of Ecology and Genetics

Type of employment: Full time , Temporary position longer than 6 months

Pay: Individuell lönesättning

Number of positions: 1

Working hours: 100%

Town: Uppsala

County: Uppsala län

Country: Sweden

Union representative: Saco-rÃ¥det saco@uadm.uu.se ST/TCO tco@fackorg.uu.se Seko Universitetsklubben seko@uadm.uu.se Number of reference: UFV-PA 2019/3840

Last application date: 2019-12-06

När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här:

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USDA-ARS Maryland EvolutionMicrobialCommunities

A post-doctoral opportunity is available to conduct research that provides critical knowledge of the fungal pathogens and plant microbiomes associated with boxwood blight, a destructive emerging disease spreading throughout the U.S. and worldwide. The post-doctoral researcher will take a lead on development and implementation of next-generation sequencing (NGS) and other advanced molecular tools to quantify, visualize and detect plant infection by the fungal pathogens. Additional work will evaluate impacts of the plant microbiome and abiotic environment on pathogen fitness and virulence. The research will yield an improved understanding of how latent, asymptomatic infection of less susceptible boxwood cultivars affects pathogen movement and persistence in the environment.

The position is located at the U.S. Department of Agriculture (USDA) Agricultural Research Service (ARS) in the Mycology & Nematology Genetic Diversity & Biology Laboratory located in Beltsville, MD, 16 miles outside of Washington, D.C. This project is a component of a multi-state, multi-disciplinary initiative focused on mitigating the negative impact of boxwood blight disease in the U.S. Exceptional in-house biological resources, computational infrastructure, and NGS/molecular biology instrumentation are in place to support accelerated research progress.

Requirements: The position requires a Ph.D. in mycology, plant pathology, microbiology, ecology or a closely related field within four years of the start date. Must have excellent molecular biology skills and experience working with filamentous fungi is required. Competitive candidates will be proficient in the use of bioinformatics and statistical analyses of multivariate data. Experience with molecular characterization of microbial communities is preferred. The successful candidate will have excellent verbal and written communication skills, including a solid record of peer-reviewed publications.

Application instructions: To apply, please send: (1) a brief cover letter detailing your research experiences, interests and career goals; (2) curriculum vitae, and (3) contact information of three references to Jo Anne Crouch at joanne.crouch@ars.usda.gov. The position is open until filled but applications received before December 12 will receive first consideration.The initial appointment period is one year, with reappointment after the first year based on successful performance and availability of funds. This position requires a preappointment background check, and is open to U.S. citizens or permanent residents only.

Jo Anne Crouch, Ph.D. Research Molecular Biologist, USDA-ARS Mycology & Nematology Genetic Diversity & Biology Laboratory 10300 Baltimore Avenue, Bldg 10A, Room 227 Beltsville, MD 20705 Phone: (301) 504-6922 Cell: (609) 933-5496 joanne.crouch@ars.usda.gov

"Crouch, JoAnne" <joanne.crouch@usda.gov>

UtahStateU FloralMicrobiome

Postdoctoral Fellow at Utah State University: Microbial Ecology of Flowers

The Schaeffer Lab (www.robertnschaeffer.com) in the Department of Biology at USU is seeking a Postdoctoral Fellow. The fellow will be expected to contribute to ongoing projects in the lab on the community and evolutionary ecology of floral-associated microbiomes, including those associated with both applied and natural systems. Considerable flexibility will be extended to the fellow however on the design and implementation of their project. Candidates interested in developing research involving one or more of the following areas are encouraged to apply: chemistry of floral rewards, plant-pollinator interactions, plant mating system evolution, and/or sustainable food production. The fellow will also have ample opportunity to both mentor and collaborate with undergraduate and graduate students.

The start date for the position is flexible, however sometime during Spring 2020 is preferred. The position offers a competitive salary and benefits, with an initial appointment of one year. A second year of funding is available to extend the position pending satisfactory performance. Review of applications will begin immediately and continue until the position is filled.

Responsibilities:

The fellow will design and carry out research studies pertaining to the basic and/or applied ecology of the floral microbiome. Moreover, the fellow will be expected to analyze data resulting from this work and present findings through presentations and peer-reviewed publications.

Qualifications

Minimum qualifications:

-Doctoral degree in botany, ecology, microbiology or related discipline.

-Experience designing and managing field and greenhouse studies.

-Strong quantitative, as well as written and verbal communication skills.

-Demonstrated record of publication of peer-reviewed literature.

To apply: Please submit 1) a cover letter outlining relevant experience and research interests pertaining to the position; 2) C.V., including contact information for three references; and 3) a writing sample (i.e. peer-reviewed publication). These documents can be submitted at the address below. Informal inquiries about the position are welcomed.

https://careers-usu.icims.com/jobs/2192/postdoctoral-fellow-ii/job Robert Schaeffer, Ph.D.

Assistant Professor

Department of Biology

Utah State University

Logan, UT 84322

robert.schaeffer@usu.edu

Robert Schaeffer <schaeffer.robert@gmail.com>

UTexas Austin 2 EvolutionaryGenomics

Two Postdocs in Evolutionary Genomics at U.T. Austin

The Kirkpatrick lab at The University of Texas at Austin is searching for two postdocs with experience in genomics, population genetics, and/or bioinformatics to join us on one of three projects funded by grants from the NIH and NSF. The first is a study of sexually antagonistic selection on sticklebacks and humans using whole genome sequences. We will use new statistical methods that we recently developed to detect and measure this key form of selection. The work on fishes is in collaboration with Dan Bolnick (UConn). The second project investigates the evolutionary forces driving the origin of new sex chromosomes, including transitions between XY and ZW sex determination. This research is in collaboration with Manfred Schartl (U Wurzburg). The third project focuses on the marine microbes that are the world's most abundant organisms. Here we are using whole genome sequences to study speciation and molecular evolution in populations that are largely free of random genetic drift. The initial appointment will be for one year, with the possibility for renewal for up to three years. The salary is $49,000 to $52,000, depending on experience, and full benefits are provided. The starting date is negotiable, but can be as soon as early 2020. If interested, please contact Mark Kirkpatrick (kirkp@mail.utexas.edu). Provide a CV and a brief statement of research interests and qualifications, and arrange to have three letters of recommendation sent.

Mark Kirkpatrick <kirkp@austin.utexas.edu>

UVienna PopGen Phylogen

A postdoc position in the fields of population genomics and phylogenomics is available at the Department of Botany and Biodiversity Research, Faculty of Life Sciences, University of Vienna, Austria. The position is available from 1st February 2020, initially for two years, with possibilities of subsequent extension. If desired, employment for 30h per week can also be discussed.

The position is funded by an Austrian Science Fund (FWF) grant focused on 1) assembling and annotating a new, high-quality genome for Nicotiana benthamiana; 2) answering ecological and evolutionary genomics questions in N. section Suaveolentes. This highly interesting group has an ancient allopolyploid origin in South America, but is exclusively found today in Australia, where it has experienced a recent adaptive radiation in the deserts. The research will use the latest DNA / RNA sequencing technologies in combination with spatial and ecological data. The project is expected to generate detailed understanding on the drivers of the evolution of this group and have implications for our knowledge of chromosomal evolution, adaptation and plant evolution in general. The project is a close collaboration with Prof. Mark Chase from the Royal Botanic Gardens, Kew (UK).

The main duties of the postdoc will be to analyze NGS and geographic/ecological data, focusing on whole genome assembly and annotation, genome scans, population genomics and phylogenomics, including the development/validation of new bioinformatics pipelines. Further duties will also include drafting corresponding publications, presenting results at international meetings and supporting supervision/mentoring of a wet-lab technician and 1-2 MSc students. The project will include at least one fieldtrip to Australia to collect leaf samples and ecological information. We have access to advanced computing resources and an active research program on this and related topics. The full-time equivalent gross salary is at least Â53k/year, split in 14 payments a year.

Formal requirements are a PhD in the natural or computer sciences, a record of quality research in evolutionary genomics, knowledge of unix/linux environments, programming skills (bash scripting; R; either Python or Perl), excellent written and oral communication skills in English, a keen interest to keep abreast with ongoing developments in bioinformatics and computational biology, and the ability to work in a team. Experience with wet lab protocols will be considered an advantage. The working language is English, knowledge of German is advantageous but not essential.

In recent years, Vienna has developed into one of the leading centers in evolutionary biology (http://www.evolvienna.at). In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life.

The position is available from February 2020, but the exact starting date is negotiable. Full applications should be sent to Rose Samuel (mary.rosabella.samuel@univie.ac.at) with CC to Ovidiu Paun (ovidiu.paun@univie.ac.at), as a single pdf containing CV, list of publications, a statement of research interests, and contact details of three potential referees. Although the search will continue until the position is filled, applications should be received by December 1st, 2019, to ensure full consideration.

Ovidiu Paun http://plantgenomics.univie.ac.at Ovidiu Paun <ovidiu.paun@univie.ac.at>

UVirginia:Coevolution

The Brodie lab (http://www.faculty.virginia.edu/brodie/) at the University of Virginia is seeking a Post-Doctoral Research Associate to study landscape-scale patterns of coevolutionary interaction between predators and prey.

Potential projects will involve analysis of the geographic and phenotypic distributions of traits that mediate the coevolutionary arms race between toxic newts and their resistant snake predators. Data collected over several decades are available to explore questions about biotic and abiotic factors that influence the geographic mosaic of coevolution. Specific projects will include spatially explicit modelling to better understand the distributions of toxicity levels of prey, phenotypic and genetic resistance of prey, as well as the development of a relational database aggregating physical, genetic, phenotypic, and digital resources related to the project. The successful candidate will be encouraged to pursue self-directed projects promoting understanding of the causes and patterns of coevolutionary processes.

The Biology Department at UVA (http://bio.as.virginia.edu/) is an excellent training environment for curious, highly motivated scientists. The successful applicant can expect to interact frequently with the department's strong, collegial group of evolutionary biologists (https://www.eebvirginia.org/). Additional opportunities for research and training are available at the Mountain Lake Biological Station (https://mlbs.virginia.edu/), in southwestern Virginia. The Brodie lab is committed to fostering diversity in evolutionary biology and ecology and to promoting a safe and inclusive working environment.

Qualification requirements: A Ph.D. in evolution, ecology, or related field is required by the start date of the appointment. Candidates must have experience with spatially explicit analysis such as ecological or mechanistic niche modelling, GIS, or related approaches, as well as proficiency in general database management and statistical analysis. A strong publication record, excellent written and verbal communication skills, and the ability to work well with others are required. The ideal candidate will demonstrate ambition, creativity, and independence.

Application procedure: Apply online at https://uva.wd1.myworkdayjobs.com/UVAJobs and attach a cover letter, a curriculum vitae, contact information for 3 references, and 1-2 writing samples (preferably first-author publications, published or in prep).

Application deadline: Review of applications will begin on Nov 1, 2019. The position will remain open until filled.

Initial appointment will be one-year with the possibilty of extension, contingent upon performance and available funding.

Interested applicants are invited to email Butch Brodie, BFD Runk Professor of Biology, at bbrodie@virginia.edu to discuss the position.

For questions about the application process, please contact Richard Haverstrom, Faculty Search Advisor, at rkh6j@virginia.edu.

For information on the benefits available to postdoctoral associates at UVA, visit postdoc.virginia.edu and hr.virginia.edu/benefits.

Butch Brodie <butchbrodie@gmail.com>

UVirginia TransmissionModeEvolution

UVirginia_TransmissionModeEvolution

The Department of Biology at the University of Virginia invites applications for a postdoctoral research-associate position in evolution and ecology of infectious disease. The position will be in the research group of Janis Antonovics as part of the project "Evolution of transmission mode: anther-smut as a model system" funded through the NSF/NIH Ecology of Infectious Disease Panel.

We seek applicants with research interests in the ecology and evolution of infectious disease with an interest in transmission modes and behavior. The successful applicant will plan, conduct, and publish research, and assist with other routine lab activities. Note that this is a short-term appointment for six months; however, the appointment may be renewed for some additional months, contingent upon available funding and satisfactory performance.

APPLICATION PROCEDURE: Apply online at https://uva.wd1.myworkdayjobs.com/UVAJobs and attach a curriculum vitae, a cover letter, and contact information for three individuals who can provide professional reference letters. The University will perform background checks on all new hires prior to employment.

APPLICATION DEADLINE: Review of applications will begin on December 5, 2019, but the position will remain open until filled. The University will perform background checks on all new hires prior to employment.

Additional Job Description For questions about the position, please contact Janis Antonovics, Associate Professor, at ja8n@virginia.edu.

For questions about the application, please contact Rich Haverstrom, Faculty Search Advisor, at rkh6j@virginia.edu

For more information on the benefits available to postdoctoral associates at UVA, visit postdoc.virginia.edu and hr.virginia.edu/benefits.

"Antonovics, Janis (ja8n)" <ja8n@virginia.edu>

UWestFlorida MolecularEvolution

Job Title: Post-Doctoral Research Associate (12710T)

Location: Janosik Laboratory, University of West Florida (UWF), Pensacola, Florida

Salary: $48,000

Job Description: The Janosik Laboratory in Department of Biology in the Hal Marcus College of Science and Engineering at the University of West Florida is seeking a full-time two-year Post-Doctoral Fellow with a research focus in molecular evolution, environmental DNA, metabarcoding, and bioinformatics. Applicants should be creative and independent, have good writing skills, a strong publication record, and have a demonstrated passion for evolutionary research and ecological genetics. The appointment can begin immediately and as a one-year appointment with possible extension to two years. Some field work is necessary.

Applicants will be expected to develop and lead projects. Candidates will be working on a funded environmental DNA project of metabarcoding of reef fish. Opportunities to explore other evolutionary projects with both Antarctic and Gulf of Mexico fishes and invertebrates will be encouraged.

Minimum qualifications are a Ph.D. from an accredited institution in Biological Sciences or a similar field of study with a demonstrated record of achievement in teaching, academic research, and service.

The ideal candidate would have strong laboratory skills, and with experience working with environmental DNA or metabarcoding in marine or freshwater systems and significant experience in using molecular tools and bioinformatics to tackle evolutionary and phylogenomic questions.

The University of West Florida is an Equal Opportunity/Access/Affirmative Action/Disabled/Veteran employer. Any individual requiring special accommodation to apply is requested to advise UWF by contacting UWF Human Resources at 1-850-474-2694 (voice) or 1-850-857-6158 (TTY). A criminal background check is required for successful candidates. E-Verify requirements may apply for employment in certain positions. All applications for employment at the University are subject to Florida public records law.

Apply online at https://jobs.uwf.edu/. Be prepared to attach a letter of application/interest stating your areas of interest and career goals, a current C.V. with expected availability date and contact information for three individuals who will serve as references. The posting will remain open until filled with a preferred response date of 1/24/2020.

Thank you!

– Alexis M. Janosik, Ph.D. Associate Professor Biology Graduate Program Coordinator University of West Florida Department of Biology Biology Building Annex 58C, 104G 11000 University Parkway Pensacola, FL 32514 (850) 857-6033 http://www.janosiklab.com/ Alexis Janosik <ajanosik@uwf.edu>

UZagreb VirusEvolution

The Jezic lab at the University of Zagreb (Croatia, https://www.pmf.unizg.hr/biol/marin.jezic) are looking for a new postdoc to work on the“Dynamics of virus infection and mycovirus-mediated biological control of a fungal pathogen. The projectutilises genomics andlaboratory experiments to examine questions related to the hypovirusCHV-1, which is an important component of Chestnut Blight biocontrol within Europe. For full information see the ad: https://euraxess.ec.europa.eu/jobs/458316?fbclid=IwAR2YYd087VqCae8vanKRR5C2IJEH6n0cgVJagmfSbhL_98AYFQ63wUbI1k Knowledge of Croatian is not required to successfully complete the project.

leigh <deborah.leigh@wsl.ch>

VIB Gent WheatGenomics

For a joint project of the VIB Center for Plant Systems Biology and BASF Agricultural Solutions Innovation Center Gent, we are looking for a postdoctoral researcher who will develop and implement computational pipelines to build and compare different biological networks for gene function analysis in cereals.

This 3-year project, starting on 1 March 2020, is fully funded by BASF and VLAIO (Flanders Innovation & Entrepreneurship). The successful applicant will be part of the Comparative Network Biology lab led by Klaas

Vandepoele in VIB, but will also closely work together with BASF data scientists and program leaders.

Job description

- Collect and integrate public and private crop expression datasets Develop computational pipelines to build and compare cross-species gene co-expression and regulatory networks to identify key transcription factors (TF) - Perform data analysis of DAP-seq high-thought experiments to identify TF binding sites and build TF regulatory networks - Perform/assistant data analysis on Y2H and build protein-protein interaction networks - Develop pipelines and methodologies to compare and integrate multiple biological networks - Integrative network analysis for gene function prediction and trait- associated gene identification - Closely work with both data scientists, biologists and wet-lab scientists in both VIB and BASF - Reporting of results through publications in peer-reviewed international journals. - Attending and presenting your results at international scientific events.

Profile

- PhD in Bioinformatics, Computational biology or similar. Good programming (Python, R) and Linux skills are a must Familiar with reporting in Jupyter notebook, bitbucket and git system for code sharing and sustainable data analysis - Strong ability and experience in high-throughput biological network and NGS data analysis - Knowledge in plant/crop genetics and molecular biology is a plus You are enthusiastic about scientific research, computational biology, and want to learn more about advanced biological concepts. - You have good writing and communication skills with both data scientists and biologists - You are proficient in English.

How to apply? Submit your application online to Jobsoid (https://vibvzw.jobsoid.com/j/23730/post-doctoral-researcher-integrative-network-analysis-for-gene-discovery-in-wheat) by sending your letter of motivation, a detailed CV and contact info of 2 references (including e-mail addresses and phone numbers).

Application deadline: 31/12/2019 or until position has been filled.

Klaas Vandepoele -Professor

Comparative Network Biology VIB-UGent Center for Plant Systems Biology Ghent University Technologiepark 71 - 9052 Ghent - Belgium Tel. +32(0)9 331 38 22 www.psb.ugent.be Klaas Vandepoele <klaas.vandepoele@psb.vib-ugent.be>

WellcomeSangerInst 4 TreeOfLife

The Tree of life is a new programme at the Wellcome Sanger Institute that will explore the evolutionary biology of genomes from across eukaryote diversity to understand pattern and process in the generation of diversity. To do this, we will generate many thousands of high quality genomes, chromosomally-resolved wherever possible, of protists, fungi, plants and animals. We are looking for up to four postdoctoral bioinformatics researchers to join Mark Blaxter's group to work on diverse aspects of the evolution of genomes, their structure, their analysis and their presentation to the wider world.

Post 1: Phylogenomics We aim to build a continually updated tree of life from the genomes generated in the Tree of Life programme at Sanger and elsewhere. This post will deliver software solutions to identify orthology, build alignments and compute phylogenies across all sequenced genomes. In addition to resolving a species-level tree, these data will be used to understand the dynamics of gene family change through evolution, and map the conflicting roles of introgression, hybridisation and horizontal gene transfer in producing conflict in tree estimation. The ideal applicant will have experience in both software pipe-lining in a production environment and in large scale phylogenetic inference. A keen interest in the diversity of life and understanding of the nuances of genome evolution would be desirable.

Post 2: Chromosome evolution While organisms and genes evolve rapidly, karyotypes appear to be relatively stable. In addition, chromosomes have internal structure that persists through phylogenetic time, such that many genes have been linked on the same chromosome for many millions of years. What maintains chromosome structures through time? What does karyotypic conservatism mean for linked gene coevolution? These questions will be explored using the breadth of genomes sequenced in the Tree of Life programme across a range of evolutionary distances. The ideal applicant for this post would be a computational biologist comfortable with large data and able to develop algorithms to describe and model chromosome evolution.

Post 3: Genomes within genomes Nearly one third of eukaryotic species are parasites, and many eukaryotes host prokaryotic endosymbionts. We have built toolkits for effective separation of cobiont genomes from their hosts, and this post will use these tools to survey and describe the diversity of symbionts within the thousands of genomes delivered by the Tree of Life programme. Do these cobionts cospeciate with their hosts, or do they jump regularly? What novel symbionts are there in the majority of unsequenced life? How do symbiont genomes evolve? The ideal applicant would be comfortable with genome assembly and interpretation, and in particular have an interest in investigating pattern and process in symbiont genome evolution.

Post 4: GenomeHubs We are developing a genome databasing package, GenomeHubs (see https://genomehubs.org) based on Ensembl, that communities of researchers can use to deliver custom solutions for sharing and analysis of genome data. This post is for a curator/developer who will support our several taxon-oriented communities in installing and maintaining their instances of GenomeHubs, train users (including generating online training materials), and assist in the development of new functionality. The post will involve considerable travel and collaborative working, and so the ideal applicant will have experience in programming and genomics databasing and a desire to communicate and train a diversity of fellow scientists worldwide. This position is funded in part by the UK BBSRC.

General The post holders will work closely with others in the Tree of Life programme and Mark Blaxter's evolutionary genomics group. Within the underpinning need to deliver a whole solution to their overarching goals, all the posts will have independence in defining research focus and in establishing key collaborations.

All posts are for 3 years in the first instance, with prospect for extension.

For informal enquiries please email mark.blaxter@sanger.ac.uk

Essential Skills Experienced in independently solving bioinformatics problems, either as part of PhD work or demonstrated by several years of on-the-job training

Good programming skills, preferably Python; Proficiency in Unix/Linux operating system

Experience with managing and processing next-generation sequencing data

Experience in genome assembly and quality assessment, and in genome interpretation

Experience and understanding of large-scale phylogenetic inference

Strong grounding in evolutionary genomics, genome biology and population genetics

Excellent communication skills

Attention to detail and highly developed problem solving skills

Ideal Skills Experience with using relational database systems

Experience with using compute cluster and batch queuing systems

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Yale 2 AntBeeDiversity

Global Biodiversity of Bees

https://bgc.yale.edu/opportunities A new, 2-3 year postdoc position is available in association with the Yale Center for Biodiversity and Global Change (BGC Center), the GEO BON Species Populations Working Group, Map of Life, and the Jetz Lab. The position is part of a larger, collaborative initiative to advance a conservation-relevant knowledgebase for focal taxa at a global scale, supported through the E.O. Wilson Biodiversity Foundation and associated sponsors, NASA and others. The postdoc will benefit from working closely with a growing group of Center-based biodiversity scientists, modelers, coordinators, and informaticians and from engaging with a global collaborative network of species group and methods experts worldwide. Support for project-related travel and workshops is available. Target start date for the position is spring through fall 2020.

We are seeking an innovative thinker with a strong quantitative background who is interested in addressing ecological, conservation, biogeographic, or macroevolutionary questions for Bees as a global study system. Qualifications for the position include a PhD in ecology, conservation, macroevolution, bio-/geography, or biological informatics, combined with experience in spatial biodiversity analysis and inference. The preferred candidate will have a deep understanding of this species group, a passion for advancing its spatial knowledge base, a strong interest in the model-based integration of large, disparate biodiversity data, a dedication toward conscientious work in a team, attention to detail, and strong communication skills. Particularly welcome is an ability to traverse ecological, evolutionary, and conservation perspectives and to address processes at different spatial and temporal scales. We expect strong analysis and scientific writing skills. Experience in several s cripting languages, database management, taxonomic name management, remote sensing, and/or biodiversity informatics are highly welcome.

The position offers broad thematic flexibility, and focal research questions may be macroecological, conservation-focused, biogeographical, macroevolutionary, or comparative. We ask candidates to briefly describe their preferred thematic interest in the cover letter.

We strongly encourage applications from women and minorities. Diversity, equity, and inclusion are core values in our group, and we believe that a diverse team will enable a broader perspective and enhance creativity.

The Yale BGC Center connects biodiversity scientists from across campus and hosts a range of speaker and workshop events. It supports research and training around the use of new technologies and data flows for model-based inference and prediction of biodiversity distributions and changes at large spatial and taxonomic scales. Flagship Center projects include Map of Life and activities supporting the Half-Earth Map and the development of the GEO BON Species Population Essential Biodiversity Variables. Other initiatives associated with the Center include the integration of macroevolutionary and biogeographic inference (e.g., VertLife, ButterflyNet), NASA-supported remote sensing-informed layers and tools for biodiversity modelling (EarthEnv), the Max Planck-Yale Center on Biodiversity Movement and Global Change, and the Wildlife Insights initiative for camera trapping data.

Yale University offers researchers and staff competitive salaries and a generous package of benefits. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. New Haven is renowned for its classic Ivy League setting, 75 miles northeast of New York City. To apply please send, in one pdf, a short motivation (i.e. cover) letter, CV and names and contact information for three referees to anna.schuerkmann@yale.edu, subject “BGC Postdoc - Bees”. Review of applications will begin on 9 December 2019 and continue until the position is filled.

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Global Biodiversity of Ants

https://bgc.yale.edu/opportunities A new, 2-3 year postdoc position is available in association with the Yale Center for Biodiversity and Global Change (BGC Center), the GEO BON Species Populations Working Group, Map of Life, and the Jetz Lab. The position is part of a larger, collaborative initiative to advance a conservation-relevant knowledgebase for focal taxa at a global scale, supported through the E.O. Wilson Biodiversity Foundation and associated sponsors, NASA and others. The postdoc will benefit from working closely with a growing group of Center-based biodiversity scientists, modelers, coordinators, and informaticians and from engaging with a

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Yale 2 DragonflyButterflyDiversity

Global Biodiversity of Butterflies

https://bgc.yale.edu/opportunities A new, 2-3 year postdoc position is available in association with the Yale Center for Biodiversity and Global Change (BGC Center), the GEO BON Species Populations Working Group, Map of Life, and the Jetz Lab. The position is part of a larger, collaborative initiative to advance a conservation-relevant knowledgebase for focal taxa at a global scale, supported through the E.O. Wilson Biodiversity Foundation and associated sponsors, NASA and others. The postdoc will benefit from working closely with a growing group of Center-based biodiversity scientists, modelers, coordinators, and informaticians and from engaging with a global collaborative network of species group and methods experts worldwide. Support for project-related travel and workshops is available. Target start date for the position is spring through fall 2020.

We are seeking an innovative thinker with a strong quantitative background who is interested in addressing ecological, conservation, biogeographic, or macroevolutionary questions for butterflies as a global study system. Qualifications for the position include a PhD in ecology, conservation, macroevolution, bio-/geography, or biological informatics, combined with experience in spatial biodiversity analysis and inference. The preferred candidate will have a deep understanding of this species group, a passion for advancing its spatial knowledge base, a strong interest in the model-based integration of large, disparate biodiversity data, a dedication toward conscientious work in a team, attention to detail, and strong communication skills. Particularly welcome is an ability to traverse ecological, evolutionary, and conservation perspectives and to address processes at different spatial and temporal scales. We expect strong analysis and scientific writing skills. Experience in several scripting languages, database management, taxonomic name management, remote sensing, and/or biodiversity informatics are highly welcome.

The position offers broad thematic flexibility, and focal research questions may be macroecological, conservation-focused, biogeographical, macroevolutionary, or comparative. We ask candidates to briefly describe their preferred thematic interest in the cover letter. We strongly encourage applications from women and minorities. Diversity, equity, and inclusion are core values in our group, and we believe that a diverse team will enable a broader perspective and enhance creativity.

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Global Biodiversity of Dragonflies

https://bgc.yale.edu/opportunities A new, 2-3 year postdoc position is available in association with the Yale Center for Biodiversity and Global Change (BGC Center), the GEO BON Species Populations Working Group, Map of Life, and the Jetz Lab. The position is part of a larger, collaborative initiative to advance a conservation-relevant knowledgebase for focal taxa at a global scale, supported through the E.O. Wilson Biodiversity Foundation and associated sponsors, NASA and others. The postdoc will benefit from working closely with a growing group of Center-based biodiversity scientists, modelers, coordinators, and informaticians and from engaging with a

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Yale GlobalPlantDiversity

Postdoc Positions - Global Biodiversity of Vascular Plants

https://bgc.yale.edu/opportunities Two 2-3 year postdoc positions are available in association with the Yale Center for Biodiversity and Global Change (BGC Center), the GEO BON Species Populations Working Group, Map of Life, and the Jetz Lab. The positions are part of a larger, collaborative initiative to advance a conservation-relevant knowledgebase for focal taxa at a global scale, supported through the E.O. Wilson Biodiversity Foundation and associated sponsors, NASA and others. The postdocs will benefit from working closely with a growing group of Center-based biodiversity scientists, modelers, coordinators, and informaticians and from engaging with a global collaborative network of species group and methods experts worldwide. Support for project-related travel and workshops is available. Target start date for the positions is spring through summer 2020.

We are seeking innovative thinkers with a strong quantitative background who are interested in addressing ecological, conservation, biogeographic, or macroevolutionary questions using all or major groups of vascular plants as a global study system. Qualifications for the position include a PhD in ecology, conservation, bio-

/geography, or biological informatics, combined with experience in spatial biodiversity analysis and inference. The preferred candidates will have a deep understanding of this species group and a passion for advancing its spatial knowledge base, a strong interest in the model-based integration of large, disparate biodiversity data, a dedication toward conscientious work in a team, attention to detail, and strong communication skills. Particularly welcome is an ability to traverse ecological, evolutionary, and conservation perspectives and to address processes at different spatial and temporal scales. We expect strong analysis and scientific writing skills. Experience in several scripting languages, database management, taxonomic name management, remote sensing, and/or biodiversity informatics are highly welcome.

The positions offer broad thematic flexibility, and focal research questions may be macroecological, macroevolutionary, comparative, biogeographical, or conservation-focused. We ask candidates to briefly describe their preferred thematic interest in the cover letter.

We strongly encourage applications from women and minorities. Diversity, equity, and inclusion are core values in our group, and we believe that a diverse team will enable a broader perspective and enhance creativity.

The Yale BGC Center connects biodiversity scientists from across campus and hosts a range of speaker and workshop events. It supports research and training around the use of new technologies and data flows for model-based inference and prediction of biodiversity distributions and changes at large spatial and taxonomic scales. Flagship Center projects include Map of Life and activities supporting the Half-Earth Map and the development of the GEO BON Species Population Essential Biodiversity Variables. Other initiatives associated with the Center include the integration of macroevolutionary and biogeographic inference (e.g., VertLife, ButterflyNet), NASA-supported remote sensing-informed layers and tools for biodiversity modelling (EarthEnv), the Max Planck-Yale Center on Biodiversity Movement and Global Change, and the Wildlife Insights initiative for camera trapping data.

Yale University offers researchers and staff competitive salaries and a generous package of benefits. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. New Haven is renowned for its classic Ivy League setting, 75 miles northeast of New York City. To apply please send, in one pdf, a short motivation (i.e. cover) letter, CV and names and contact information for three referees to anna.schuerkmann@yale.edu, subject “BGC Postdoc - Plants”. Review of applications will begin on 9 December 2019 and continue until the positions are filled.

walter.jetz@yale.edu

YaleU BiodiversityChange

Postdoc Position - Quantitative Ecology and Biodiversity Change

A new 2-3 year postdoc or longer-term staff position is available in association with the Yale Center for Biodiversity and Global Change (BGC Center), Map of Life, and the Jetz Lab. We are seeking a highly quantitative ecologist with strong R programming skills and a background in geospatial analysis, remote sensing, and species distribution modelling. The project is supported by NASA and other sources with the goal of demonstrating the power of novel quantitative approaches and data for addressing central questions in large-scale ecology and conservation. The successful candidate is expected to work with an array of biodiversity data (e.g., survey, citizen science, GPS tracking, and camera trapping) as well as a range of remote sensing products and sources, including hyperspectral data. While there is thematic and taxonomic flexibility, a particular focus of the position will be the collaborative development and use of multi-species models at large spatial scales. We therefore expect a background in Bayesian and/or machine-learning approaches to model species and/or assemblage distributions and changes. Experience in Python, Jupyter Notebooks, Google Earth Engine, SQL, and HPC is a plus.

The preferred candidate will be dedicated to conscientious work in a team and have excellent writing and communication skills. The position is formally supervised by Walter Jetz, and the successful candidate will collaborate closely with an international working group of leading biodiversity modelers associated with Map of Life and the Yale BGC Center. Support for project-related travel and workshops is available. Target start date for the position is spring to summer 2020. Depending on experience and preference, employment as either postdoctoral researcher, research scientist, or longer-term Yale Center staff is possible.

The position will benefit from interacting closely with a growing group of Center-based biodiversity scientists, modelers, coordinators, and informaticians. The Yale BGC Center connects biodiversity scientists from across campus and hosts a range of speaker and workshop events. It supports research and training around the use of new technologies and data flows for model-based inference and prediction of biodiversity distributions and changes at large spatial and taxonomic scales. Flagship Center projects include Map of Life and associated activities supporting the Half-Earth Map and the development of the GEO BON Species Population Essential Biodiversity Variables. Other initiatives associated with the Center include the integration of phylogenetic information with spatial distributions (e.g., VertLife, ButterflyNet), NASA-supported remote sensing-informed layers and tools for biodiversity modelling (EarthEnv), Movebank, which supports the management and integration of movement data, and the Wildlife Insights initiative for camera trapping data.

We strongly encourage applications from women and minorities. Diversity, equity, and inclusion are core values in our group, and we believe that a diverse team will enable a broader perspective and enhance creativity.

Yale University offers researchers and staff competitive salaries and a generous package of benefits. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. New Haven is renowned for its classic Ivy League setting, 75 miles northeast of New York City.

To apply please send, in one pdf, a short motivation (i.e. cover) letter, CV and names and contact information for three referees to anna.schuerkmann@yale.edu, subject “BGC Postdoc - Biodiversity Modelling”. Review of applications will begin on 2 December 2019 and continue until the position is filled.

“Jetz, Walter” <walter.jetz@yale.edu>

YorkU BeeEcologyEvolution

Wild Bee Behavioural Genomics and Molecular Ecology Positions (1 postdoc + 1 graduate student)

The Rehan Lab (www.rehanlab.com) is hiring 2 positions to study behavioural genomics and molecular ecology of wild bees. The Rehan lab is a collaborative group of researchers, staff, and students focusing on bee behaviour, ecology and evolution. We are located at York University in Toronto, Canada. The candidates will join a vibrant team of integrative biologists passionate about all things bee.

Behavioural Genomics Position

This postion will examine nutritional ecology of wild bees to determine pollen preference and nutritional requirements of native pollinators. There is increasing evidence that bee health is mediated not only by the quantity, but also quality of food provided during development. This researcher will conduct field and lab experiments to determine optimal diets for bee nutrition and pollinator health. We are also interested in the effects of maternally provisioned diet and mother-offspring interactions on social behaviour. We encourage the candidate to develop research projects on the social evolution and behavioural genomics of wild bees.

The successful candidate will have skills in a relevant area, and a strong background in behavioural ecology and evolution. Analytical and writing skills as well as familiarity with transcriptomic and genomic data is highly desirable.

*Molecular Ecology and Population Genomics Position *

This position will develop genomic reference material and environmental samples for the wild bees across eastern North America. We have a rich database of existing material and are actively working to develop robust dataset for wild bees in the northeast as well as understanding habitat requirements and floral hosts using a mix of metabarcoding, phylogenomics, historic reference data and ongoing field surveillance. This researcher will help manage a field crew, analyze complex genomic and ecological data, write manuscripts and and engage in public outreach and educate events across Toronto.

The successful candidate will have skills in a relevant area, and a strong background in molecular ecology and population genetics. Analytical and writing skills as well as familiarity with genomic data and bioinformatics is highly desirable.

York University is an Equal Opportunity Employer and encourages applications from women and underrepresented groups. If interested, please send a CV, names of three references, and a short statement of interests to Sandra Rehan *sanrehan@y <sandra.rehan@unh.edu>orku.ca* by December 6, 2019. Graduate students are encouraged to apply by January 2020 for Fall 2020 admission considerations. A Postdoctoral Fellowship position is available for one year (starting January 2020) and renewable up to three years with successful progress and performance.

– Sandra Rehan, FRES | Assistant Professor of Molecular Evolution Department of Biology | Faculty of Science | York University 4700 Keele Street | 109 Farquharson Building | Toronto ON | M3J 1P3 Email: sanrehan@yorku.ca | Web: www.rehanlab.com | Tel: 416.736.2100 ext. 77822

Sandra Rehan <sandra.rehan@gmail.com>

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Armidale Australia Genetics Feb3-7

Registration is now open for the 2020 Summer course in Armidale

The search for selection

Teachers: Professor Bruce Walsh University of Arizona (USA) Dr Michael Morrissey University of St Andrews (UK)

Dates: Monday 3 February 2020- Friday 7 February 2020

More information about course content on this link. https://jvanderw.une.edu.au/aabc2020.htm jbwalsh@email.arizona.edu

Barcelona GeometricMorphometrics Jan20-24

Dear colleagues,

Registration is opened for Transmitting Science course 'GEOMETRIC MORPHOMETRICS IN R - 7th edition'.

Dates: January 20th-24th, 2019.

Instructor: Dr. Julien Claude (Institut des Sciences de l'Ãvolution de Montpellier, France).

Place: Capellades, Barcelona (Spain)

Registration and more information: https://www.transmittingscience.org/courses/geometric-morphometrics/geometric-morphometrics-r/ Course Overview

Concepts in geometric morphometrics will be taught using a series of original data sets and working in R for solving a series of tasks. The course will start with an introduction to R and will rapidly go into shape analysis with measurements, landmark data and outlines. The participants are welcome to bring their own data and problems so that we may find R solutions.

This is not an introductory course to Geometric Morphometrics, therefore, basic knowledge of Multivariate Statistics, R and Geometric Morphometric is recommended in order to take this course.

This course is organized by Transmitting Science.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards,

Sole

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

Berlin DatavizInRggplot Mar2-6

Dear all,

we will run a 5-day course on "Data visualization IN R with ggplot2" in March (2-6) at the Free University Berlin (Germany): https://www.physalia-courses.org/courses-workshops/course56/ Registration deadline: 6th February 2020

In this course, you learn how to use R to load, transform, explore and visualize data. The course also covers the basic concepts in data visualization and a suite of different chart types and tricks to make appealing and informative-rich plots using 'ggplot2'.

This workshop is aimed at researchers and technical workers with a background in any data-related field. In general, no programming experience is needed. The course teaches all relevant steps to load, transform and visualize the data. However, basic knowledge of R is beneficial.

After completing the workshop, students should be in a position to:

- know and apply the principles of good data visualization such as the right choice of colors and chart types - load and transform data in R using 'tidyverse' - the layered structure of 'ggplot2' - the data in multiple ways using 'ggplot2' - publication quality and easy understandable figures - reproducible by using version control and project organization

Session content: https://www.physalia-courses.org/courses-workshops/course56/curriculum56/ Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Best regards,

Carlo

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

Berlin GWAS Mar2-6

Introduction to genome-wide association studies (GWAS)

(https://www.physalia-courses.org/courses-workshops/course49/)

Where: Free University (FU) Berlin (Germany)

When: 2-6 March 2020

General Topic: Bioinformatics pipeline for GWAS analysis

Instructors: 1) Dr. Filippo Biscarini (CNR, Italy); 2) Dr. Oscar González-Recio (INIA, Spain); 3) Dr. Christian Werner (University of Edinburgh, UK)

OVERVIEW

This course will introduce students, researchers and professionals to the steps needed to build an analysis pipeline for Genome-Wide Association Studies (GWAS). The course will describe all the necessary steps involved in a typical GWAS study, which will then be used to build a reusable and reproducible bioinformatics pipeline.

FORMAT

The course is structured in modules over five days. Each day will include introductory lectures with class discussions of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, results will be interpreted and discussed in group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at students, researchers and professionals interested in learning the different steps involved in a GWAS study using them to build a structured pipeline for semi-automated and reproducibile GWAS analyses. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of GWAS and bioinformatics pipeline building, progressively describing all steps and putting there seamlessy together in a general workflow. Attendees should have a background in biology, specifically genetics; previous exposure to GWAS experiments would also be beneficial. There will be a mix of lectures and hands-on practical exercises using R, Linux command line and custom software. Some basic understanding of R programming and Unix will be advantageous. Attendees should also have some basic familiarity with genomic data such as those arising from NGS experiments.

LEARNING OUTCOMES

*Understanding the different steps involved in a typical GWAS analysis and how to build them together in a general workflow / bioinformatics pipeline

Programme: (https://www.physalia-courses.org/courses-workshops/course49/curriculum49/)

Full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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

Berlin IntroductionBayesianStatistics Mar16-20

Dear all,

registration is now open for our course "An introduction to computational Bayesian methods" :

Website: (https://www.physalia-courses.org/courses-workshops/course46/)

Where: Free University (FU) Berlin (Germany)

When: 25-29 March 2019

Instructors: Prof. Shravan Vasishth and Bruno Nicenboim (University of Potsdam, Germany)

In this course, we seek to cover this gap, by providing a relatively accessible and technically non-demanding introduction to the basic workflow for fitting different kinds of linear models using Stan. To illustrate the capability of Bayesian modeling, we will use the R package RStan and a powerful front-end R package for Stan called brms.

After completing this course, the participant will have become familiar with the foundations of Bayesian inference using Stan (RStan and brms), and will be able to fit a range of multiple regression models and hierarchical models, for normally distributed data, and for log-normal, poisson, multinomial, and binomially distributed data. They will know how to calibrate their models using prior and posterior predictive checks; they will be able to establish true and false discovery rates to validate discovery claims, and to carry out model comparison using cross-validation methods, and Bayes factors

Session content: (https://www.physalia-courses.org/courses-workshops/course46/curriculum46/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Best regards,

Carlo

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

#!forum/physalia-courses)

"info@physalia-courses.org" <info@physalia-courses.org>

Berlin NanoporeGenomeAssembly Feb10-14

Course: GENOME ASSEMBLY USING OXFORD NANOPORE SEQUENCING

Course website: (https://www.physalia-courses.org/-courses-workshops/course59/)

Where: Free University Berlin (Germany)

When: 10 'V 14 February 2020

COURSE OVERVIEW

New advances in sequencing technologies have opened the door to more contiguous genome assemblies due to the increased length of obtained fragments. Although there is a setback in accuracy, a broad range of algorithms has been developed to cope with it. This course will introduce the audience with a spectre of methods which are present in a usual assembly workflow, starting from raw data and finishing with a fully assembled genome. We will see how to obtain nucleotide sequences from raw signals, dive deeper into the most used assembly paradigm for long fragments, try out and compare several state-of-the-art assemblers, and at last, assess the quality of the obtained assembly with and without a reference genome. Structured over five days, this course consists of both theoretical and practical aspects which are intertwined through each day. The presented theoretical foundation will be applied on small bacterial datasets and visualized in order to better grasp the algorithms at hand.

TARGETED AUDIENCE

This course is intended for researchers interested in learning the concepts of algorithms for de novo genome assembly with Oxford Nanopore Technologies data. Both beginners and more advanced users will find useful information in the presented matter. Course attendees should bring a laptop with either macOS or any Unix version. Some background in using mentioned operating systems via the command line is desirable, but we will cover the needed essentials throughout the hands-on sessions.

LEARNING OUTCOMES * Learn the advantages and disadvantages of third generation of sequencing. * Understand the concepts of de novo genome assembly. * Obtain practical experience on using state-of-the-art tools for de novo assembly and assembly quality assessment.

Outline

Monday 'V Session1: Introduction

This course starts with a general introduction to sequencing and assembly. The audience will get familiar with Oxford Nanopore sequencing, how it works, its advantages and disadvantages. Afterwards, we will transform a subset of a bacterial dataset, containing electric current signals, into a set of nucleotide sequences with error rate higher than previous generations of sequencing.

Session2: Stitching fragments

Sequencing technologies are still unable to read the whole genome at once, therefore the obtained fragments need to be joined together. We will first try and use sequence alignment, the basis of many bioinformatics tools. As it is not feasible for larger amounts of data, we will investigate a heuristic approach that uses short substrings of predefined length (Minimap). We will discuss the trade-off between execution time and sensitivity, and its impact on assembly contiguity, and apply this method on a small bacterial dataset.

Tuesday 'V Session3: Unknotting graphs

Given the set of pairwise overlaps between fragments, we will build an assembly graph from which the genome can be reconstructed (Miniasm). The graph will look like a yarn ball due to the sheer amount of overlaps. Step-by-step, we will introduce and apply several simplification methods to untangle the graph. There will still be knots in the graph which occurred due to sequencing errors. We will examine and try to resolve them. Afterwards, contiguous chains of fragments will be extracted and used in the next phases.

Session4: Polishing until it shines

Contigs from the assembly graph will have accuracy as the sequencing yield and will be unusable for most downstream analyses. Therefore, we will map all fragments to the assembly and create a multiple sequence alignment with partial order graphs (Racon). Retaining the most frequent base in all fragments at a given assembly position, we will iteratively try to increase the overall accuracy. Once we reach the maximum, we will see if we can further improve the assembly by using signal level data (Nanopolish).

Wednesday 'V Session5: Quality assessment

Quality of the assembly is important for downstream analysis so we will assess it in three different aspects: base accuracy (MuMmer) and completeness (QuastLG) given the reference genome, and protein prediction (orthologs (BUSCO) and ORFs (Ideel)). We will cover each appropriate tool and apply them on our assembly.

Session6: State-of-the-art

We will go through the basic concepts of several state-of-the-art assemblers such as Canu, Redbean, Flye, etc. We will apply each of them on the same dataset and create an evaluation consisting of contiguity, accuracy and the amount of resources needed.

Thursday 'V Session7: State-of-the-art continued

Session8: Group task

Attendees will get several sets of fragments obtained with Oxford Nanopore

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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

Berlin Phylogenomics May25-29

3rd edition of the Phylogenomics Course

Where: FU University Berlin (Germany)

When:25-29 May 2020

Instructor: Dr. Michael Matschiner (University of Basel (Switzerland))

Course website: (https://www.physalia-courses.org/courses-workshops/course21/)

Overview: In this workshop we will present theory and exercises to infer time-calibrated phylogenies from multilocus, RADseq, and whole-genome data sets while accounting for these confounding factors.

Who Should Attend: This workshop is aimed at researchers, PhD or postdoc level planning to infer phylogenetic relationships and divergence times from multilocus, RADseq, or whole-genome data.

Requirements: Attendents should have basic knowledge of UNIX and will need to use the command line on their laptops. Familiarity with a scripting language such as Ruby, Python, or Perl will be helpful but is not required. Full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

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

Best regards, Carlo

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

"info@physalia-courses.org" <info@physalia-courses.org>

Berlin PopulationGenomics May18-22

Dear all,

happy to inform you that we will run the 5th edition of our Workshop "Introductory Population Genomics: From Data to Inference" in Berlin.

When: 18-22 May 2020

Instructors:

Dr. Martin Taylor (University of East Anglia, UK)

Dr. Lewis Spurgin (University of East Anglia, UK)

Course website: https://www.physalia-courses.org/courses-workshops/course9/ Course Overview

Next generation sequencing has revolutionized evolutionary biology allowing unprecedented resolution and insight into evolutionary questions that appeared intractable only a few years ago. The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Targeted audience & ASSUMED BACKGROUND

This workshop is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an underpinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and FST are desirable. The course will use a range of software including the Linux operating system and R.

TEACHING FORMAT

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of a combination of lectures and practical exercises, with breaks at the organisers' discretion. There will also be time for students to discuss their own problems and data.

Session content: https://www.physalia-courses.org/-courses-workshops/course9/curriculum9/ Here is the full list of our courses and Workshops: https://-www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

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

Berlin scRNAseq Mar23-27

Course: "Analysis of single cell RNA-seq data"

Where: Free University (FU) Berlin (Germany)

When: 23-27 March 2020

Course website: https://www.physalia-courses.org/-courses-workshops/course18/ Instructors:

Dr. Kirk Gosik (Broad Institute of MIT and Harvard)

Dr. Dana Silverbush (Broad Institute of MIT and Harvard)

Dr. Orr Ashenberg (Broad Institute of MIT and Harvard)

Course overview

In recent years single-cell RNA-seq (scRNA-seq) has become widely used for transcriptome analysis in many areas of biology. In contrast to bulk RNA-seq, scRNA-seq provides quantitative measurements of the expression of every gene in a single cell. However, to analyze scRNA-seq data, novel methods are required and some of the underlying assumptions for the methods developed for bulk RNA-seq experiments are no longer valid. In this course we will cover all steps of the scRNA-seq processing, starting from the raw reads coming off the sequencer. The course includes common analysis strategies, using state-of-the-art methods and we also discuss the central biological questions that can be addressed using scRNA-seq.

Targeted Audience & Assumed Background

This course is aimed at researchers and technical workers who are or will be analyzing scRNA-seq data. The material is suitable both for experimentalists who want to learn more about data-analysis as well as computational biologists who want to learn about scRNASeq methods. Examples demonstrated in this course can be applied to any experimental protocol or biological system.

The requirements for this course are:

i- Working knowledge of unix (managing files, running programs)

ii- Programming experience in R (writing a function, basic I/O operations, variable types, using packages).

iii- Bioconductor experience is a plus.

iv- Familiarity with NGS data and its analyses (using alignment and quantification tools for bulk sequencing data)

Teaching Format

The course will be delivered over the course of five days. Each day will include a lecture and laboratory component. The lecture will introduce the topics of discussion and the laboratory sessions will be focused on practical hands-on analysis of scRNA-seq data. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using a combination of tools installed on the attendees laptop computer and web resources accessed via web browser.

EXAMPLE DATA

Please find example datasets here: https://-support.10xgenomics.com/single-cell-gene-expression/-datasets Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Should you have any questions, please do not hesitate to contact us : info@physalia-courses.org

Best regards,

Carlo

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ColoradoStateU GenomicsDiseaseWildlife May31-Jun6

Where: Colorado State University What: The 4th Genomics of Disease in Wildlife Workshop When: May 31 to June 6, 2020 Website for more information and application instructions:

https://gdwworkshop.colostate.edu Application Deadline: January 3, 2020

Email inquiries: CSU_gdw@colostate.edu

Overview: Title: Genomics of Disease in Wildlife: A Workshop

Location: Lory Conference Student Center, Colorado State University, Fort Collins, CO

Dates: May 31 to June 6, 2020

Website: https://gdwworkshop.colostate.edu Application deadline: January 3, 2020.

GDW2020 is an intensive, hands-on workshop focused on the application of powerful genomic tools to monitor, detect and investigate the role of pathogens within both wildlife and domesticated species. To date, the GDW 2017-2019 series has trained 73 researchers (43 women, 30 men) of which 25% were international scientists. Post-workshop participant surveys gave high scores for GDW workshops with a cumulative average of 4.7 of 5 for overall scientific value and 4.8 of 5 for overall venue experience.

Why is the workshop needed? Advances in genomic technology now provide an extraordinary opportunity to rapidly assess the impact of disease in wildlife biodiversity, management, and conservation. Wildlife and animal health researchers are uniquely positioned to merge ecological, biological, and evolutionary studies with genomic technologies to generate unprecedented Big Data tools in disease research. The workshop will provide a venue to accomplish this goal, will provide networking opportunities for colleagues from intersecting interests, and will advance genomic tools in wildlife and animal health disease investigations.

How will the workshop address the need? GDW2020 will provide essential training to those with skills and interest in some or all of the following: Wildlife Biology and Ecology, Disease Ecology and Modeling, Evolutionary Biology of Host and Pathogen, Pathogen Surveillance and Discovery, Animal Health and Veterinary Sciences, Genome Science and Bioinformatics, Diseases of Domesticated Species and Livestock

Attendees will conduct analyses of genomic data of both host and pathogen. The course will provide: an overview of current bioinformatics developments and approaches; guidance to implement genomic tools in study design; NGS data analysis and interpretation; and, opportunities for interaction with peers, core faculty, and invited experts.

Workshop Syllabus The workshop will cover a typical workflow commonly used in NGS analyses starting with the initial raw sequence through the final stages of identifying host:pathogen variants linked with disease. Each day of the workshop will cover an essential component of the NGS workflow in succession.

Morning sessions will be a series of instructional lectures and demonstrations that will concisely present the purpose, justification and implementation of the specific workflow unit. Short and exciting flash talks presented by CSU faculty will present some of their ongoing investigations using genomic tools in both host and pathogen.

The afternoon sessions will be computer intensive labs in which attendees will perform analyses with genomic data for each workflow topic.

Evening plenary lectures from invited faculty will conclude each day's activities.Teaching tools will include exercises using NGS data from a range of pathogens and host species.

Participants will learn the importance of integrating NGS data from both host and pathogen in order to better understand current epidemics in wildlife.For the duration of the course, each attendee will be provided with a MacBook Pro computer and peripheral equipment, and prepared genome datasets from several host species and associated pathogens. These datasets will be organized into various files and formats prior to the course, demonstrate key concepts, and be the foundation for computer exercises and teaching tools.

Summary of Workshop Schedule: Optional PreWorkshop Clinic. Sunday May 31, 2020 (10 a.m. to 4 p.m.)

An optional preworkshop clinic preceding the opening reception and activities on Sunday May 31, 2020. The crash course in basic coding skills will introduce conceptions of interacting with UNIX-based (Mac or Linux) platform, command line structure, navigating folders, and reading/writing files. The clinic will emphasize commands and terminology that will be used during GDW2020, and is designed for those with little or no experience in coding.

Day 1 Sunday May 31, 2020 Official Opening of GDW Workshop at 6 p.m.

The workshop begins in the evening of Sunday May 31, 2020 at the Lory Conference Center. A welcome session will introduce faculty and an overview of the workshop. NGS workflow projects for teams will be introduced. An informal welcome reception follows with faculty, staff and participants.

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Crete ComputationalMolEvol May10-21

Dear Community,

This is a reminder that the 12th summer school on Computational Molecular Evolution organized by Ziheng Yang, Alexis Stamatakis, Adam Leaché, and Cilia Antoniou, will take place from May 10 - 21 2020 in HCMR Crete, Greece.

Please visit the course web-site for further details: http://meetings.embo.org/event/20-comp-evolution The application deadline of 18th November 2019 is approaching!

Please feel free to circulate this message.

Course: “Computational Molecular Evolution”

Where: Heraklion, Crete, Greece

When: 10-21 May 2020

Course website: http://meetings.embo.org/event/20-comp-evolution Instructors: Ziheng Yang, University College London, UK Alexandros Stamatakis, Heidelberg Institute for Theoretical Studies, Germany Cilia Antoniou, Hellenic Centre for Marine Research, Crete, GR Maria Anisimova, ZHAW, Zurich, CH Brian Moore, UC Davis, USA Adam Leache, University of Washington, Seattle, USA Jeff Thorne, North Carolina State University, USA Tom A. Williams, University of Bristol, UK James Pease, Wake Forest University, USA Bruce Rannala, UC Davis, USA Asif Tamuri, University College London, UK Ben Redelings, Duke University, USA Bastien Bousseau, CNRS, Lyon, FR

Teaching assistants: Emmanouela Karameta, University of Cyprus, GR Pavlos Pavlidis, Foundation for Research and Technology Hellas, Crete, GR Rebecca Bengtsson, Liverpool, UK Sandra Alvarez Carretero, Queen Mary, UK Sarah Lutteropp, Heidelberg Institute for Theoretical Studies, Germany

Course details: The need for effective and informed analysis of biological sequence data is increasing with the explosive growth of biological sequence databases. A molecular evolutionary framework is central to many Bioinformatics approaches used in these analyses. Additionally, explicit use of molecular evolutionary and phylogenetic analyses provide important insights in their own right, e.g., analysis of adaptive evolution in viruses providing clues of their interaction with host immune systems.

To this end, we aim to provide graduate and postgraduate researchers with the theoretical knowledge and practical skills to carry out molecular evolutionary analyses on sequence data. The course will entail data retrieval, alignment techniques, phylogeny reconstruction, hypothesis testing, and population genetic approaches. The course will cover sessions on analysis of both protein and nucleotide sequences, including NGS data.

Also, the EMBO Practical Course will offer a unique opportunity for direct interaction with some of the world-leading scientists and authors of famous analysis tools (Maria Anisimova, Bastien Bousseau, Bruce Rannala, Alexandros Stamatakis, Benjamin Redelings, Ziheng Yang, etc.) in evolutionary Bioinformatics.

Note that the last three courses in Crete were heavily over-subscribed. The expected participant acceptance rate is below 20%. Experience from previous years has led to preference being given to candidates who:

are doctoral candidates in the early to middle stages of their thesis research already have some familiarity (i.e. have already used some of the relevant tools) with phylogenetic methods have already collected/assembled a molecular sequence dataset to analyze in their work have experience working in a Unix/Linux command-line environment We will also select a small fraction of participants that already work in Bioinformatics labs, to intensify collaboration between early career stage Biologists and Bioinformaticians. Applicants from labs with a strong focus on computational molecular evolution methodology need to carefully outline their motivation for attending the course in this context, since they have ready access to expert supervision and are likely to be very skilled already in the topics we teach, or are in the course of becoming very skilled therein.

Travel grants: A limited number of travel grants are available for participants. Applicants do not need to apply separately for travel grants for this event but should indicate on the registration form if they wish to be considered for a travel grant. Selection of awardees is handled directly by the organizer who will notify all eligible participants. More information is available at EMBO Travel Grants' page.

Best,

Adam D. Leaché, PhD Professor of Biology, Department of Biology Curator of Genetic Resources Curator of Herpetology Burke Museum of Natural History and Culture University of Washington, Seattle, WA 98195 USA leache@uw.edu

Adam Leache <leache@uw.edu>

Crete IntroQuantGen Mar30-Apr03

Dear evoldir members,

Transmitting Science is offering the course 'INTRODUCTION TO EVOLUTIONARY QUANTITATIVE GENETICS'.

Instructor: Dr. Erik Postma (University of Exeter, UK) and Dr. JesÃºs Martínez-Padilla (Universidad de Oviedo, Spain) Dates: March 30th-April 3rd, 2020 Location: Crete, Greece Early-bird deadline: November 30th, 2019

COURSE OVERVIEW: The response to both natural and artificial selection critically depends on the additive genetic variances and covariances underlying the traits subject to selection. As a consequence, understanding the genetic basis of complex morphological, life-history, physiological, ornamental and behavioural traits is crucial if we are to understand their evolutionary potential, and the evolutionary process in general.

Quantitative genetics uses the phenotypic resemblance among related individuals to infer the role of genes and the environment in shaping phenotypic variation. Depending on the species, we can use data obtained from breeding experiments under controlled conditions (e.g. insects, plants), or from individual-based monitoring programs in the wild (e.g. birds and mammals). Especially the latter has benefited greatly from the application of animal model methodology, originally developed in animal breeding to identify individuals of high genetic merit. By simultaneously using the resemblance among all individuals in the pedigree, these methods provide more precise and accurate estimates of genetic and non-genetic variance components (heritabilities and genetic correlations). Furthermore, they allow for the estimation of individual-level genetic effects (breeding values), and thereby the inference of evolution.

In this course we will cover everything from basic quantitative genetic theory and statistics to advanced mixed model-based approaches. You will learn how to estimate genetic variances and covariances in wild and captive populations, and how to test for evolutionary change. Along the way, you will be exposed to a range of general statistical methods (including generalised and mixed models), the R packages MCMCglmm and ASReml-R in particular. Furthermore, we will discuss a number of landmark papers that have put the concepts and methods covered during the lectures and practicals into practice to address fundamental evolutionary questions. You are strongly encouraged to bring your own data (if you have them), which you will be able to work on during the course and which will allow you to put the theory into practice.

PROGRAM: Monday, March 30th, 2020.

Morning: - Lecture: Key concepts in evolutionary biology. - Lecture: Quantitative genetic theory. - Lecture: Basic statistics. Afternoon: - Lecture: Heritability and its estimation. - Practical: Estimating heritability. - Lecture: Quantifying evolvability. - Discussion of research paper.

Tuesday, March 31st, 2020.

Morning: - Lecture: Quantitative genetic theory - Lecture: Mixed models. - Practical: Mixed models. Afternoon: - Lecture: Pedigree reconstruction. - Practical: Pedigrees. - Discussion of research paper.

Wednesday, April 1st, 2020.

Morning: - Lecture: The animal model. - Practical: Fitting animal models in ASReml-R. Afternoon: - Lecture: Selection and its response. - Analysis of own (or simulated) data. - Discussion of research paper.

Thursday, April 2nd, 2020.

Morning: - Lecture: Breeding values. - Practical: MCMCglmm Afternoon: - Lecture: Generalised linear models and animal models. - Analysis of own data - Discussion of research paper.

Friday, April 3rd, 2020.

Morning: - Lecture: Advanced topics. - Presentations

For more information and registration: http://bit.ly/intro-evol-quant-genetics . Contact: courses.crete@transmittingscience.org

All the best, Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.org haris.saslis@gmail.com

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INRA-Morocco FarmAnimalGenomics

Dear all,

The National Institute of Agronomic Research in Morocco INRA-Morocco < https://www.inra.org.ma/ > organizes a 4-day course, in the framework of the EU Horizon 2020 project IMAGE < http://www.imageh2020.eu/ >. This event will follow the 1-day workshop < https://www.inra.org.ma/fr/content/13112019-workshop-conservation-farm-animal-genetic-resources-fangr-january-20th-2020-rabat#overlay-context=fr/content/registration-workshop-farm-animal-genetic-resources-fangr > that will be organised within IMAGE project with Moroccan decision makers and stakeholders.

Title: Biobanking for a sustainable management of Farm Animal Genetic Resources (FAnGR): novel approaches in genomics, reproductive technologies and economics.

Aim: Give an update on the role of biobanking for a sustainable management of farm animal genetic resources (FAnGR) with a focus on the use of novel methods in genomics, reproduction, economics and the possibility to carry out practical cases of interest to participants.

Date: 21-24 January 2020

Location: Beni Mellal city Morocco

Level: postgraduate (experience with Unix and SNP data is preferred. Laptops required for the exercices)

Language: French & English

Infos, agenda & pre-registration not later than December 20, 2019: here < https://www.inra.org.ma/fr/content/13112019-post-graduate-image-training-course-21-24-january-2020-beni-mellal-morocco#overlay-context=fr/content/13112019-post-graduate-image-training-course-21-24-january-2020-beni-mellal-morocco > (the form can be filled in French also) Learning goals

- How to assess neutral and adaptive genetic diversity in the era of whole genome data? - How to effectively conceive and manage efficient genebanks? - How could the use of cryo-conserved material help to restore profitable traits? - Can we facilitate the effective use of gene bank samples in breeding by novel genome-assisted methods and tools? - How to sustainably manage indigenous populations?

Course content Assessment of genomic diversity Progress in genotyping Adaptive/productive introgression Functional genomics Economic assessment of conservation Conservation strategies Conception and use of animal genebanks Sustainable Management of livestock populations Legal issues Practical exercises

Confirmed lecturers Michèle Tixier-Boichard (INRA France) Badr Benjelloun (INRA Morocco) Sipke-Joost Hiemstra (Wageningen University & Research) Dominic Moran (Edinburg Univ.) Julie Demars (INRA France) Gwendal Restoux (INRA France) Philippe Monget (INRA France) Bouchra ElAmiri (INRA Morocco)

Jack Windig, (Wageningen University & Research)

Organising committee (workshop & training) Abdelmajid Bechchari Abdessamad Ouhrouch Badr Benjelloun Bassou Bouazzama Bouchra El Amiri Fatima Ezzahra Labdidi Fouad Elame Hayat Lionboui Ichrak Hayah Imane Thami Alami Kaoutar Elfazazi Marouane Jbilou Michèle Tixier-Boichard Mohammed BenBati Mouad Chentouf Moussa El Fadili Mustapha Ibnelbachyr Otman Sebbata Paul Boettcher Reddad Tirazi Samir Fakhour Sipke-Joost Hiemstra Tarik Benabdelouahab

We will have slots for poster sessions during the 1-day workshop and the training. People applying for the training may optionally submit their abstracts related to the topics of the events using the email address image.trainingmorocco2019@inra.org.ma A book of abstracts will be edited at the end of the training.

If you have further questions please check this link < https://www.inra.org.ma/fr/content/13112019-post-graduate-image-training-course-21-24-january-2020-beni-mellal-morocco#overlay-context=fr/-content/13112019-post-graduate-image-training-course-21-24-january-2020-beni-mellal-morocco >. You can also contact me or email the address image.trainingmorocco2019@inra.org.ma

On behalf of the organising committee, Badr Benjelloun

Badr Benjelloun, PhD Livestock genomics INRA Tadla, Morocco Other email: benjelloun@inra.org.ma Phone: +212 662351942 Skype: b.badr66

Benjelloun Badr <badr.benjelloun@gmail.com>

Madrid Phylogenetics Mar10-20

Dear Colleagues,

Registration is open for MadPhylo 2020, a course on statistical phylogenetics, to be held in Madrid, Spain.

Dates: March 10-20, 2020

Place: Royal Botanical Garden, Madrid, Spain

Details, including information for registering, can be found on the MadPhylo website, https://-www.madphylo.com . Please feel free to distribute information about the course to interested students and postdocs.

Sincerely,

John Huelsenbeck

John Huelsenbeck <johnh@berkeley.edu>

Malta ConservationGenomics Jan20-22

Dear all, we are pleased to announce that applications are now open for the first Training School of our COST Action G-BIKE which will be held in *La Valletta (Malta) from January 20th to 22nd, 2020*: *Genomic tools for conservation: a practitioner's guide*

Overview This Training School will be mainly, but not exclusively oriented towards practitioners, with the aim of presenting, in the simplest and yet most comprehensive manner, the contribution that can be provided by genetics and genomics for effectively tackling practical conservation and management problems. The underlying rationale for the School is to create a bidirectional information flow between scientists and practitioners to explore and clarify where and when genomics can make a difference in every day conservation within an EU policy and legislative framework, but with global application. To this end, trainees will be asked to offer at the beginning a short presentation about the main conservation challenges of their current jobs where they think genetic tools might help. At the end of the School, we will revisit these presentations, discussing the options and potential strategies that can be applied using the genomic and analytical tools described during the School. We hope to enable those involved to go back to their respective positions armed with a plan that they can then put into practice! This School may also be relevant to graduate students about to embark on conservation genomics projects to help them develop workplans, and just as important, to allow them to make their work policy and management oriented from the outset.

For details, please visit the G-BIKE website < https://-sites.google.com/fmach.it/g-bike-genetics-eu >.

Deadline for applications is December 8th, 2019. Selected trainees will be granted a full reimbursement (travel, lodging) from G-BIKE COST Action

Best regards Cristiano

Cristiano Vernesi Forest Ecology and Biogeochemical Cycles Unit Research and Innovation Centre- Fondazione Edmund Mach via E. Mach, 1-San Michele all'Adige 38010 (TN), Italy tel: +39 0461 615 671, mobile + 39 331 6471339 skypename:cvernesi Personal webpage < https://sites.google.com/fmach.it/cristianovernesi/home > G-BIKE COST Action < https://sites.google.com/fmach.it/g-bike-genetics-eu/ > ORCID ID: 0000-0001-7534-5669 < http://orcid.org/0000-0001-7534-5669 >

Please, do not print this email unless strictly necessary

cristiano.vernesi@fmach.it

MNHN Paris IntegrativeTaxonomy Mar30-Apr3

The course “Integrative taxonomy in the ”big data“ era” will be from the 30th of March to the 3rd of April, 2020 at the MNHN of Paris, France.

This course is also part of the DEST- Taxonomy training program (http://www.taxonomytraining.eu/).

The course is in English. To register, please fill the form on the website of the course (https://sites.google.com/site/coursbarcode/inscription-1) before the 13th of January, 2020.

If you have any question, please contact: Line Le Gall (legall@mnhn.fr) Nicolas Puillandre (puillandre@mnhn.fr) Sarah Samadi (sarah@mnhn.fr)

Nicolas Puillandre <nicolaspuillandre@gmail.com>

Online LandscapeGenetics Jan15-May6

Online Landscape Genetics Graduate Student Course Jan 15 - May 6, 2020, Wed 8:30 - 10:30 PST (also can be taken at any time using taped lectures) [Buffer]Cost $500 individuals, $1000 Groups Course Organizers: Helene Wagner, Melanie Murphy, and Lisette Waits Co-Instructors: Niko Balkenhol, Jeff Bowman, Anne Charpantier, Katalin Csilléry, Marie-Josee Fortin, Caren Goldberg, Nusha Keyghobadi, Erin Landguth, Stephanie Manel, Yessica Rico, Sean Schoville, Steve Spear, Kathy Zeller

Course description This course on Landscape Genetics provides a unique opportunity for interdisciplinary training and provides an overview of the field of landscape genetics. The course caters to students in basic and applied ecology, conservation and population genetics, landscape ecology, evolutionary biology and conservation biology. A key objective of landscape genetics is to study how landscape modification and habitat fragmentation affect organism dispersal and gene flow across the landscape. Landscape genetics requires highly interdisciplinary specialized skills making intensive use of technical population genetic skills and spatial analysis tools (spatial statistics, GIS tools and remote sensing). Even when students receive disciplinary training in these areas, educational programs often lack the necessary linkage and synthesis among disciplines. This linkage can only be accomplished after experts from each discipline work together to develop guiding principles for this new research area.

Landscape Genetics will be concurrently offered at multiple universities across the globe, giving students the opportunity to learn from international experts and work with peers from outside institutions. For students who are not members of the participating institutions, we are offering a web-based online course to reach a broader audience. Each course meeting will start with a live webcast lecture (no special software required) by an expert on the topic that introduces foundations and methods and highlights points for discussion in local seminar groups. After breaking out into local course group discussion (including a discussion group for online course students), a web-based discussion across campuses will wrap up the weekly topic. Students who are unable to make it to live-cast of lectures can view taped lectures. In addition, students can choose to participate in an optional lab section using R and/or interdisciplinary group term projects with web-based collaboration across institutions. The final two options are provided to help students develop analytical skills in Landscape Genetics. Students who participate in group projects will have the option of applying to attend a project synthesis meeting in Toronto Canada in May 13-17 2020 after the IALE North America meetings. See more information here: https://sites.google.com/site/landscapegeneticscourse/ Course Textbook: Landscape genetics: Concepts, methods, applications. 2015. Balkenhol, Cushman, Storfer, Waits, eds, Blackwell.

How to register?

Use this link: https://docs.google.com/forms/d/e/1FAIpQLScw_IIpr_7x7xysH0UMzMe34N-om0iWbAtVO2AfXghQdzi2Zg/viewform?usp=sf_link

When to register: by January 8

Faculty who would like to add a local section of the course at their university can register as a group or multiple students at one institution can register as a group. For faculty who set up local sections, we would expect you to set up course credit at your institution, participate in the course with the students and grade assignments (we provide answer keys for assignments). For individual students or students in small groups (<4) without a local instructor) who need course credit, you can have your advisor set up an independent study course at your home institution and turn in specific assignments during the semester that will be evaluated by our online instruction team. This can be set up as pass/fail or grading on A-F scale. It is easiest for us if you pick the pass/fail option. In the US system, this would count as a 2 credit course for the lecture portion, and students who choose to do all labs or participate in a group project would receive an additional credit.

You will be invoiced for the course in early January and can pay by credit card or check.

Class Schedule:

Overview section Jan 15 - Introductions and overview of landscape genetics (Spear) Theoretical Background section Jan 22 - Landscape ecology (Zeller) Jan 29 - Population genetics (Waits) Feb 5 - Metapopulation dynamics (Keyghobadi) Feb 12 - Study design (Fortin) Feb 19 - Adaptation and quantitative genetics (Charpantier) Feb 29 - Basics of spatial data analysis (Wagner) Students read one background paper (generally book chapter) and watch tutorials if needed

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Smithsonian MeiofaunaDiversityTaxonomy Jun7-21

2020 Smithsonian Marine Station (SMS) Meiofauna Diversity and Taxonomy Workshop

Dates: June 7-21, 2020 Location: Fort Pierce, FL Cost: Free - need-based support for travel expenses is available; most meals will be catered during the workshop Application deadline: February 1, 2020

Organizers: Kevin Kocot - University of Alabama, Tuscaloosa Ashleigh Smythe - Virginia Military Institute

Mentors: Michael Boyle - Smithsonian Marine Station - Sipuncula & confocal microscopy Rick Hochberg - University of Massachusetts Lowell - Gastrotricha & Rotifera Oleksandr Holovachov - Swedish Museum of Natural History - Nematoda & scientific illustration Ulf Jondelius - Swedish Museum of Natural History - Acoela & (some) Platyhelminthes Kevin Kocot - University of Alabama Tuscaloosa - Mollusca, Entoprocta, Hemichordata, & genomics Francesca Leasi - University of Tennessee Chattanooga - Rotifera & metagenetics/metagenomics Jon Norenburg - Smithsonian Institution - Nemertea & diverse other invertebrates Thomas Schwaha - University of Vienna - Bryozoa, Phoronida, 3D anatomical reconstruction Ashleigh Smythe - Virginia Military Institute - Nematoda

Course Description The term “meiofauna” refers to tiny animals capable of passing through a ~0.5-mm mesh. Many meiofaunal animals are interstitial, meaning they burrow in marine sediments. Several entire phyla (such as kinorhynchs, gastrotrichs, and gnathostomulids), major clades of other invertebrate phyla (especially arthropods, nematodes, annelids and flatworms), and miniaturized representatives of most other animal phyla are meiofaunal. Meiofaunal animals have been estimated to account for half of the biodiversity in complex biotopes such as coral reefs, with most of it associated with sediments. While the great phylum- and class- level diversity of meiofauna is well-known, the species-level diversity remains largely unexplored and undocumented. By some estimates, the number of species of meiofaunal nematodes alone that waiting to be formally named dwarfs the number of already described meiofaunal species by two orders of magnitude. Morphological studies of meiofauna have led to groundbreaking insights about their evolution, adaptation, and functional biology (e.g., adhesive and sensory structures), as well as fundamental insights into the evolution of the major animal groups in the tree of life. More recently, advances in molecular biology ranging from DNA barcoding to metabarcoding to whole-genome sequencing have accelerated the pace of the study of all aspects of the biology of meiofauna.

The overarching goal of this course is to help train the next generation of marine invertebrate taxonomists. Specifically, the course is designed to familiarize participants with the vast biodiversity of marine meiofauna through field and laboratory work. We will take a taxon-survey approach to emphasize the development or enhancement of practical skills essential for collection, identification, characterization, preservation, and molecular analysis of meiofauna. Sampling of diverse habitats near Fort Pierce (e.g., Capron Shoal and local beaches) and the Florida Keys (e.g., coral reefs, rubble fields, mangroves, and beaches) by snorkeling, SCUBA diving, and boat (grabbing/dredging) will provide a wealth of specimens of diverse taxa for our investigations. Note that SCUBA-certified participants will have the opportunity to dive recreationally in the Florida Keys at their own expense/risk, but the course will not involve scientific diving.

Morphological laboratory work will emphasize the preparation of specimens for microscopic examination and sorting to the level possible with light microscopy. Participants will have the opportunity to collect specimens of meiofaunal animals for their own research (if desired) and will be expected to compile and contribute species lists, images, and metadata to public databases.

Molecular laboratory work will begin with training in basic molecular lab skills and DNA barcoding for participants not already familiar with these techniques. Subsequently, participants will learn transcriptome (cDNA) and genomic DNA sequencing library preparation techniques that can be used on single meiofaunal animals. Each participant will have the opportunity to sequence at least one transcriptome or one mitochondrial genome as part of the course.

The course is limited to 8 students and will be taught in English. We use the term “student” broadly and will consider applicants at diverse career stages interested in studying meiofauna.

How to Apply Send your CV and a 1-2 page statement explaining your background and reasons for taking the course to Dr. Kevin Kocot at kmkocot@ua.edu before February 1st, 2020. Please be sure to describe your ultimate career goals and how participation in this course will help you excel in your career. It is anticipated that significant and lasting interactions

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SmithsonianTropInst PolycladTaxonomy Jun23-Jul12

Course title: Systematics and biology of Ctenophora and Medusozoa Dates: June 23, 2020 - July 12, 2020 Location: Bocas Research Station, Bocas del Toro, Panama Organizer: Dr. Rachel Collin STRI, Panama Registration Fee: $995 Application deadline: January 31st, 202 Course webpage: https://stri-sites.si.edu/sites/taxonomy_training/course/understanding-basal-metazoan-relationships-jellyfish-and-ctenophores/ Instructors: Steven Haddock Ph.D., is a Senior Scientist at the Monterey Bay Aquarium, USA Otto M. P. Oliveira Ph.D., is an Associate Professor at the Federal University of ABC in Brazil Erik V. Thuesen Ph.D., is a Member of the Faculty in Zoology at the Evergreen State College in Washington, USA Stefano Piraino Ph.D., is a Professor of Zoology and Marine Biology at the University of Salento in Lecce, Italy Rachel Collin Ph.D, Smithsonian Tropical Research Institute, Panama

Course description: This course is intended for graduate students, post-docs, or professionals who are interested in learning and applying knowledge about the taxonomy, evolution, and ecology of ctenophores, Medusozoa and other gelatinous zooplankton.

The students participating in this course will achieve the following:

1. learn to describe and identify ctenophores and pelagic cnidarians, focusing on the most common species living in the Bocas del Toro region; 2. learn general biological and ecological characteristics of other gelatinous groups; 3. gain hands-on ecological and taxonomic experience with tropical ctenophores and medusae; 4. learn fundamental sampling and survey techniques; and 5. learn how to conduct physiological experiments with fragile gelatinous organisms.

This course seeks to give the participants the necessary tools to continue studies on the taxonomy, systematics, ecology, and/or evolution of ctenophores and medusozoa. This edition of the course will also include discussions of the origins of Metazoa, and the relative phylogenetic placements of sponges, cnidarians, and ctenophores. The course will last 21 days, with the first week mostly dedicated to taxonomic training. During the second week, students will study ecological and physiological aspects of gelatinous zooplankton with special attention to techniques used to work with these very fragile animals. During the last week of the course, students will carry out a focused research project and present their results.

Daily activities will include morning and afternoon lectures, fieldwork, laboratory work, and evening seminars or talks.

Application: This course is directed towards advanced graduate students, post-docs, and young investigators, and will be conducted in English. Please e-mail your CV, 1 letter of recommendation, and a 1-2 page statement explaining your background and reasons for taking the course, to bocasresearchstation@gmail.com before January 31, 2020. To be considered for a need-based fellowship, applicants should send a description of their need, their efforts to obtain funding from other available sources, and a travel budget. For more information see: http://www.stri.si.edu/sites/taxonomy_training "Madrid, Maycol" <MadridM@si.edu>

Spain ConservationGenetics Jan27-31

Many conservation genetics tools have been developed for use in temperate other high latitude habitats, and so not all of these tools translate to the tropics. Tropical habitats share some features which complicate the application of some conservation genetics tools which are heavily relied upon in higher latitudes, and also share some basic questions and problems that are less of an issue in higher latitudes or other, better studies and/ or less diverse habitats.

This course will discuss practical issues, genetic and genomic theory, tools and analyses as applied to issues relevant to conservation in the tropics. Some basic questions of conservation importance include describing species diversity, determining species distributions, characterizing the basic biology of species, and understanding demographic history and population size and structure. Underlying biogeographic histories that have shaped communities, and the biotic interactions within those communities are also of fundamental importance. There is an optional, personalized conservation genetics project immediately following the lecture and computer practical week.

This course is designed with students and practitioners of Conservation Biology or Conservation Genetics in the tropical regions of America, Africa and Asia in mind.

This course will take place January 27-31, 2020 in the Biological Reserve of Doñana (Spain).

For more information, check out the website:

https://www.consevol.org/consgentropicscourse.htm

Jennifer Leonard Conservation and Evolutionary Genetics Group Estación Biológica de Doñana Avd. Americo Vespucio 26 41092 Sevilla, Spain

www.consevol.org Jennifer Leonard <jleonard@ebd.csic.es>

Toulouse SPAAM2 Sep21-22

Workshop: Standards, Precautions and Advances in Ancient Metagenomics (SPAAM2) PROPOSED DATES: 21-22nd September 2020 (prior to the ISBA9 conference) PROPOSED LOCATION:TBA, Toulouse, France

Dear all, We are circulating a 'registration of interest' survey for an ancient metagenomics workshop, possibly to be held as a satellite-meeting the two days prior to ISBA9 (https://isba9.sciencesconf.org/). This workshop will revive the Standards, Precautions and Advances in Ancient Metagenomes workshop that was held in 2016, which resulted in the guidelines published in A Robust Framework for Microbial Archaeology (https://doi.org/10.1146/annurev-genom-091416-035526). We are currently developing a proposal to hold this meeting and ask for your input.

We would like to have a round table discussion meeting between active PhD and postdoc researchers working in this area of research to share experiences, challenges, and propose practical solutions for the field in both data generation and analysis. We aim to announce the outcomes of this workshop at the closing ceremony of ISBA9, including an (in-)formal 'community'/network for continued interaction, and to develop an opinion paper in which we: -Discuss major issues -Outline recommended technical best-practices in ancient microbial genomics -Define metadata standardsAnnounce the network

We would be grateful if you could forward the above information your students and early career researchers to get their feedback and register their interest.

Please submit your registration of interest form by 30th January 2020.

The registration of interest form can be found here: https://docs.google.com/forms/d/1fKkW7WSXhojBZCxk7DY38Qljk-zORg_-nL5-82DZ024 Kind Regards, SPAAM2 Organizing Committee James Fellows Yates (MPI-SHH, Jena. Email: fellows@shh.mpg.de) Irina Velsko (MPI-SHH, Jena) Alexander Hübner (MPI-SHH, Jena) Andaine Seguin-Orlando (UMR5288, CNRS, University Toulouse 3) Clio Der Sarkissian (UMR5288, CNRS, University of Toulouse 3) Ãshild VÃ¥gene (Globe Institute, University of Copenhagen) Anna Fotakis (Globe Institute, University of Copenhagen)

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UIceland Reykjavik SLiMEvolModeling Mar6-10

Hi all.

March 6-10, 2020, a five-day SLiM workshop will be offered at the University of Iceland (Reykjavík, Iceland). It will be hosted by SnÃbjörn Pálsson and Arnar Pálsson, of the University of Iceland (Háskóli íslands). It will be free, and open to participants outside of the university. HOWEVER, registration is required, a limited number of seats are available, and priority will be given to registrants affiliated with the University. To apply, please send an email to BOTH SnÃbjörn and myself (snaebj@hi.is, bhaller@mac.com) with the info below. The deadline for applying is the end of the day on 10 January (late applicants may be considered if there is room), but priority for University applicants will end on 13 December; after that date it will be first-come-first-served so that we can notify everyone of their acceptance in time to make travel arrangements. Early application is advised.

As background: SLiM is a software package for creating evolutionary models/simulations that are individual-based and genetically explicit. It is scriptable, flexible, fast, and includes an interactive graphical modeling environment. You can read more about it on its home page (https://messerlab.org/slim/).

THIS IS THE ONLY WORKSHOP I AM LIKELY TO RUN IN EUROPE UNTIL MID-2021. The dates for it have been chosen to dovetail with the Oikos conference in Reykjavík, which is March 3-5 (https://www.oikos2020.org); we hope that this will make the workshop more convenient for many to attend. Note that early registration for Oikos lasts until December 2nd, and then the price goes up, so if you wish to attend the conference as well, act quickly.

For this workshop, your application email should include: (1) your name, (2) your university or institutional affiliation, (3) a link to a research website or similar academic page, if you have one, (4) a 1-2 sentence description of your level of experience with SLiM and any other forward genetic simulation software, if any, (5) a 1-2 sentence summary of why you want to attend the workshop (i.e., the connection to your research), and (6) 1-2 sentences about any specific topics within SLiM that you hope to learn about in the workshop. Note that you will be responsible for your own lodging and your own transportation. Please do not apply to the workshop unless you are sufficiently serious that you will actually attend, if accepted.

The plan is to cover all the major topics in the SLiM manual, starting with lots of introductory material to get beginners up to speed with SLiM and its associated scripting language Eidos, and ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, and nucleotide-based models. We won't cover everything in the manual - that would be overwhelming! - but we'll try to cover all the big topics. There will also be time for attendees to work on their own models with help from me, and we may also have time to explore some optional side topics that are of particular interest to those attending each workshop. The workshop will be taught principally using SLiMgui on macOS. Every attendee will need their own Mac laptop, but a limited number of Mac laptops *might* be available on-site for those who do not have one, and running macOS inside VirtualBox on another operating system is also possible. (A Mac is required to run SLiMgui, which is necessary for teaching purposes.)

I'm hoping to continue doing workshops in future; if you would like to invite me to give a workshop at your institution, please send me an email (off-list).

Cheers,

Benjamin C. Haller Messer Lab Cornell University

Ben Haller <bhaller@mac.com>

UIdaho BiologyVectorBorneDiseases

The Center for Health in the Human Ecosystem of the University of Idaho (Moscow, ID, U.S.A.) hosts the annual Biology of Vector-borne Diseases six-day course. This course provides accessible, condensed training and "knowledge networking" for advanced graduate students, postdoctoral fellows, faculty and professionals to ensure competency in basic biology, current trends and developments, and practical knowledge for U.S. and global vector-borne diseases of plants, animals and humans. We seek to train the next generation of scientists and help working professionals to more effectively address current and emerging threats with holistic approaches and a strong network of collaborators and mentors.

The course is both lecture- and discussion-based and is delivered by internationally recognized experts, with integrated case studies of emerging vector-borne pathogens to highlight parallels and key distinctions in biology across plant, animal and human vector-borne diseases. This course sets an example of new vision, through leadership of the Center for Health in the Human Ecosystem, to create an enduring community of participants and instructors to expand the impact and sustainability of these approaches.

The course is scheduled for Sunday through Friday, June 21-26, 2020. The applications portal is open now. Applicants will be notified of their acceptance and invited to register for the course. The course registration fee (USD $1,500) includes housing, meals, course materials and social activities. Registration fee will be due following acceptance into the course.

For more information and to apply see: https://www.uidaho.edu/cals/center-for-health-in-the-human-ecosystem/education/vector-borne-diseases "Borowiec, Marek (mborowiec@uidaho.edu)" <mborowiec@uidaho.edu>

UOulu SpeciesIdentification Dec16-20

Time: December 16-20, 2019 Place: University of Oulu, Finland Extent: 3 ECTS

The workshop lectures will cover an introduction to the concept and idea of DNA barcoding, BOLD and mBRAVE barcode repositories and analyzing tools, international DNA barcoding activities (iBOL), metabarcoding methods and high-throughput sequencing platforms, analyses of ancient DNA, analyses of microbial communities, bioinformatic pipelines of genomic-scale data and use of some ecological analyses using R statistical platform.

The practicals will include lab exercises on both standard DNA barcoding and metabarcoding (for Ion Torrent), exercises on using bioinformatics tools and R statistical platform and exercises on using BOLD and mBRAVE.

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. …plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.