E v o l D i r

May 1, 2021

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

Foreword

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

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

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

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Conferences

Online AncientMetagenomics Sep1-3

We are delighted to inform you it's time to submit abstracts for *Standards, Precautions, and Advances in Ancient Metagenomics 3 (SPAAM3)*.

Like its predecessor, SPAAM3 will be held virtually on *September 1st-3rd* and will consist of the following topics:

§*Session 1*: Ancient Pathogens §*Session 2*: Ancient Microbiomes §*Session 3*: Ethics §*Session 4*: Bioinformatic tools

Please register and submit your abstracts here: https://pennstate.qualtrics.com/jfe/-preview/SV_6hZFd1jk3OEquTc?Q_CHL=-preview&Q_SurveyVersionID=current *The DEADLINE FOR ABSTRACT SUBMISSION is the 21st of MAY, 17:00 EDT.*

Please share this email with other labs and colleagues that may be interested in the event.

If you have any questions or comments, don't hesitate to reach out to any member of the organisation committee (contact info on the SPAAM website: https://spaam-community.github.io/#/?id=-standards-precautions-and-advances-in-metagenomics).

Looking forward to seeing you at SPAAM3, SPAAM3 Organisation Committee Aida Andrades Valtueña Elizabeth A. Nelson Kelly E. Blevins Miriam Bravo López Sterling L. Wright

– Kelly Elaine Blevins < https://shesc.asu.edu/-people/kelly-blevins >, M.Sc.   *She, her, hers < https://www.glsen.org/sites/default/files/-GLSEN%20Pronouns%20Resource.pdf >*   Ph.D. Candidate | Research Fellow School of Human Evolution and Social Change Arizona State University m. 404-247-5601

Kelly Elaine Blevins <blevinske1@gmail.com>

tion (CCDH) Dept. of Environmental and Molecular Toxicology Oregon State University

Monica Munoz-Torres <monimunozto@gmail.com>

Online Bioinformatics Jul29-30

Join us at BOSC 2021, part of ISMB/ECCB Online!

The 2021 Bioinformatics Open Source Conference (BOSC; https://www.open-bio.org/events/bosc-2021) is a forum for developers and users to interact and share research results and ideas in open source bioinformatics and open science. Topics include software development practices that promote open science standards and sharing of biological data and code, as well as approaches for building diverse communities. BOSC is a track of the conference on Intelligent Systems in Molecular Biology / European Conference on Computational Biology 2021 (ISMB/ECCB; https://-www.iscb.org/ismbeccb2021), and it will be held online on July 29-30. The main Abstract Deadline is May 6th; see our announcement on the BOSC website for a full list of deadlines and other details at https://www.open-bio.org/2021/03/24/join-us-at-bosc-2021 Requesting registration fee assistance: We realize that the cost of ISMB/ECCB may be prohibitive for some. If you are submitting an abstract to BOSC and would have difficulty covering the cost of registration, you can request registration fee assistance during abstract submission.

Increasing diversity in participation: Please share this announcement with people and groups who might be interested. We are particularly interested in reaching out to diverse communities who may not yet be aware of BOSC!

Key Dates - May 6, 2021: Deadline for submitting one-page talk/poster abstracts at https://www.open-bio.org/events/bosc/submit/ - May 27: Talk/poster acceptance notifications - June 3: Late poster (and Late-Breaking Lightning Talk) submission deadline - June 10: Late poster / Late Breaking Lightning Talks (LBLT) acceptance notifications - July 29-30: BOSC 2021 Online (part of ISMB/ECCB 2021 Online; https://-www.open- bio.org/events/bosc/) - July 31-Aug 1: CollaborationFest (CoFest) (https://www.open-bio.org/-events/bosc- 2021/collaborationfest/)

Sincerely, The BOSC 2021 Organizing Committee: Nomi Harris (chair), Karsten Hokamp (co-chair), Peter Cock, Chris Fields, Jessica Maia, Monica Munoz-Torres, Malvika Sharan, Jason Williams

– Monica Munoz-Torres, PhD Assistant Professor Director of Operations, Center for Cancer Data Harmoniza-

Online Botany UndergradMentoringGrants Jul19-23

PLANTS—Undergraduate—travel/mentoring—grants:—Enhancing—diversity—at BOTANY 2021 virtual meetings, July 19-23, 2021.

Deadline—for—grant—applications:——April   15, 2021.—Apply—soon!

PLANTS (Preparing Leaders and Nurturing Tomorrow's Scientists: Increasing the diversity of plant scientists) is a travel/mentoring grant to allow diverse and talented undergraduates to attend the BOTANY 2021 virtual meeting July 19-23, 2021. Now in its eleventh year, the program will support up to 12 undergraduates to attend the meeting, receive individual mentoring throughout the meeting (and beyond) from graduate students, postdocs, and/or faculty and professionals, and participate in networking events including diversity events and career-oriented activities.

Topics at the conference range across all levels of botany and include presentations on conservation, biodiversity and ecology, plant genomics, evolution, plant systematics, and botanical education. Several social functions are specifically for students with networking opportunities and engaging informative activities. The meetings are a great way to understand the breadth of botanical research and education, explore job opportunities, meet undergraduate and graduate students with similar interests and network with professionals in your area of interest.

For an overview of the scientific conference see http://2021.botanyconference.org/ —— For PLANTS: https://botany.org/home/awards/travel-awards-for-students/plants-grants.html DEADLINE:—April 15, 2021.—Apply—soon!

APPLICATIONS: The application includes completion of the online form providing your statement of interest, a letter of recommendation, and unofficial transcripts. Applications are welcome from all domestic undergraduates from the US and Puerto Rico (we are unable to accept applications from international students) who are interested in plant science; the ad-

missions goal is to create a diverse pool of students attending the conference. You do not need to be a current BSA member to apply. The application form is online at— https://botany.org/home/awards/travel-awards-for-students/plants-grants.html We encourage you to review the online instructions and application form thoroughly before filling it out. Please send letters of reference and unofficial transcripts directly to bsa-manager@botany.org

CONTACTS:—For—further—inquiries,—please—contact—one—of—the—organizers: Ann—Sakai —aksakai@uci.edu Anna Monfils —anna.monfils@cmich.edu— Heather Cacanindin —hcacanindin@botany.org

aksakai <aksakai@uci.edu>

Online BraithwaiteMemorial Apr28

Dear colleagues,

I would like to welcome you to a virtual memorial symposium for Victoria Braithwaite on Wednesday April 28: https://spark.adobe.com/page/5eNmtjPObmuWJ/ This memorial symposium will feature a series of 8 talks from people in the fields of animal cognition (including the evolution of) and animal welfare. They are spread across three continents and five countries which I think demonstrates the breadth of Victoria's influence on the field. Most of the speakers worked directly with Victoria in some capacity and all were heavily influenced by her careful and elegant research that was cut short all too soon.

In addition to these talks, there will be time for people to share their memories, reflections, and thoughts if they wish.

Please feel free to share widely the website in any way you wish. You will find that to actually attend, you need to click on the "Registration Link" button which will have you register in Zoom, at which point you will get emailed a personal Zoom link and the password.

Thank you,

Jason Keagy Assistant Research Professor of Wildlife Behavioral Ecology Department of Ecosystem Science and Management Penn State University email: keagy@psu.edu <jxk6051@psu.edu> web: https://www.personal.psu.edu/jxk6051/ Jason Keagy <keagy@psu.edu>

Online CICENE Apr14

Dear EvolDir members,

We are pleased to announce the coming talk at the online CIGENE seminar by Kara Layton (University of Aberdeen) on 14th April 2021 at 12:00-12:50 (Oslo time). She will talk about: "Using genomics to untangle marine mimicry systems".

Abstract: Mimicry has evolved multiple times across the tree of life, it is maintained by both evolutionary and ecological mechanisms and it contributes to speciation through the generation of adaptive phenotypic diversity. While these processes have been extensively studied in terrestrial taxa, less is known about mimicry in marine systems. Here, I present a novel mimicry system in a group of aposematic and toxic nudibranchs (sea slugs) where multiple polychromatic species have recently been discovered. I use exon capture data to provide evidence for multiple scenarios of mimicry evolution in this group and discuss how future work will look to identify the genomic basis of mimicry.

For more information on CIGENE seminars, please visit: https://cigene.no/cigene-seminar-series/ Anybody interested except for Zoombomber is welcome. Recording is planned; if successful, the video will be available upon request.

Best wishes,

Marie SAITOU, Ph.D. 'V will be hiring a PhD student soon Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences https://sites.google.com/view/saitou-lab Marie Saitou <marie.saitou@nmbu.no>

Online CICENE May5

Dear EvolDir members,

We are pleased to announce the coming talk at the online CIGENE seminar.

Date: 5th May 2021 Presenter: Daniel Machado Title: Genome-scale models of microbial communities and

their application to biotechnology

Abstract: From controlling our gut-brain axis to regulating the planetary geochemical cycles, the role of microbes in our lives seems endless. Microbes are everywhere, and they are usually not alone, but rather operating as part of complex microbial ecosystems. It thus becomes fundamental to understand how microbes interact with each other and with their environment. Next-generation sequencing technologies are shedding a light on the vast taxonomic and functional diversity of microbial communities. In this talk, I will discuss how we are using these data to build genome-scale models of single species and communities, and how we use such models to simulate the metabolic phenotype of microbial communities and their response to different kinds of perturbations. These are some of our preliminary steps towards the design and control of synthetic communities for application in industrial biotechnology.

For more information on CIGENE seminars, please visit: https://cigene.no/cigene-seminar-series/ Anybody interested except for Zoombomber is welcome. Recording is planned; if successful, the video will be available upon request.

We are hiring!!! https://cigene.no/vacancies/ Marie SAITOU, Ph.D. Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences https://sites.google.com/view/saitou-lab Marie Saitou <marie.saitou@nmbu.no>

Online CIGENE Apr21

Dear EvolDir members,

We are pleased to announce the coming talk at the online CIGENE seminar.

Date: 21st April 2021, 12:00-12:50 (Oslo time).

Presenter: Fernando Racimo

Title: Dynamic and descriptive models for spatiotemporal population genomics

Abstract: Ancient genome sequencing provides the opportunity to study population genomic processes as they unfolded in time and space. We can now directly observe how and when alleles moved across a landscape over succeeding generations with unprecedented detail. Here, I will describe several methods developed in our group to relate these spatiotemporal observations to

informative parameters about migration, admixture and species ranges. First, I will present new way to model the spread of ancestry in ancient genomes through time and space. We have recently applied this method to a dataset containing thousands of ancient human genomes and inferred the geographic spread of major population movements in the past 13 millennia of Western Eurasian history. Our group has also developed a new dynamic framework for inferring the diffusion of a positively selected allele in a landscape, and a new wrapper to a forwards simulation framework, which makes it easy for users to readily gene rate spatiotemporal genetic processes programmatically. Finally, I will present a model to jointly infer changes in species distributions, using a combination of fossil records, sedimentary DNA data and paleo-climate records. We have applied this model to an arctic Pleistocene mega-fauna dataset and demonstrate that incorporating different types of data allows us to evince patterns that would not be visible if these were studied in isolation.

For more information on CIGENE seminars, please visit: https://cigene.no/cigene-seminar-series/ Anybody interested except for Zoombomber is welcome. Recording is planned; if successful, the video will be available upon request.

Best wishes,

Marie SAITOU, Ph.D. - will be hiring a PhD student soon Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences https://sites.google.com/view/saitou-lab "marie.saitou@nmbu.no" <marie.saitou@nmbu.no>

Online ESEB EvolOfSenescence Jul6-7

Abstract submissions are invited for 10 min talks and posters at the online ESEB 2021 satellite symposium: How have biomarkers improved our understanding of the evolution of senescence?

6-7 July 2021: talks, 12:30-16:30 CEST; posters, evening of 6th July

As individuals reach older ages their bodies deteriorate - a process known as senescence. Individuals within the same species can differ greatly in the age they start to senesce, and the rate at which they senesce. However, why individuals senesce so differently remains unresolved

and is one of the biggest unanswered questions in evolutionary biology. Understanding the drivers of senescence has important ramifications for veterinary medicine, conservation, health and society, as it could help individuals to live longer, healthier lives. This symposium will seek to address this knowledge gap by bringing together researchers with expertise in senescence from theoretical, laboratory and field settings. In particular it will focus on how our understanding of health and the evolution of senescence has been altered with the development of indicators and biomarkers of senescence such as epigenetic clocks and telomeres. These biomarkers have shed light on the relative impact of social, environmental, genetic and trans-generational effects on senescence. A synthesis of advances in the evolutionary theory of senescence, the occurrence and life-history consequences of senescence, and the underlying genetic and non-genetic mechanisms driving variation in individual senescence will significantly further the field. This knowledge is vital to understanding why senescence has evolved and how variance is maintained.

Invited speakers: Emma Teeling, University College Dublin Katharina Gapp, ETH Zurich Jenny Tung, Duke University

Organisers: Hannah Dugdale, University of Groningen Julia Schroeder, Imperial College London Alex Sparks, University of Leeds

Abstract submission: through the ESEB website https://www.eseb2021.cz/en/satellite-symposia-2021, which will open on 20 April 2021

Registration: free of charge, through the ESEB website https://www.eseb2021.cz/en/satellite-symposia-2021 Abstract and registration deadline: 15th May 2021

h.l.dugdale@rug.nl

Online ESEB SexAsexuality Jun16-17

Dear all!

Please do check out our ESEB satellite meeting Genomic signatures and consequences of sex and asexuality here https://worm-lab.eu/sex-asex-genomics-satellite. We are very much looking forward to receiving your abstracts and seeing you in June.

Philipp and Astrid

Online EvolutionEcol Apr28

Dear EvolDir,

Join us for the next talk in our popular, weekly, online seminar series in Evolution and Ecology.

—

Wed 28 April

Prof. Pat Monaghan

Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow, UK

"Stress exposure and longevity; organismal and cellular level effects at different life history stages"

—

When: 5PM BST/ 9AM PDT

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

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

How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg Please follow our Twitter feed and join the Slack group for details of future upcoming talks.

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

Many thanks,

Dr. Elizabeth Duxbury Dr. Iulia Darolti Dr. Wouter van der Bijl Dr. Emily Fowler

—- Dr. Elizabeth Duxbury

Senior Postdoctoral Research Associate

Prof. Alexei Maklakov Group

School of Biological Sciences

University of East Anglia

Norwich Research Park

UK

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

Online EvolutionEcology Apr14

Dear EvolDir,

Join us for next week's talk in our popular, weekly, online seminar series in Evolution and Ecology.

—

Wed 14 April

Prof. Tracey Chapman

School of Biological Sciences, University of East Anglia, UK

"Sexual selection, sexual conflict and evolutionary change"

—

When: 5PM BST/ 9AM PST

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

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

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

Many thanks,

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

—- Dr. Elizabeth Duxbury

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

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

Online EvolutionEcology Apr21

Dear EvolDir,

Join us for next week's talk in our popular, weekly, online seminar series in Evolution and Ecology.

—

Wed 21 April

Prof. Anjali Goswami

Natural History Museum and Dept. of Genetics, Evolution & Environment, University College London, UK

"From development to deep time: Reconstructing the evolution of diversity with a phenomic approach"

—

When: 5PM BST/ 9AM PST

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

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

How to join: our Slack Evolution and Ecology Seminars here https://join.slack.com/t/evolutionecol-xl54980/-shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg Please follow our Twitter feed and join the Slack group for details of future upcoming talks.

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—- Dr. Elizabeth Duxbury

Senior Postdoctoral Research Associate

Prof. Alexei Maklakov Group

School of Biological Sciences

University of East Anglia

Norwich Research Park

UK

"Elizabeth Duxbury (BIO - Staff)"

<E.Duxbury@uea.ac.uk>

Online FishComparativeTranscriptomics Apr13

The National Center for Genome Analysis Support (NC-GAS, ncgas.org) helps researchers nationwide with the demanding'Xand often confusing'X computations that genomics research requires. In this monthly webinar series, scientists supported by NCGAS present their genomics research in pursuit of answers to some of the most confounding biological questions. They discuss their work as well as the nationally available tools they used to get it done.

This month's speaker: April 13, 2021: Comparative transcriptomics of spotted seatrout (Cynoscion nebulosus) populations to cold and heat stress. Presented by Jingwei Song, Research Scientist, University of Florida.

Full abstract, information, and registration here: https://itnews.iu.edu/events/20210413-ncgas-webinar.php Sheri Sanders, Ph.D. [she/her] Manager, Bioinformatic Analyst National Center for Genome Analysis Support (NCGAS)

NCGAS is a management unit of the Research Technologies division of UITS; NCGAS is affiliated with the Indiana University Pervasive Technology Institute.

"Sanders, Sheri" <ss93@iu.edu>

Online GenomeEvolution May19-21

Dear EvolDir,

Join us for the virtual symposium on "Models of Genome Evolution from Populations to Species" hosted by the Swedish Collegium for Advanced Study during the 19th - 21st of May 2021, http://www.swedishcollegium.se/-Symposium5/Symp_Home.html 19 - 21 May, 2021

Studies of genome evolution are generally based on two approaches, phylogenetic methodology that relies on inter-species variation, and population genetics methodology that relies on intra-species variation. The two approaches, thus, focus on two different time-scales, and

different models and methods have emerged in both disciplines. Different model assumptions have led to a separation of the two disciplines, and informa- tion content extracted by each of the two approaches is rarely combined. However, motivated by the recent increase in genome sequence data, efforts in method development have been made to counteract the distinc- tion between phylogenetic and population genetics methodology.

The idea of this symposium is to discuss and compare different approaches that cross the bridge between inter- and intra-specific studies. The discussions shall improve our understanding of the information content provided in genome sequence data across time-scales and stimulate further method development to efficiently use the increasing amount of data available.

Organizing committee: Laurent Guéguen, Laboratoire de Biométrie & Biologie Ãvolutive, Université Lyon 1 (Convener) Carolin Kosiol, Centre for Biological Diversity, School of Biology, University of St Andrews Carina Farah Mugal, Department of Ecology and Genetics, Uppsala University

The symposium consists of 15 contributed talks and is open for everyone that wishes to attend. Pre-registration is required. A schedule for the symposium together with information about registrations can be found at, http://www.swedishcollegium.se/-Symposium5/Symp_Home.html Everybody welcome!

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

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

Online GreatLakesEvolutionaryGenomics Aug2-6

The 2021 Great Lakes Annual Meeting in Evolutionary Genomics will be held online the week of Aug 2.

GLAM-evogen is an annual symposium that brings together faculty and trainees in the Great Lakes region from a range of backgrounds who work at the interface of genomics and evolutionary biology. The meeting is trainee-oriented and a great venue to meet others, present your work, and hear about undergraduate, graduate, and postdoctoral research projects. Our keynote speaker will be Dr. Yasir Ahmed-Braimah from Syracuse University.

We are planning for live talks via zoom on -Mon 2 Aug 10 am 'V 2 pm ET -Wed 4 Aug 10 am 'V 2 pm ET -Fri 6 Aug 2 'V 5 pm ET, followed by a zoom happy hour

Posters and discussion will be hosted the entire week on Slack.

Registration for the meeting is now open here: https://forms.gle/xSRysDsTUTPogfn78. The abstract submission deadline is July 2. Registration will remain open, but all participants must register to get zoom and slack information. More information is online at: http://blogs.rochester.edu/EEB/?page_id=30552 . If you would like to stay updated and receive information about the meeting, you can join the GLAM-evogen group here: https://groups.google.com/forum/-#!forum/glamevogen – *Nancy Chen, Ph.D.* Assistant Professor Department of Biology University of Rochester popgenchenlab.github.io/

Pronouns: she/her/hers

Nancy Chen <nancy.chen@rochester.edu>

Online InsectPlantRelationships Jul19-23

The 17th Symposium on Insect Plant relationships (SIP2021) is open for registration. The symposium will be held online from Sunday 25 July 2021 till Friday 30 July 2021. See https://www.universiteitleiden.nl/-sip2021 In this event you can: - enjoy lectures by 11 keynotes introducing the different topics on insect-plant relationships (see the list below) - give an oral presentation (limited number of places) - give a poster presentation of 3 minutes. - organize small discussion groups for your favorite topic in insect-plant relationships - arrange meetings with people you would like to meet - meet companies looking for jobs - meet with funding organizations

Deadline for submissions : 31 May 2021 Deadline for registration: 20 June 2021

Contact: SIP17@Biology.Leidenuniv.nl

Program: 1. Plenary lecture André Kessler (Cornell University, USA) 2. The ecology of plant-insect interactions Nicole van Dam (iDiv Halle-Jena-Leipzig, Germany) 3. Genomics of plant-insect interactions Heiko Vogel (Max Planck Institute for Chemical Ecology Germany) 4. Metabolomics of Plant-Insect interactions Caroline Müller (University of Bielefeld, Germany) 5. Multitrophic Interactions Consuelo De Moraes (Swiss Federal Institute of Technology (ETH), Switzerland 6. Insects and weeds Ruth Hufbauer (Colorado State University, United States) 7. Phylogenetic, evolution and novel interactions Niklasz Jans (Stockholm University, Sweden) 8. Plant- insect pollinator interactions Geraldine Wright (University of Oxford, UK) 9. Community ecology and plant insect interactions John Vandermeer (University of Michigan, United States) 10. Innovations and new topics in insect plant interactions Matthias Erb (University of Bern, Switserland) 11) Closing lecture Marcel Dicke (Wageningen University, The Netherlands)

"Vrieling, K." <k.vrieling@biology.leidenuniv.nl>

Online NLSEB Apr19-20 Reminder

The Third Conference of the Netherlands Society for Evolutionary Biology (NLSEB) is approaching! It will be held online in the afternoons of 19 and 20 April 2021 (see www.nlseb.nl).

We have three exciting keynote speakers (Thijs Ettema, Toby Kiers, Mark van Vugt), there will be parallel sessions with contributed presentations and there are poster sessions. The program is online now at http://nlseb.nl/-nlseb2021-nlseb-phd-postdoc-meeting/ . Registration for the meeting is free and there is still opportunity to submit an abstract for a poster presentation.

Please register and submit your abstract now, by going to https://www.formdesk.com/nlseb/NLSEB2021, The deadline for registration is 12 April 2021.

In the mornings of 19 and 20 April, there will be the first NLSEB PhD/Post-doc meeting (online) with many interesting workshops. See: http://-nlseb.nl/nlseb2021-phd-postdoc-meeting/ "Bemer, Marian" <marian.bemer@wur.nl>

Online SMBEv2021 CallForAbstracts DeadlineMay3

Dear Colleagues,

SMBEv2021

A Virtual Meeting to Beat All Virtual Meetings 4-8 July (3-7 July in the United States)

We invite you to submit an abstract for the 2021 annual conference of the Society for Molecular Biology and Evolution (SMBEv2021) at http://smbe2021.org/ < http://smbe2020.org/abstracts/abstract-submission/ >

SMBE 2021 is taking place online 4-8 July (3-7 July in the United States)

*** The deadline for abstract submission is Monday 3 May 2021, 23:59 (GMT). ***

* Note: Due to constraints imposed on SMBE because of the virtual format, we will require all accepted speakers (oral and poster) to submit their video files and posters to their symposium organisers before 28th May at the latest to be included in the conference.

SMBE 2021 will run across three geographical hubs. We hope in this way to make the conference as accessible as possible across our global community. All presentations will be pre-recorded and discussion rooms will be available for all participants to interact live online with speakers. There will also be designated poster space and live interactive poster sessions.

Registration for the conference is free for members of the society. There are also several conference associated awards available for members V applications can be made during abstract submission. SMBE membership is for 3 years and costs $10 for students and $30 for others. Membership can be applied for at https:/-/www.smbe.org/smbe/MEMBERSHIP.aspx . *Please contact us via email (contact details below) if you would like to become a member but feel that this membership fee is prohibitive for you.*

Awards include:

1) The SMBE Graduate Student Excellence Award honors the best presentation at the Graduate Student Excellence symposium, which provides a forum for young investigators to showcase their exemplary research at the annual meeting. Eligibility: Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society (minus any career disruption or delay). A candidate for the award must become a member of the Society at least a month before the first day of the annual meeting. Approximately eight winners will be selected every year to cover the broad spectrum of research covered by SMBE.

*** The deadline for applications for this award is 30 April 2021. You must also email your CV to *smbe@allenpress.com*.

2) The Undergraduate Mentorship Award provides support, advice and networking opportunities for undergraduate students (including Masters students under a 3+2 system) as they navigate their first international conference. Applicants for this award must be presenting their own work as a poster or talk at the conference. Applicants must email 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 (e.g. 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 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.

*** The deadline for applications for this award is 26 April 2021.

3) Carer awards can be applied for during registration, or by email to smbe.contact@gmail.com if an earlier response is needed. Open to members with expenses for the care of children or dependent adults (including adult children with a disability or elderly relatives) during their attendance at the annual SMBE meeting.

4) Internet Access Assistance Award for those who need financial assistance with internet access to attend the conference (relevant mainly for countries or areas with insufficient WiFi cover).

If interested in sponsorship of the meeting, for any queries over abstracts or registration, please direct all questions regarding SMBE 2021 to *smbe@allenpress.com* (please cc *smbe.contact@gmail.com*).

We look forward to welcoming you in soon on gather.town.

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

We look forward to welcoming you in soon on gather.town.

smbe2021.org

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

Online SMBEv2021 Jul3-8 RegistrationIsOpen

*** SMBEv2021 Registration is Open! ***

SMBEv2021 A Virtual Meeting to Beat All Virtual Meetings 4-8 July (3-7 July in the United States)

Dear Colleague,

SMBE Council would like to welcome you to SM-BEv2021! This year' Âs conference will be fully online and run across three geographical hubs. We hope in this way to make the conference as accessible as possible across our global community. All presentations will be pre-recorded and discussion rooms will be available for all participants to interact live online with speakers. There will also be designated poster space and live interactive poster sessions.

Registration is FREE for all active SMBE members. *** You must be an active member of SMBE to be able to register ***. SMBE membership is for 3 years and costs $10 for students and $30 for others. If you wish to become a member or need to update your membership details, please go to https://www.smbe.org/-smbe/MEMBERSHIP.aspx. Please contact us via email (smbe.contact@gmail.com) if you would like to become a member but feel that the membership fee is prohibitive for you.

*** Registration is now open at http://smbe2021.org/ *** Registration closed on 25 June 2021, 23:59 (GMT).

Registration is very quick and simple with your member login details. You will *not* receive a confirmation email (we recommend that you print out the last page of the process with your registration details). *** All registrants will be sent access instructions on June 28, 2021 ***. If you have a question about the registration process please contact smbe@allenpress.com.

Member log-in: by default, a person' Âs Username is the email address we have on file in the membership database (unless you asked to have it changed). We cannot send passwords via email but our system does have a password reset option in case you forgot your password. If you cannot log in to your member space please contact smbe@allenpress.com.

Several conference-associated awards are available for members 'V applications can be made during abstract submission.

Online TempleU Epistasis Apr7

Epistasis - April 7th, 2021 (Wednesday) A Convergence of Epistasis and the Neutral Theory

Virtual Symposium (9 am to 4:30 pm) https://-igem.temple.edu/epi/ You are welcome to attend a virtual symposium on Epistasis. It will be on ZOOM in a few days (April 7th, Wednesday).

Registration is free (https://igem.temple.edu/epi/-registration)

We can also accommodate a few more Lightning Talks (5 minutes). Submit your talk title at the time of registration (deadline is April 2nd). A selection decision will be sent this weekend.

We look forward to seeing you

Sudhir Kumar s.kumar@temple.edu

PorquerollesIsland France MCEB Jun13-17 Reminder

———— ————— ———— REMINDER – DEADLINE FOR SUBMISSION: 9th of April

Dear all,

The 2021 edition of the MCEB conference will take place on June 13-17 in Porquerolles, France:

https://mceb2021.sciencesconf.org/ We are aiming at having a "regular" conference, with all participants spending a week on the island. Yet, current restrictions limit the number of attendees to 60. Other restrictions (e.g., wearing masks, keeping physical distances between two persons to at least one meter, etc.) will likely apply too.

*Submissions of posters and/or talks will open the 24th of March and close the ** **9th of April*. Notifica-

tion of acceptance or rejection will be sent by the 26th of April. Registration to the conference will open the following day (the 27th of April). Registration fees (about 500 euros, refundable in case of cancellation of the event) will cover accommodation plus breakfast, diner and supper.

The main focus of this year's edition will be on "Climate Changes and their Impacts on Evolution", in particular the preservation of biodiversity, the conservation of species, the study of ecosystems and their dynamics, and the reconstruction of major past changes of climate and living conditions on Earth.

We will also welcome contributions dealing with mathematical and computational techniques that improved our understanding of the COVID-19 pandemic. The design and application of integrative approaches that incorporate genetic data along with other sources of information (e.g., geography) in order to decipher the processes governing the evolution of SARS-CoV-2, will be of particular interest.

The list of invited speakers for this year's edition is given below:

- Bastien Boussau (Laboratoire de Biométrie et Biologie Evolutive,CNRS, Lyon, FR) - Lounes Chikhi (Instituto Gulbenkian, Lisboa and CNRS, Toulouse, FR) - Christophe Dessimoz (University of Lausanne, CH) - Simon Gravel (Mc Gill University, Montreal, CA) - Emma Hodcroft (ISPM, University of Bern in Switzerland) - Michel Milinkovitch (Université de Genève, CH) - Tandy Warnow (University of Illinois , USA)

Best regards,

The MCEB Organizing Committee

Stephane Guindon <stephane.guindon@lirmm.fr>

Snowbird Utah ConservationGenomics Oct10-13

Save the date for AGA2021: October 10-13, 2021

The American Genetic Association Council is thrilled to announce that we will be holding President Kelly Zamudio's symposium this October, in Snowbird, Utah —

Conservation Genomics: Current Applications and Future Directions

The meeting will include sessions on o Climate change,

adaptation, and genomics o Genetic monitoring and genomic rescue o Genomics of disease and conservation of wildlife o Conservation genomics in action

The AGA holds the friendliest symposia - small meetings in lovely settings, providing great opportunities to interact with the best in the field.

Student and postdoc members will receive free registration if they submit a poster abstract, and have the chance to be selected for oral presentations and travel awards.

Watch for further announcements on EvolDir, the AGA website < https://www.theaga.org/index.php >, and Twitter < https://twitter.com/theAGA_org >, coming soon!

Anjanette Baker <theaga@theaga.org>

Switzerland ForestGenomicsAdaptation Sep21

First EVOLTREE Conference 2021: Genomics and Adaptation in Forest Ecosystems

The first EVOLTREE Conference, hosted by WSL Birmensdorf (Switzerland) from 14-17 September, 2021, focuses on the genomics and adaptation of trees and interacting species from evolutionary, demographic, and ecological perspectives.

We welcome contributions that apply innovative approaches and consider the relevance of their research in the context of biodiversity conservation through natural dynamics or silvicultural interference.

Registration and abstract submission is now open! https://conf.wsl.ch/evoltree/ For more details, visit our conference website: http://www.evoltree.eu/index.php/-10-news/news-middle/180-evoltree-conference Due to the COVID-19 pandemic, for now you can register only for the online conference. In early June 2021, we will decide if and how many attendees can participate on-site (although this will be subject to government travel restrictions that may change at short notice). You will then be able to acquire an additional on-site package.

EVOLTREE is a European network of research institutions and universities engaged in studying the evolution and functioning of forest ecosystems, in particular trees as the foundation species in forest stands. A prime topic in the face of ongoing climate change is to elucidate how trees, together with their associated organisms such

as mycorrhizal fungi, respond to rapid environmental changes.

The organizing committee:

Felix Gugerli, WSL Christian Rellstab, WSL Susanne

Senn-Raschle, WSL

evoltree@wsl.ch

christian.rellstab@wsl.ch

GradStudentPositions

AuburnU EvolutionMalaria

I am looking to fill a newly funded PhD assistantship in the School of Forestry and Wildlife Sciences at Auburn University, beginning as early as Fall 2021. Research in the lab is broadly focused on conservation genetics/genomics of wildlife, and typically relies on whole genome sequencing data and bioinformatic tools. Current research the lab includes investigation of the evo-

lution of fitness in kangaroo rats, understanding the complexities of population recovery from recent crashes in Steller sea lions, and developing methods for efficiently tracking large populations in terms of census size and movement patterns in caribou. (Please see the lab webpage for additional information about ongoing work < http://wp.auburn.edu/willoughbylab/ >.) PhD students are given a lot of flexibility in designing their research questions. The applicant hired to fill this position will focus on the evolution of malaria-transmitting mosquitos in a collaborative project between the Willoughby lab and Dr. Sarah Zohdy. In

some African mosquito populations, treating with pesticides inside family homes has resulted in behavior shifts where mosquitos now congregate and bite outside the home. However, we don't know how this behavioral change has manifested in the genome or how these changes may ultimately alter our ability to control these populations. Critically, these mosquitos carry malaria, so control is important! Possible topics include for the PhD projects in this general research space include: quantifying genomic adaptation to common mosquito control measures, modeling of mosquito populations responses to human activities, genetic determination of how mosquitos move via water collection, and many more that could be developed collaboratively. Auburn University is an R1 institution located in a mid-sized city in the foothills of the Appalachian Mountains. Local attractions include farmers markets, Auburn City Fest, and the newly constructed Gouge Performing Arts Center. The nearby Kreher Forest Ecology Preserve and Tuskegee National Forest offer additional recreational opportunities year-round. Successful applicants for this assistantship will be prepared to take on a new research project that combines molecular lab work with bioinformatics and modeling and perhaps a small amount of field work. For interested students, outreach and science communication opportunities can be made available, in support of the land-grant mission of Auburn University. Graduate students in the School of Forestry and Wildlife Sciences are provided with a competitive stipend and tuition remission.

Diversity and inclusion are a high priority of this lab group; all interested applicants are encouraged to get in touch with me directly prior to applying to the graduate program. To do so, please send me an email (janna.willoughby@gmail.com) with your background and interests and a copy of your CV. Although familiarity with bioinformatics and molecular techniques is desirable for this position, previous experience in this area is not required. Please do not self-select yourself out of applying as there are many ways to acquire skills that will set you up for a successful graduate experience.

jrw0107@auburn.edu

CzechRepublic CommunityEvolution

PhD in eco-evolutionary dynamics of communities

We invite prospective candidates for a four-year fully funded PhD Studentship to explore exciting questions on the interface of population genetics and community ecology. How is genetic variation maintained within populations? And how do species coexist in diverse communities? These processes are typically studied separately, but likely interact to structure diversity in ecological communities. Our collaborative project utilizes a novel experimental community model system of wild Drosophila species and their parasitoids from tropical Australia. Specifically, the candidate could develop individual based eco-evolutionary dynamics models of our study system investigating the interactive effect of genetic variation and species diversity, conduct experimental evolution with the study system, investigate cellular immunity of Drosophila species in the community, or take part in field surveys.

The successful applicant will join the Laboratory of Experimental Ecology [http://lab.hrcek.net] at the Biology Centre, Czech Academy of Sciences, Ceske Budejovice, Czech Republic, under the supervision of Dr Jan Hrcek. The laboratory is a multinational team of postdocs, PhD students and technicians and the applicant will have the opportunity to work extensively with other team members. The laboratory obtained prestigious high-level funding for five years from 2020 to 2025 (ERC-CZ grant) and therefore can provide substantial resources and support for exceptional research. The laboratory is part of the Department of Ecology, a dynamic international centre for research on interaction networks.

Together with the PhD student we will choose a co-supervisor from current collaborators (listed at the bottom of [http://lab.hrcek.net/people.html] page) or start new collaborations. The position includes a research stay abroad and possibility of fieldwork in Australia.

The deadline for applications is 6th May 2021, with interviews on 10th or 11th May. The position can start from September 2021 onwards. Interested candidates who could only start in spring 2022 are also encouraged to get in touch. The student will receive a salary which comfortably covers living expenses in the Czech Republic. The working language is English and applicants from all countries are eligible. A MSc degree is required to enter PhD in Czech Republic. We are looking for candidates with:

-——— Experience in eco-evolutionary dynamics or population genetic modelling -——— Experience with population genetics -——— Research experience with laboratory experiments, insect ecology or molecular ecology -——— Driving licence and fieldwork experience

To apply please send one document comprising a CV,

contact details for two references, and a motivation letter to Jan Hrcek [janhrcek@gmail.com].

Jan Hrcek <janhrcek@gmail.com>

DanishTechU
BioinformaticsAncientDNA

DTU Health Tech is looking for 2 qualified candidates for 2 vacant PhD positions in bioinformatics. In these positions, you will develop algorithms and computational methods to deal with the analysis of large datasets from modern and ancient sources. More specifically, these algorithms will be aimed at analyzing sedimentary DNA and microbial DNA. The bioinformatics section of DTU Health Tech performs research in the areas of different metagenomics, machine learning, cancer genomics and population genomics.

Current bioinformatics algorithms and software are often ill-equipped to deal with DNA extracted from ancient soil samples. This ancient DNA shows high levels of fragmentation and accumulated chemical damage. Furthermore, ancient sediments often contain DNA from multiple species and often multiple individuals. Fortunately, several problems pertaining to ancient DNA can be described in a maximum-likelihood framework and computer science techniques can help us to solve such numerical problems efficiently via numerical algorithms and data structures. You will work in collaboration with other partners including the University of Copenhagen and McMaster University in order to develop the next generation of algorithms and software applied to DNA extract from fossils, ancient soils and sediments.

Given the COVID19 pandemic, we will happily accommodate requests for remote work until in-person work is deemed safe.

Applicable for all scholarships

Qualifications You must have a two-year masters degree (120 ECTS points) or a similar degree with an academic level equivalent to a two-year masters degree. Ideally, your degree should be in computer science, mathematics or biological science with a focus on quantitative and mathematical aspects.

More specifically you should ideally have the following qualifications:

* Knowledge of a programming language like Python, Perl, C++ and/or Java (C/C++ is preferred) * Abil-

ity to work in a UNIX environment, ideally in a high-performance computing environment * Thorough understanding of basic algorithms and data structures used in computer science * Knowledge of probabilities and statistics * Firm grasp of first-year university mathematics (differential calculus/linear algebra) * Experience in bioinformatics and knowledge of metagenomics are a plus * Expertise in next-generation sequencing data generation and processing are also a plus

We offer DTU is a leading technical university globally recognized for the excellence of its research, education, innovation and scientific advice. We offer a rewarding and challenging job in an international environment. We strive for academic excellence in an environment characterized by collegial respect and academic freedom tempered by responsibility.

Salary and appointment terms The appointment will be based on the collective agreement with the Danish Confederation of Professional Associations. The allowance will be agreed upon with the relevant union. The period of employment is 3 years.

Potential start date around September 1st 2021 (or according to mutual agreement).

Application Your complete online application must be submitted no later than 10 June 2021 (Danish time).

Apply at https://www.dtu.dk/english/about/job-and-career/vacant-positions/job?id=3D8741fe36-7c69-4955-9e0b-bf5574dc3af6   Gabriel Renaud <gabriel.reno@gmail.com>

GeorgeMasonU
FishConservationGenetics

PhD Position in salmonid epigenetics and adaptation to captivity at George Mason University

A PhD position is available to start in Fall 2021at George Mason University in Fairfax, Virginia. We are seeking a highly motivated prospective graduate student to investigate adaptation to captivity conditions in salmonids. This project combines a wide array of skills, including field work, bioinformatics, genomics, and transcriptomics.

The selected student will work in the lab ofDr. Ylenia Chiari (Dept. of Biology;www.yleniachiari.it). The Chiari Lab uses integrative approaches from molecular biology to behavior to computational modeling to

study vertebrate ecology and evolution. This project is in collaboration with Dr. Gordon Luikart (Flathead Lake Biological Station, University at Montana) and Dr. Matt Boyer (Montana Fish, Wildlife and Parks) and includes the possibility of conducting field work sampling wild and captive fish in the Rocky Mountains of Northeast Montana with wild biologists from the University of Montana and Montana Fish, Wildlife and Parks.

Successful candidates will have some previous research experience and a strong interest in ecology and evolution. Candidates interested in fisheries are encouraged to apply. Some background or experience in molecular laboratory techniques and/or bioinformatics and field work is encouraged.The Chiari Lab is committed to promoting and supporting diversity and a multicultural environment and we encourage underrepresented students to apply.

Support will be provided through a teaching assistantship. However, the successful candidate will be expected to apply for graduate fellowships during his/her PhD.

Prospective students should send a short description of their research interests, past research experience, and a description of why they are interested in this project and in joining the Chiari Lab along with a resume or CV (including the names of three people who could serve as a reference on your behalf) toychiari@gmu.edu. Selection of candidates will begin immediately.

For information about the program, please visit

https://catalog.gmu.edu/colleges-schools/science/-systems-biology/biosciences-phd/   Ylenia   Chiari, PhD

Assistant Professor

P(703) 993-4467 Eychiari@gmu.edu

George Mason University, Department of Biology SciTech Campus, 10900 University Blvd., Colgan Hall 407 Manassas, VA 20110

www.yleniachiari.it   Ylenia Chiari <ychiari@gmu.edu>

Hungary EvolutionCooperation

The Ecological Research Centre is recruiting one early stage researcher to work on scientific problems related to the evolution of cooperation and multi-level selection. The position is part of a H2020 ITN project EvoGamesPlus (www.evogamesplus.eu).

Qualification: Applicant require to have an MSc by the time they would be hired (so they could finish in the spring/summer). MSc in mathematics, physics or computer science is preferred, but anyone with strong mathematical background is welcome.

*Country of origin: *Anyone can apply (but see limitations).

Limitation: Only early stage researches who has finished their MSc in the last four years and do not have a PhD can apply (finished after 1st September, 2017). The mobility requirement of the grant require that the candidate should not have finished her/his MSc in Hungary, nor should she/he be working/studying in Hungary for more than 12 months in the last 3 years. (To put it into plain English, we are seeking someone, who has not spent any considerable time in Hungary yet.)

Employment: Successful candidate will have a fixed-term employment contract with the Ecological Research Centre.

Start date: The successful candidate should start her/his work at the 1st of September 2021.

Place of work: Institute of Evolution of the Ecological Research Centre, Budapest, Hungary. The institute is located in the hills surrounding the capital of Hungary. Successful candidate will also have the opprotunity to receive training in the UK and in the USA.

We have an equal opportunity employment.

If you are interested, please send your CV as pdf file to Ãdám Kun (kun.adam@ecolres.hu) and József Garay (garay.jozsef@ecolres.hu).

Application deadline: 15th of May, 2021

Selected candidates will be interviewed on the week following the deadline via Zoom or GoogleMeet.

This project has received funding from the European Union's Horizon 2020 Research and Innovation Programme under the Marie SkÂ³odowska-Curie grant agreement number 955708 (https://cordis.europa.eu/-

project/id/955708).

kunadam@elte.hu

Iceland BirdEcologicalGenomics

Ph.D. studentship in Rock ptarmigan ecological genomics at the University of Akureyri, Iceland

We???re seeking a highly motivated Ph.D. student to work on a fully funded project on genomics and ecology of rock ptarmigan (Lagopus muta) in Iceland. The project is funded for 36 months, starting in June 2021.

The project Ecological genomics encompasses ecology, genomics and evolutionary biology, and utilizes genomic approaches to address consequential ecological questions. In this project we will apply an ecogenomic approach, by analysis of genome diversity and gene expression, assessing the association of genetic variants to population cycling or intermediate phenotypes of rock ptarmigan. Within the frame of the recently completed comprehensive project, ???Rock ptarmigan health and population change??? spanning the years 2006-2018, a unique tissue-, and dataset have been created by the annual collection of data on this wild bird population. We aim to explore the impact of trophic interactions such as diversity of the gut microbial community, plant-herbivore interactions, and the role of toxins. The health parameters and tissue collection of Icelandic rock ptarmigan are unique with no such comparable dataset available elsewhere. To convey ecogenomic approach we will generate genomes and transcriptomes from the rock ptarmigan to carry out our comparative genomics and tissue-specific expression analysis with the goal to map and characterize genomic regions involved in selection/adaption and to examine how genes are involved in various biological processes such abiotic and biotic stress responses.

The main supervisor of the PhD student will be Professor Kristinn P. Magn??sson at the Faculty of Natural Resource Sciences, Universtity of Akureyri (UNAK) and Icelandic Institute of Natural History (IINH). Other advisors are Professor Jacob H??glund at the Instititute of Ecology and Genetics, University of Uppsala, Sweden. Professor Sn??bj??rn P??lsson, Faculty of Life and Environmental Sciences, University of Iceland, Assoc Professor Eva Charlotte Halapi Faculty of Natural Resource Sciences, UNAK and Professor Jennifer Forbey Dep. of Biological Sciences, Boise State University, Boise, USA. The bulk of the work will be carried out at the UNAK/IINH laboratories in Akureyri, but the stu-

dent will also attend secondments in Uppsala, Sweden.

The role of the doctoral student In accordance with the rules and regulations for doctoral studies at the University of Akureyri, the student will prepare and submit their own study plan, and otherwise submit to the obligations and attain the rights of doctoral students at UNAK. The doctoral studies will conclude with the public defense of a Ph.D. thesis consisting of peer-reviewed publications in internationally recognized academic journals.

Qualifications A successful applicant will have a first-class M.Sc.-degree or equivalent in a relevant field, such as genomics, bioinformatics, evolutionary biology or molecular genetics. The applicant will furthermore have a genuine, interest in science, as well as a willingness to learn new methods of research and excellent interpersonal and collaborative skills. Excellent reading, writing, and communication skills in English are an absolute must.

Application process Applications for doctoral student positions at the University of Akureyri are twofold. Firstly, the applicant applies to a relevant research project should be submitted to the principal investigator for that project, Prof. Kristinn P??tur Magn??sson, kpm@unak.is.

This application should consist of: 1. A cover letter, wherein the applicant states the reasons for their interest in the project, explains how they fulfill the eligibility criteria, and outlines their proposed contribution to the project. 2. A curriculum vitae, listing all relevant qualifications and work experience. 3. A copy of any relevant diplomas and/or transcripts. 4. Contact information of at least two reference persons.

Guidance can also be obtained from the doctoral studies program at doktorsnam@unak.is.

Further information Salaries and benefits are according to the F??lag ??slenskra N??tt??rufr????inga contract (www.fin.is). The University of Akureyri (www.unak.is) strives for equality regarding age, gender, race, nationality, and sexual orientation. The project is fully funded by a grant from the Icelandic Research Fund.

The application deadline is May 15th, 2021. The applicant should be able to commence employment in June 2020.

For further information, please contact Professor Kristinn P??tur Magn??sson at kpm@unak.is

Kristinn P??tur Magn??sson Pr??fessor / Professor Au??lindadeild Vi??skipta- og raunv??sindasvi?? / School of Business and Science Skrifstofa / Office: Borgir ranns??knarh??s - R421 S??mi / Phone: 5900578

Fars??mi / Mobile: 8918778 ORCiD: 0000-0003-4528-6826

Lagalegur fyrirvari / Legal disclaimer

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IdahoStateU PlantEcologicalGenomics

Funded PhD position available at Idaho State University in plant ecology and genomics!

We are looking for a PhD student and future collaborator to join our team on a recently-funded project investigating the ecological impacts of ploidy and genome size variation in the iconic foundational species, big sagebrush (Artemisisa tridentata). This student will be involved in a large and collaborative network of trans-disciplinary scientists and stakeholders across Idaho as part of the NSF/Idaho EPSCoR GEM3 project (see idahogem3.org for more information on this state-wide initiative). The PhD student will be co-advised by Dr. Josh Grinath (https://jbgrinath.wordpress.com/) and Dr. Kathryn Turner (kathryngturner.com) in the Department of Biological Sciences at Idaho State University (isu.edu/biology). The student will be supported on a research assistantship for two full years (tuition is waived, and there is guaranteed summer funding and no TAing during that time). After that, the student will transition to a teaching assistantship or other funding support. This work represents 1-2 chapters of the student's dissertation; the student will develop additional, perhaps related, projects for the rest of their dissertation work.

The project:

Ploidy level and genome size are genetic traits that greatly influence the performance of phenotypes in ecological communities. In particular, organismal demands for nitrogen (N) and phosphorus (P) are expected to increase with genome size because genetic architecture requires larger amounts of these resources than other biomolecules. As N and P have limited availability in most natural systems, these demands translate into stronger limitation in the performance of polyploids vs. diploid relatives. In plants, restrictions on polyploid performance may be even more severe for species that are co-limited by both N and P supply. Co-limitation occurs when plant access to one resource is impeded by the lack of another resource, and performance only improves greatly when multiple resources are simultaneously available. In addition, water availability can affect plant access to N and P, and co-limitation may occur among all three of these resources. Though resource co-limitation is common for plants, it is currently unclear how ploidy level and genome size affect the strength of co-limitation and plant competitive ability across various resource environments. Moreover, it is unclear how these resource relationships affect the spatial distribution of individuals within and across populations. In this project, we will study the effects of ploidy level, genome size, and resource availability (N, P, and water) on the performance of big sagebrush (Artemisia tridentata s.l.). Focusing on the establishment life-history phase, we will use greenhouse and field experiments to evaluate how these factors affect sagebrush resource requirements, co-limitation, competitive ability, and spatial patterning.

To apply:

If interested, please contact Dr. Grinath (grinjosh@isu.edu) and Dr. Turner (turnkat2@isu.edu) as soon as possible. For more information on applying, please see the Department of Biological Sciences at ISU (isu.edu/biology/degree-programs). Ideally, this position would begin August 2021.

– Dr. Kathryn G. Turner Dept. Biological Sciences Idaho State University kathryngturner.com

Kathryn Turner <turnkat2@isu.edu>

Krakow InsectOutbreakGenomics

PhD Student position in Population genomics of outbreaks - one week left to apply!

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

About the project

A major goal in evolutionary biology is to understand which processes shape genetic diversity observed in natural populations. Classic population genetic theory

provides a solid mathematical framework to study genetic variation and predict efficacy of natural selection relative to drift in equilibrium conditions, for example under constant population size. However, the majority of natural populations often experience large size fluctuations that make prediction less straightforward. The main purpose of this project is to test how extreme fluctuations in population size of outbreaking species affect the dynamics of neutral and adaptive genetic variation. Many pests experience epidemic outbreaks characterized by sudden changes in population size, often spanning orders of magnitude. Such outbreaks are known from ecological studies of closely monitored species of economic importance. However, little is known about how genetic variation changes during outbreak cycles. Specifically, the rate of adaptive evolution during relatively short periods of large population size remains unknown. This can be studied in species which experience extreme fluctuations of population size, such as spruce bark beetle (Ips typographus). Spruce bark beetle is the most destructive pest of Norway spruce forests because under specific conditions (e.g. storms) populations may outbreak, causing mass mortalities of spruce stands. We will compare populations of spruce bark beetle that have experienced frequent, recent outbreaks and populations that did not experience outbreaks in the recent past. By combining existing knowledge on biology and ecology of the species with newly generated, large-scale genomic data, we will address specific questions about the relationship between genome-wide variation and fluctuating effective population size: How outbreaks affect species genetic structure? Are adaptations in frequently outbreaking populations mainly driven by soft sweeps? How demographic history of the spruce bark beetle and historical fluctuations of effective population size over time affect current patterns of neutral and adaptive variation and more.

The PhD student will be working with large, whole genome resequencing data obtained from several populations and >500 individuals (short and linked-read sequencing). Part of the sequencing data is already available. The PhD student will investigate selection patterns along the spruce bark beetle and among outbreaking and non-outbreaking populations. The analysis will include standard selection scans as well novel approaches to detect and distinguish between hard and soft sweeps. The PhD student will gain a wide range of scientific experience including genome-wide sequence data analysis as well as wet lab practice and will be encouraged to develop his/hers own projects using extensive datasets available.

About the place and salary

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

The PhD student will be supported by a 48-month, tax-free research stipend: 4500 PLN (˜1000 EUR) per month. This stipend may be combined with the standard PhD program scholarship (for those that will pass the entrance exam to PhD graduate school at Institute of Environmental Sciences, approximately 2200 - 3500 PLN, https://wb.uj.edu.pl/ksztalcenie/szkola-doktorska/phd-programme-in-biology). Note that in Poland, the living costs are relatively low (check out a cost-of-living calculator such as www.numbeo.com) and even without additional funding from graduate school the salary is more than enough to fully enjoy life in Krakow.

Requirements

The successful candidate will have an M.Sc. degree in a relevant field by October 2021. We are looking for a student with strong interest in Evolution, Molecular Ecology, Population Genetics and/or Genomics as well as experience with, or a keen interest in learning, Bioinformatics and Computational Biology; and strong English language, communication, and

— / —

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

Krakow OutbreakInsectGenomics

PhD Student position in Population genomics of outbreaks

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

About the project

A major goal in evolutionary biology is to understand which processes shape genetic diversity observed in natural populations. Classic population genetic theory provides a solid mathematical framework to study genetic variation and predict efficacy of natural selection relative to drift in equilibrium conditions, for example under constant population size. However, the majority of natural populations often experience large size fluctuations that make prediction less straightforward. The main purpose of this project is to test how extreme fluctuations in population size of outbreaking species affect the dynamics of neutral and adaptive genetic variation. Many pests experience epidemic outbreaks characterized by sudden changes in population size, often spanning orders of magnitude. Such outbreaks are known from ecological studies of closely monitored species of economic importance. However, little is known about how genetic variation changes during outbreak cycles. Specifically, the rate of adaptive evolution during relatively short periods of large population size remains unknown. This can be studied in species which experience extreme fluctuations of population size, such as spruce bark beetle (Ips typographus). Spruce bark beetle is the most destructive pest of Norway spruce forests because under specific conditions (e.g. storms) populations may outbreak, causing mass mortalities of spruce stands. We will compare populations of spruce bark beetle that have experienced frequent, recent outbreaks and populations that did not experience outbreaks in the recent past. By combining existing knowledge on biology and ecology of the species with newly generated, large-scale genomic data, we will address specific questions about the relationship between genome-wide variation and fluctuating effective population size: How outbreaks affect species genetic structure? Are adaptations in frequently outbreaking populations mainly driven by soft sweeps? How demographic history of the spruce bark beetle and historical fluctuations of effective population size over time affect current patterns of neutral and adaptive variation and more.

The PhD student will be working with large, whole genome resequencing data obtained from several populations and >500 individuals (short and linked-read sequencing). Part of the sequencing data is already available. The PhD student will investigate selection patterns along the spruce bark beetle and among outbreaking and non-outbreaking populations. The analysis will include standard selection scans as well novel approaches to detect and distinguish between hard and soft sweeps. The PhD student will gain a wide range of scientific experience including genome-wide sequence data analysis as well as wet lab practice and will be encouraged to develop his/hers own projects using extensive datasets

available.

About the place and salary

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

The PhD student will be supported by a 48-month, tax-free research stipend: 4500 PLN (~1000 EUR) per month. This stipend may be combined with the standard PhD program scholarship (for those that will pass the entrance exam to PhD graduate school at Institute of Environmental Sciences, approximately 2200 - 3500 PLN, https://wb.uj.edu.pl/ksztalcenie/szkola-doktorska/phd-programme-in-biology). Note that in Poland, the living costs are relatively low (check out a cost-of-living calculator such as www.numbeo.com) and even without additional funding from graduate school the salary is more than enough to fully enjoy life in Krakow.

Requirements

The successful candidate will have an M.Sc. degree in a relevant field by October 2021. We are looking for a student with strong interest in Evolution, Molecular Ecology, Population Genetics and/or Genomics as well as experience with, or a keen interest in learning, Bioinformatics and Computational Biology; and strong English language, communication, and

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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

MississippiStateU MicroEukaroyteEvolution

Graduate Assistantship(s) in Microbial Eukaryotic Evolution, Ecology, and Genomics
**

The Brown lab (http://amoeba.msstate.edu) seeking potential graduate students (M.S. or Ph.D.) interested in studying evolution, ecology, and/or comparative genomics of amoeboid protists.

The Brown lab is broadly interested in the evolution, ecology, and genomics of microbial eukaryotes. We are currently funded through a multiyear US National Science Foundation project through the PurSUiT category, which is "meant to encourage biodiversity discovery and description in poorly known, or dark areas, of the Tree of Life."

The project title is "PurSUiT: Sampling amoeboid protists as a reservoir of unknown/undescribed eukaryotic diversity" and more information on this project can be found at https://www.nsf.gov/awardsearch/showAward?AWD_ID!00888 Generally, the Brown lab examines the deep evolution of eukaryotic lineages. We are using novel approaches in phylogenomics to examine how the various major groups of eukaryotes evolved over the course of the last 2 billon years. However, we are currently most focused on the evolutionary histories of amoeboid organisms.

The Brown lab is also developing model systems to look at the commonalities among the greatest examples of convergent evolution known to date. We have discovered that a great diversity of single celled eukaryotic microbes (AKA protists) are capable of working with one another to form a complex body made of thousands of individual cells. This is one of the simplest and most striking examples of emergent behavior. In many cases, this behavior is sacrificial where some of the cells that become part of the multicellular body die for the "greater good" of others. To examine the commonalities amongst the various social protists, we are taking a multi-pronged approach using comparative genomics and developmental transcriptomics to elucidate the genetic basis of sociality. Aspects of this project may also be pursued by new graduate students.

**

Funding for students will be provided through NSF funded research assistantships with some semesters of teaching assistantships within the department so that graduate students can gain formal teaching experience. I will also provide a summer salary. Information on Graduate Studies in the Department of Biological Sciences is available at http://biology.msstate.edu/degrees/graduate/ ** Mississippi State University is a Carnegie classified R1: Doctoral University (i.e., Very high research activity). The Department of Biological Sciences is home to faculty with broad research & teaching interests in ecology, evolution, and systematics. My group has a strong recent record of attracting

federal funding from the NSF and the department as a whole has a strong record of USDA, NSF, NIJ, and NIH funding. We use a wide array of approaches ranging from field studies and experimentation to molecular approaches including next-generation DNA sequencing and bioinformatics.

**

Please contact Dr. Matthew Brown (matthew.brown{at}msstate.edu) for more information. Also, a CV that includes information regarding prior education and research experience would be appreciated, along with a statement of your specific research interests.

**

For more information about the Brown Lab @ MSU, please visit: http://amoeba.msstate.edu **

####

Matthew W. Brown, Ph.D. Associate Professor

Sanderson Excellence Dean'sEminent Scholar Biological Sciences Mississippi State University 312 HARN Hall (Office) 351A HARN Hall (Lab) 662-325-2406(Phone)

President-Elect, International Society of Protistologists|www.protistologists.org Lab Website|http://amoeba.msstate.edu Google Scholar| https://scholar.google.ca/citations?user=UvN4AQsdfygC&hl=en Fedex/UPS Shipping Address MSU-BIO SCI 295 Lee Blvd. HARN 219 MS State, MS 39762

"Brown, Matthew" <mbrown@biology.msstate.edu>

MNHN-CNRS France ExtinctionHistoricalDNA

PhD Studentship in population genetics - Using a genetic time series and historical DNA to understand extinction risk

A fully-funded 3-year PhD studentship is available at the French National Museum of Natural History in Paris (MNHN), working closely with the CAGT ancient DNA lab at the University of Toulouse. The student will be supervised by Ben Warren (Principal Supervisor), Guillaume Achaz and Stefano Mona.

The PhD is part of a wider project on birds (SusceptExt) funded by the French National Research Agency (ANR) aimed at understanding the role of evolutionary

history in determining why some species are threatened with extinction, while others are at comparatively little risk.

Co-investigators are Ludovic Orlando, Catherine Thèves, Lounès Chikhi and Eric Crubézy at the University of Toulouse, and Julian Hume at the Natural History Museum, London.

Details of the project:

Evolutionary history is expected to play a major role in determining which species decline in population size to extinction in response to environmental change, but the processes by which this comes about are poorly understood. Although population genetic studies provide much promise to understand the microevolutionary processes behind macroevolutionary patterns of extinction risk, inferences can be limited by our confidence in the timescales inferred, and by the scale of such studies, which frequently include only one lineage. The PhD student will tackle both of these issues, applying population genetic methods to a genome-wide time series for multiple Mascarene island bird lineages that differ in abundance and other biological traits. The student will help develop the time series which will contain not only modern DNA but also historical DNA from museum samples (historical and subfossil).

Islands in the Mascarene archipelago (Mauritius & Réunion), Indian Ocean, are unusual among sizable and biologically diverse landmasses worldwide, in that they had no human population until European arrival 400 years ago. For birds, there exist museum samples and subfossils spanning the full duration of anthropogenic environmental change, allowing a real-time assessment of genetic response to environmental changes of known timing and across multiple species following first human presence.

The student will be in charge of population genetic analyses aimed at making inferences of selection, and comparing selective responses to common (and severe) environmental changes across multiple species that differ in abundance - common species versus rarer ones (most of which are IUCN threatened). Another aim is to test the significance of correlations between the timing of genetic and environmental changes. The student will work alongside a postdoc (Alexander Verry) with experience in ancient DNA lab techniques, and who will be focussed on demographic analyses for the same time series. It is expected that the student will help generate the genetic time-series, with guidance in the lab from the postdoc. Furthermore, there is much potential for the student to contribute to demographic analyses or method development, in collaboration with the postdoc. Such demographic analyses should be used to inform

inferences of selection.

We are looking for a highly-motivated student with: - first-rate academic credentials in population genetics in particular, - a strong interest in the broad theme of the study - understanding the role of evolutionary history in determining which species decline towards extinction in response to environmental change.

A minimum requirement is to have obtained excellent grades in a substantial (Undergrad and/or Masters) course(s) in population genetics. Experience in population genetic or genomic analyses in previous research projects would be ideal. Other fields particularly relevant to this project are Evolutionary Biology (ideally a broad background and interest), Conservation Biology, Mathematics or Bioinformatics.

The student will be based at the MNHN (Muséum National d'Histoire Naturelle, UMR ISYEB CNRS), which is a renowned centre for biodiversity research and collections in the heart of Paris. S/he will also spend 4 months of their first year in a globally leading ancient DNA lab in the south of France (UMR CAGT, CNRS-University of Toulouse) for the wet lab component of their thesis.

Start date: December 2021 or January 2022

Applications should ideally be submitted by May 19th (deadline: May 31st).

For informal enquiries please contact Ben Warren (bwarren@mnhn.fr)

To apply: Please submit your application to Ben Warren (bwarren@mnhn.fr) and Stefano Mona (stefano.mona@mnhn.fr) as a single pdf file containing: 1) a short covering letter (1-2 pages) explaining your motivation, and why you would be well suited to this PhD including achievements and research experience; 2) a full CV, including grades obtained in the final year of Undergraduate & Masters to date;

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MPIO Seewiesen EvolutionCognition

Opportunity!

Projects available for Master's/Bachelor's students and self-funded Interns in Comparative Cognition Research Station at Tenerife, Spain run collaboratively between the Max-Planck Institute for Ornithology and the Loro Parque Foundation

The Max-Planck Comparative Cognition Research Group (CCRG)

https://www.orn.mpg.de/Comparative-Cognition-Research-Group-von-Bayern invites applications from Postgraduate/Undergraduate students and Interns who want to assist in research projects and bird care, enrichment and management. The CCRG is part of collaboration between the Max-Planck Institute for Ornithology, Germany, and Loro Parque Fundación (LPF) in Tenerife, Spain. We are currently carrying out several projects on parrot intelligence. We work with mostly tame, captive parrots of LPF, which owns the largest collection of parrots and genetic reserve in the world (approximately 350 subspecies) for conservation and research purposes. Interested candidates are encouraged to contact us to request information about ongoing projects. Selected applicants will gain experience in the field of cognitive research, as well as working with and training exotic parrots in a highly dynamic international research environment. A unique opportunity!

Preferable time of joining: It is highly preferable if students can join by April-May 2021

Logistics: The projects for Master's/Bachelor's theses and internships require minimum of 4 months but ideally 6 months of continuous commitment at the research station in Tenerife, Spain. Accommodation can be provided in a shared student apartment (Puerto de la Cruz, Tenerife, Spain), with affordable facilities. Students with their own funding or grants can apply for the posts.

Important skills/qualifications:

Selected candidates need to have:

- High motivation and commitment to the care of our birds

- Preferably pursuing Bachelor's or Master's degree in Bi-

ology/ Psychology/Animal Science or related subjects.

- Reliability, efficiency and ability to work independently

- Confidence to interact with animals

- Good verbal English skills

- Good teamwork attitude and social skills

Submit your request!

For more information on how to apply, please email Dr. Anastasia Krasheninnikova (akrashe@orn.mpg.de), the Msc Esha Haldar (ehaldar@orn.mpg.de) or the Msc. Sara Torres (storres@orn.mpg.de).

"akrashe@orn.mpg.de" <akrashe@orn.mpg.de>

MPI Seewiesen AvianEvolution

The Max Planck Institute for Ornithology (MPIO) in Seewiesen (located near Starnberg about 50 km from Munich) is an internationally renowned research institution with more than 200 employees working in two departments and seven research groups. The MPIO employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology. It features an exceptional infrastructure with state-of-the-art laboratories dedicated to hormone, neurological and genetic research. A fully funded PhD position is available in the research group of Clemens Kuepper (https://www.orn.mpg.de/Research-Group-Kuepper) at the Max Planck Institute for Ornithology (MPIO) in Seewiesen, Germany. PhD opportunity in Behavioural and Evolutionary Genomics We are interested in the evolutionary and ecological mechanisms that maintain diversity in social behaviour using an integrative approach. Example publications are here: https://www.orn.mpg.de/3872051/publications . The project, which is funded by the German Research Foundation (DFG), builds on our description of genomic differences between the three male mating morphs in Ruffs Philomachus pugnax (Küpper et al. 2016 Nature Genetics https://doi.org/10.1038/ng.3443). Ruffs, provide a flamboyant avian model system to understand the genomic underpinnings of male alternative reproductive strategies.

Over the course of the project, we will characterize comprehensively transcriptomic differences of several brain and organ tissues from embryos, chicks and adults to determine differences in gene regulation and alternative splicing between morphs.

The current project is a collaboration with Katja Nowick, FU Berlin. Tissue sampling and laboratory work will be conducted in the captive Ruff population at MPIO. Candidates should have a Master's degree (or equivalent) in Biology with a specialization in e.g. neurogenetics, genetics/genomics and/or computational biology. Experiences with RNA Seq methodology and bioinformatic analysis are desirable. The candidate will have the opportunity to join the Nowick lab (https://www.bcp.fu-berlin.de/en/biologie/-arbeitsgruppen/zoologie/ag_nowick/index.html) for customized bioinformatic training. Strong self-motivation, an ability to work independently and in a team are an absolute must for successful candidates in this highly collaborative research effort. For further questions please contact ckuepper@orn.mpg.de. The position is funded for three years. The salary will be paid in accordance with the German Tarifvertrag des öffentlichen Dienstes (TVöD Bund), salary group 13 (65%). Qualified PhD candidates can apply to join the International Max-Planck Research School for Organismal Biology that offers unique training opportunities. The Max-Planck Society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals. Your application To apply please send (1) your CV, (2) a letter of motivation, and (3) the contact details of at least two referees under this link: https://s-lotus.gwdg.de/-mpg/maor/perso/orni_w003.nsf/application Review of applications will begin on 10 May 2021 until the position is filled. The starting date is negotiable, ideally the 1st June 2021 but no later than 1 September 2021.

Lilly Mros Max-Planck-Institute for Ornithology Auszubildende in der Verwaltung Eberhard-Gwinner-Straße 82319 Seewiesen -Germany-

Telefon: +49 8157 932-221 Fax: +49 8157 932-209 E-Mail: lilly.mros@vw.orn.mpg.de

"Mros, Lilly" <lilly.mros@vw.orn.mpg.de>

NHM Geneva CarabinaePhylogenomics

We are seeking a PhD student (4 year-position) to work on Carabinae phylogenomics and evolution at the Natural History Museum of Geneva in Switzerland in the Toussaint Lab starting in January 2022.

Details:

A PhD position is available in the Toussaint Lab at the Natural History Museum of Geneva to work on a SNSF-funded project that focuses on species delimitation, phylogeography, phylogenomics, macroevolution, genome architecture and wing evolution of Calosoma ground beetles and related genera. You will be working in a welcoming and inclusive institution located in a beautiful region surrounded by lakes and mountains. The position is located in the largest Natural History Museum of Switzerland with 15 million specimens where you will be developing new skills in molecular biology, data analysis, writing and evolutionary biology theory alongside the PI, a postdoc, other students, the Museum staff and scientists from the Universities of Geneva and Lausanne.

Qualifications:

- M.Sc. in evolutionary biology (ideally in entomology) - Strong interest in entomology and systematics - Experience with wet lab techniques (ideally NGS oriented) - Experience with molecular data analysis/bioinformatics - Ideally at least one peer-reviewed publication - Fluency in English and/or French is expected

How to Apply?

Send a cover letter, CV, two reference letters and copies of academic transcripts to Emmanuel.touss1@gmail.com before the 1st of June 2021.

"Emmanuel F.A. Toussaint" <emmanuel.touss1@gmail.com>

NMBU Norway SalmonSeaLiceResistance

PhD scholarship: Novel ex vivo experimental approaches to decode sea lice resistance mechanisms in salmonid fishes

About the position The Department of Animal and Aquacultural Sciences, Faculty of Biosciences at the Norwegian University of Life Sciences (NMBU) has a vacant 3-year PhD'Vposition related to salmon cell biology and mechanisms of sea lice resistance in salmonid species.

The PhD project will focus on development of cutting-edge cell culturing technology in two salmonid species, differing in their resistance properties to sea lice. One of the main efforts will be directed on developing new immortalized skin cells lines from susceptible (Atlantic

salmon) and resistant (Coho) salmonids. In addition, the candidate will work to develop approaches to map the responses of sea lice infestation in these cells, thereby gene editing approaches. The candidate will work in close collaboration with other PhD-students and post-doctoral researchers.

For more information, visit https://www.jobbnorge.no/-en/available-jobs/job/204067/phd-scholarship-novel-ex-vivo-experimental-approaches-to-decode-sea-lice-resistance-mechanisms-in-salmonid-fishes   For detail, please contact Dr. Guro Sandvik, E-mail: guro.sandvik@nmbu.no

Marie SAITOU, Ph.D. Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences https://sites.google.com/view/saitou-lab Marie Saitou <marie.saitou@nmbu.no>

Norway GenomeBioinformatics

Dear Evoldir colleagues,

Hi, I hope all is well.

I am currently looking for a PhD student (3yrs) with full funding in my group at the Norwegian University of Life Sciences, to understand the phenotypic/adaptife effects of structural variants by using statistical genomics and Nanopore data sets of Atlantic salmon. A candidate with masters degree in genomics, and with skills in statistics and big-data analysis would be appreciated.

If you know students who potentially may be interested, please forward this information to them. For more details on the position and to apply please visit this page: https://www.jobbnorge.no/-en/available-jobs/job/204786/phd-scholarship-on-functional-and-evolutionary-genomics   And here is a video: https://www.youtube.com/watch?v=-3DASfE6RWQZvA The applications can be submitted until May 23rd through the webpage above.

Thank you very much,

Marie

Marie SAITOU, Ph.D. Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences https://sites.google.com/view/saitou-lab Marie Saitou <marie.saitou@nmbu.no>

TexasAM Genomics Hybrid Birds

The Delmore Lab at the University of Texas A&M is looking for a PhD student to join our group in Sept 2021.

We study speciation using hybrid zones and work at both the micro and macroevolutionary scale. One of our research streams focuses on speciation genomics and includes work on the processes that generation genome-wide variation in estimates of differentiation. We use both genomic data and computer simulations to address this question.

Another research stream focuses on behaviour 'V how variation in behavioural traits contributes to speciation and the molecular basis of these traits. One of the behaviours we study is seasonal migration. Much of this work focuses on a hybrid zones between Swainson'Âs thrushes but we are constantly expanding the scope of this work. Another behaviour we study is courtship behaviour using a hybrid zone between ruby-thorated/black-chinned hummingbirds.

We are located in the Biology Department (https://-www.bio.tamu.edu/) which has a collaborative, enthusiastic and supportive environment. We have students from many different international backgrounds and you will be able to develop knowledge in evolution and substantial genomic and computational skills while you'Âre here.

Texas A&M is a Tier 1 institution with an amazing number of facilities to support research. College Station itself is a friendly university town located between Austin and Houston. It is the perfect venue for getting work done while having access to vibrant city centers full of entertainment and culture.

You can find out more about our lab at delmorelab.com. If you are interested please email a CV (including names and contact details of two-three references) and a one-page cover letter stating your motivations to Kira Delmore (kdelmore@bio.tamu.edu) with the subject line "PhD application".

"Delmore, Kira" <kdelmore@bio.tamu.edu>

ToulouseU MusselGenomicMorphologicalEvolution

PhD position: Genomic and Morphological Evolution of Mussels - CAGT Toulouse France

We are hiring a PhD student to join our International and multidisciplinary team investigating the Genomic and Morphological Evolution of Mussels.

Applications can be submitted through the website https://emploi.cnrs.fr/ ONLY starting May, 3rd 2021, but interested applicants can now get in touch by emailing Clio Der Sarkissian at clio.dersarkissian@univ-tlse3.fr.

Hosting organisation: Centre for Anthropobiology and Genomics of Toulouse, France Supervision: Clio Der Sarkissian/José Braga Duration: 3 years, full time Starting date: October 1st 2021 Salary: 2,135 euro per month (net) Application deadline : June 13th

***Project description The proposed program is part of a multidisciplinary project aimed at better understanding the impact of environmental conditions on mussels of the Mytilus genus through time and space. Using the latest 3D morphometry and ancient genomics methods, the objective will be to characterize the relationships between biological (phenotypic and genomic) responses and environmental changes.

The research work of the future PhD student will be based on a collection of modern and ancient mussel shells sampled along environmental gradients. It will consist in generating and analyzing ancient and modern genomic data, as well as acquiring and processing 3D micro-CT scans, in order to identify candidate traits influenced by environmental factors. For more information, see our previous work: Der Sarkissian et al., 2017 Molecular Ecology Resources, and Der Sarkissian et al., 2020 Frontiers in Ecology and Evolution; as well as Orlando et al. 2021, Nature Reviews Methods Primers for a review on ancient DNA.

***Context This project is funded by the French National Research Agency (ANR; MEET, website: https://cagt.cnrs.fr/meet/) and the student will join a team of experts in ancient genomics, statistical analyzes of shapes, and ecology. The PhD student will be hosted as part of the team AGES (Archeology, Genomics, Evolution and Societies) headed by Ludovic Orlando at the Centre for Anthropobiology and Genomics of

Toulouse (CAGT, UMR5288 CNRS, website: https://cagt.cnrs.fr/, Twitter: @CAGToulouse), University of Toulouse 3, France. The PhD project will be supervised by Clio Der Sarkissian, a researcher in ancient genomics. She develops pioneering approaches applying state-of-the-art techniques to study mollusk shells from archaeological archives and museum collections. The second supervisor will be José Braga, a paleoanthropologist who implements cutting-edge statistical methods for the modelling of shape variability.

CAGT is an International and multi-disciplinary research environment bringing together (ancient) geneticists, palaeontologists, anthropologists, archaeologists and experts in 3D-imaging in order to better understand the complex interactions between human populations, biodiversity and the environment through time. CAGT benefits from privileged relationships with the Natural History Museum of Toulouse next door to the laboratory. Located on the campus of the Faculty of Medicine of Purpan, CAGT offers a pleasant working environment in the center of Toulouse, a city known for its large student population, quality of life and proximity to the Pyrenees, the Mediterranean Sea and the Atlantic Ocean.

***Requirements We are seeking highly motivated and committed applicants with a strong interest in interdisciplinary research.

The PhD project is intended for applicants with knowledge and experience in molecular biology, genomics, evolutionary biology, population genetics, ecology, and/or bioinformatics. A French Master 2 Research (M2R) / DEA degree or equivalent in the research fields concerned is required (see degree equivalence on the doctoral school website: https://ed-bsb.univ-toulouse.fr/as/ed/page.pl?site=3Dedbsb&page=3Dequivalence). Prior experience in a molecular biology (ancient DNA) laboratory or computational analyses of high-throughput genomic data is a plus, as is coding proficiency in R, Bash and/or Python (Perl).

The applicant must be fluent in English as CAGT is an International environment.

The applicant will ideally have skills in taking initiatives and working independently, as much as in communicating progress (in oral and written forms) and working on a team.

The future PhD student will be expected to participate in the life and activities of AGES and CAGT, and to communicate research with the members of CAGT, the scientific community and the general public.

*** Further information Applications must be submitted on the CNRS Employment Portal ONLY. Candidates are invited to send: - a letter detailing their previous

research work, as well as their

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Tubingen EvolutionSocialLearning

The ???Human and Machine Cognition??? lab of the Cluster of Excellence ???Machine Learning: New Perspectives for Science??? and the ???T??bingen AI Center??? invites applications for an open PhD position (m/f/d; E13 TV-L, 65%) to be filled as soon as possible. The position is limited to three years.

About the group: The HMC lab is led by Dr. Charley M. Wu and operates at the intersection of Human Cognitive Science and Machine Learning research. The focus of this position will be to study the strategies that humans use to learn from and interact with other people in social settings. Potential topics include the integration of social and individual information, computationally tractable implementations of Theory of Mind inference, and cumulative cultural evolution in online communities, in addition to the interests of the candidate.

Members of the lab are working on a diverse set of topics including, structure learning in planning and search, developmental changes in learning and exploration, inductive biases in compositional learning, and many more. Our research methods include online experiments (commonly in the form of interactive games), lab-based virtual reality experiments, computational modeling of behavior, evolutionary simulations, developmental studies (comparing children and adults), fMRI/EEG, and analyzing large scale real-world datasets. We have a rich collaboration network of researchers from Harvard, Princeton, UCL, and several Max Planck Institutes around Germany. To find out more, visit the lab website at www.hmc-lab.com . About the position: The candidate should hold a MSc degree in cognitive science, computer science, psychology, computational neuroscience, statistics, or any relevant discipline. The ideal candidate should be self-motivated, comfortable with both analytic and critical thinking, and have a passion for science. Please indicate in your application if you have prior experience with conducting experiments, computational modeling, machine learning, and/or neuroimaging (EEG/fMRI). Skills in computer programing

languages (e.g., R, Python, Matlab, Javascript, Java, etc.), mathematics, writing (in English), and the ability to independently manage a project (of any type) should also be mentioned.

About T??bingen: Tu??bingen is a scenic university town on the Neckar river in South-Western Germany. The quality of life is exceptionally high and the atmosphere is diverse, inclusive, and most locals speak English. Tu??bingen offers excellent research opportunities due to the University, four Max Planck institutes, the University Hospital, and Europe???s largest AI research consortium. You can find out more about Tu??bingen here: https://www.tuebingen.de/en/ How to apply: Please send a cover letter, a description of your research interests (max 1 page), your CV, the names and email addresses of 2-3 referees, and unofficial copies of your University degrees as a single PDF to Charley Wu (charley.wu[at]uni-tuebingen[dot]de). If you have any questions about the position, please do not hesitate to contact Charley directly. The university seeks to raise the number of women in research and teaching and therefore urges qualified women academics to apply for these positions. Equally qualified applicants with disabilities will be given preference. The employment will be carried out by the central administration of the University of T??bingen. Please submit your application by May 15th, 2021.

UBasel
SticklebackEvoDevoGenomics

PhD position in evo-devo/genomics at the University of Basel

OVERVIEW The research group of Dr. Daniel Berner at the Dept. Environmental Sciences of the University of Basel offers a PhD position focusing on the developmental genetic basis of adaptive diversification in threespine stickleback fish. The four-year position is fully funded by the Swiss National Science Foundation (SNF) known for generous salaries, and can start as soon as the candidate has been chosen.

FOCUS The successful candidate will investigate the molecular basis of phenotypic diversification among natural populations of threespine stickleback adapted to ecologically different environments. This work will make use of a top model system for evolutionary genomics and will involve the establishment and maintenance of laboratory lines, characterizing developmental divergence

between populations at the phenotypic and molecular level, and performing developmental genetic experiments to discover and validate candidate genes. Techniques to be used include genome-wide association mapping, RNAseq, in situ hybridization, genome editing with CRISPR/Cas9, and the bioinformatic analysis of the resulting data. This work will be aided by the collaboration with two other research groups specialized in developmental biology and evolutionary genetics. Depending on individual interests, there will be opportunity for the development of side projects.

PROFILE OF CANDIDATES Students applying for this position should hold a master degree in biology and possess excellent verbal and written English expression. Candidates should be eager to conduct research bridging ecology, genomics and developmental biology, and to develop competence in molecular genetic techniques and bioinformatics. Experience in molecular bench work and/or programming (e.g., R, Python) is considered an asset, but is not required. Applications from diverse research backgrounds are encouraged.

APPLICATION Applications and queries should be sent to daniel.berner@unibas.ch. The application should be prepared as a single pdf document including a concise letter of motivation (< 1 page), your CV (including the contact details of 2-3 referees), and a copy of your academic transcripts. The evaluation of applications will start on April 30 and will continue until the suitable candidate has been found.

Dr. Daniel Berner Group leader Zoological Institute University of Basel daniel.berner@unibas.ch http://salzburgerlab.org/team/daniel_berner/ "daniel.berner@unibas.ch" <daniel.berner@unibas.ch>

UCopenhagen ArcticAncientDNA

PhD fellowship on ancient DNA and palaeoecology of Arctic marine mammals We are looking for a highly motivated and dynamic candidate to fill a 3-year PhD studentship to work on ancient DNA of Arctic marine mammals. The project will be based at GLOBE Institute, University of Copenhagen, in the Molecular Ecology and Global Climate Change group led by Associate Professor Eline Lorenzen. The project is fully funded by the Danish Council for Independent Research (DFF - Sapere Aude Research Leader programme).

Deadline for applications is 9 May 2021. Project start is 1 September or as soon as possible thereafter.

Full advertisement can be found here: https://employment.ku.dk/phd/?show=153884 Project description The Arctic is one of Earth's most fragile ecosystems, and the scale of change taking place in the Arctic marine environment due to rises in temperature and loss of sea ice cover is overwhelming. The PhD fellowship will integrate palaeogenomics, palaeoecology, and palaeoclimatology to elucidate how climatic perturbations have affected the ranges and abundances of Arctic marine mammal species in the past.

The PhD project aims to retrieve ancient mammalian DNA from marine sediments and subfossil remains of Arctic marine mammal species to document their occurrence and diversity throughout the Late Pleistocene/Holocene. The DNA data will be combined with other proxy data on the timing and magnitude of changes in the abundance and species composition of organisms at the base of the food web (e.g. phytoplankton, sea ice algae, zooplankton), to investigate how past patterns of climatic shifts have impacted species, with the ultimate goal of improving our understanding of how these species might fare in the near future of increased global warming under different future scenarios of climate change.

The PhD fellow will be supervised by Associate Professor Eline Lorenzen and co-advised by Senior Researcher Sofia Ribeiro at the Department of Glaciology and Climate, Past Climate and Environments Research Group, Geological Survey of Greenland and Denmark (GEUS) also in Copenhagen.

Contact: Eline Lorenzen, GLOBE Institute, elinelorenzen@sund.ku.dk, +45 26 70 10 24

Eline Lorenzen PhD, MSc Associate Professor Deputy Head of Department for Research

YIP+ Villum Fonden Young Investigator Carlsberg Foundation Distinguished Associate Professor DFF: Sapere Aude Research Leader

University of Copenhagen GLOBE Institute Section for Evolutionary Genomics

Ãster Farimagsgade 5, CSS Building 7, 2nd floor 1353 Copenhagen K, Denmark

Tel.: +45 26701024 Email: elinelorenzen@palaeome.org, elinelorenzen@sund.ku.dk

https://globe.ku.dk/research/evogenomics/lorenzen-group/ Eline Lorenzen <elinelorenzen@palaeome.org>

UFribourg
AncientDNABioinformatics

PhD position in Ancient DNA Bioinformatics

Statistical and Computational Biology Group (Daniel Wegmann) University of Fribourg, Switzerland

Who we are We are a young, international, interdisciplinary and enthusiastic research group at the University of Fribourg, Switzerland, aiming at understanding the evolutionary and ecological processes shaping the realm of biological diversity we see today. To achieve this, we design and develop new statistical and computational approaches, and apply them to big data from many biological fields. A current focus of the lab is on dedicated tools for ancient DNA (aDNA) bioinformatics and their use to study past human societies.

Your tasks We develop ATLAS (https://bitbucket.org/wegmannlab/atlas), a dedicated tool to conduct bioinformatic analyses from raw-sequence data to population genomics. We seek a highly motivated PhD student to extend the machine learning models of ATLAS that are used for genotyping, in particular regarding post-mortem damage and recalibration, and to support the analysis of ancient DNA data within larger consortia.

The position is fully funded with a competitive salary for three years, with the possibility to extend by one additional year. The successful candidate should ideally start in Summer 2021. The project does not involve lab work, unless specifically desired by the candidate.

What we offer We offer a stimulating research environment, well embedded in the strong bioinformatic and conservation communities in western Switzerland. We are part of the Swiss Institute of Bioinformatics (SIB) and boost excellent research facilities, including state-of-the-art high-performance computational infrastructures. Fribourg is a lively university town with pleasant surroundings (such as the Alps) and an excellent quality of life. It is located only 20 minutes from the capital of Switzerland, Bern, and just a little over an hour from Geneva and Zürich. While some knowledge of German or French is beneficial for living in Switzerland, it is not essential. The working language in our lab and institute is English.

What you bring You should have a master degree in bioinformatics, computational biology, computer science, statistics or a related field, and a strong interest in applying these skills to bioinformatics. While a plus, experience in programming is not strictly required. But we expect candidates to be highly motivated to acquire skills in programming and statistical inference, for which we are happy to provide state-of-the-art training. Good knowledge of written and spoken English is expected.

How to apply To receive full consideration, apply before May 15 at https://forms.gle/7ehFod3uo59CizNx8 with a single PDF file including a cover letter with a brief summary of your previous research and motivation for the position. a Curriculum Vitae. copies of degree certificates and list of coursework, including grades. names, addresses and emails of two professional references.

Further information on our lab http://www.wegmannlab.com https://www.sib.swiss/daniel-wegmann-group **Recent papers on the topic** https://doi.org/10.1101/105346 https://doi.org/10.1534/genetics.116.189985 https://doi.org/10.1016/j.cub.2020.08.033 https://doi.org/10.1126/science.aaf7943 https://doi.org/10.1073/pnas.1523951113 – Prof. Dr. Daniel Wegmann Department of Biology University of Fribourg Chemin du Musée 10 1700 Fribourg Switzerland

wegmannlab.com

+41 (0)26 300 89 49 daniel.wegmann@unifr.ch

Daniel Wegmann <daniel.wegmann@unifr.ch>

UGothenburg
ConservationGeneticsSeagrass

Graduate position: UGothenburgTjärnö.ConservationGeneticsSeagrass

PhD student in Conservation Genetics of Seagrass

Ref PAR 2021/511

The University of Gothenburg tackles society's challenges with diverse knowledge. 37 000 students and 6 000 employees make the university a large and inspiring place to work and study. Strong research and attractive study programmes attract scientists and students from around the world. With new knowledge and new perspectives, the University contributes to a better future.â€â€ The University of Gothenburg promotes equal opportunities, equality and diversity.

Type of employment: Fixed-term employment, 4

yearsâ€Extent: 100 %â€Location: Department of Marine Sciences, University of Gothenburg First day of employment: As soon as possible

The Department of Marine Sciences, the Faculty of Science, University of Gothenburg, was recently launched (July 1, 2015) with the purpose to achieve the vision of "A University with marine research, teaching and cooperation of the highest international class" (https://www.gu.se/en/marina-vetenskaper) . The department has about 110 employees - researchers, teachers, PhD students, technicians and administrators. The department carries out teaching and research in the various marine specializations, biology, oceanography, chemistry, marine geology, conservation of underwater cultural heritage, and environmental science. The Department is situated in Gothenburg and at the University's research stations at Tjärnö and Kristineberg. This position is placed at the Tjärnö Marine Laboratory, a stimulating work place on an island on the Swedish west coast, ca 2hrs North of Gothenburg (https://www.gu.se/en/tjarno).

Project description We have one PhD position available to work on the new research project funded by the research council FORMAS "Genetic population structure of Baltic Sea eelgrass - urgent information for conservation of a foundation species under climate change". Biodiversity loss and climate change are two of the grand challenges of our time. Maintaining biodiversity, within and between species and ecosystems, will become increasingly important to avoid the worst impacts of climate change. Despite the fact that genetic diversity is the level where natural selection and evolution of new adaptations affect individual and species survival, genetic diversity is rarely considered in environmental conservation.

The seagrass Zostera marina (eelgrass) is one of the most important habitat-forming species along northern temperate coasts world-wide, as well as around the Swedish coast. Eelgrass meadows have declined considerably and are at risk of further decline due to climate change, not least in the Baltic Sea. To mitigate further losses, genetic diversity must be taken in to consideration when developing management plans. This is clearly demonstrated by our earlier work showing a surprising genetic complexity of eelgrass on the Swedish west coast. Focusing on the Baltic Sea, we will use I) genomics to provide a baseline of current genetic diversity and connectivity for future genetic monitoring of Baltic eelgrass and to explore local adaptation; II) oceanographic modelling of current and future climate scenarios, useful for prioritizing meadows for protection and restoration; and III) demographic modelling to assess meadows' ability to recover and adapt in the future. We encourage applicants

that are keen to develop their own research within and beyond the above described project.

We are seeking an independent and collaborative person with a background in population genetics/genomics to pursue PhD studies in Marine Sciences. The PhD project will focus on population genomic assessments of a seagrass in the Baltic Sea to provide a baseline for future temporal conservation genetic monitoring of eelgrass in Sweden. Investigating into local adaptation, genetic demographic modelling and species distribution modelling can then help to address persistence and adaptation potential under predicted climate change. The research project itself is very collaborative and will involve collaboration with international and Swedish researchers.

Job assignments The main task is to conduct a PhD thesis under supervision within the research theme described above. Techniques used within the project include: molecular lab skills (DNA extractions, PCR, library preparation, gel electrophoresis etc), bioinformatic skills for genomic data analysis, statistical analyses, writing of scientific articles and dissemination of scientific results at both international and national conferences and seminars. There will also be opportunities for field work and mesocosm experiments.

Previous knowledge on molecular lab and bioinformatic analyses of SNP

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UInnsbruck HeatwaveAdaptation

A PhD student position is available in the group of Aquatic Evolutionary Ecology at the University of Innsbruck (Research Department for Limnology, Mondsee), Austria.

In this position, you can experimentally examine the evolutionary ecology of the responses of the freshwater snail Lymnaea stagnalis to changing environmental conditions under climate change. The specific goals are to evaluate (1) evolutionary potential (i.e., quantitative genetic variation) in snails' phenotypic responses to heatwaves, (2) the relative importance of different

genetic and non-genetic factors in determining these responses, and (3) the dependence of the expression of genetic variation on ecological factors that vary in nature (e.g., food availability). Available resources for research include inbred snail lines for quantitative genetic breeding designs. The project is linked to other work in the research group that focuses on the evolutionary adaptation of organisms to environmental change and natural enemies.

General information about the research group and the institute can be found at https://www.uibk.ac.at/limno/ The Research Department for Limnology is located on the edge of the Alps in the small town of Mondsee (Upper Austria). The nearest city is Salzburg, which offers history, culture and entertainment at a convenient distance from Mondsee.

We invite highly motivated students with a strong background in evolutionary ecology and experimental research to apply for this position. A master's degree (or equivalent) is required. Earlier experience with the study system is not necessary.

The project is funded by the Austrian Science Fund (FWF) for 4 years. The salary is based on the personnel cost rates of the FWF https://www.fwf.ac.at/-en/research-funding/personnel-costs . Earliest starting date: July 1, 2021.

Qualified persons are invited to apply by email. Please attach a single PDF file including a letter of motivation, CV, a research statement (max 2 pages), and names plus contact information of two references to otto.seppaelae@uibk.ac.at. The subject line should read "PhD-position 2021". Evaluation of the applications starts May 17, 2021. Only complete applications are considered. Top candidates will be interviewed.

Prof. Otto Seppälä

Universität Innsbruck

Forschungsinstitut für Limnologie, Mondsee Mondseestraße 9, A-5310 Mondsee E-Mail otto.seppaelae@uibk.ac.at

"Burggraf, Sonja" <Sonja.Burggraf@uibk.ac.at>

About 400 species of carabid beetles form an abundant and diverse assemblage in agricultural systems throughout the Canadian Prairies. Most of these species are considered beneficial by virtue of being parasitoids or predators of pest insects, or by feeding on weed seeds. The taxonomy, distribution and life-history for most of these beetles is well-known, and large numbers of specimens can be readily collected with use of pitfall traps. Because of these features, carabid beetles have been extensively studied as biological indicators of environmental change.

The gut microbiome of insects plays a critical role in the breakdown and assimilation of food items by the host. Factors that affect the microbiome (e.g., diet, chemical residues, temperature) can influence the survival and reproduction fitness of the host and the ecosystem services that they provide. Few studies have described the gut microbiome of carabid species.

The proposed research will use next generation sequencing methods to compare the gut microbiome of selected carabid species representing different trophic levels (e.g., parasitoid, predator, seed-feeder) under different conditions such as diet, crop type (e.g., cereal, oilseed), and exposure to agricultural chemicals (e.g., herbicides, fungicides). Results will describe the core microbiome of these species and their resilience to abiotic and biotic factors.

The successful applicant will be co-supervised by Drs. Theresa Burg < https://directory.uleth.ca/-users/theresa.burg > (Department of Biological Sciences, University of Lethbridge) and Kevin Floate < https://profils-profiles.science.gc.ca/en/profile/dr-kevin-floate > (Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada).

Students interested in pursing this opportunity are encouraged to send an email to Dr. Theresa Burg (theresa.burg@uleth.ca) before April 20. Applications receive after this date will not be considered.

theresa.burg@uleth.ca

ULethbridge BeetleMicrobiome

A MSc position is anticipated starting September, 2021 to study the gut microbiome of carabid beetles (Coleoptera: Carabidae).

UPadua EvolutionEcolConservation

Call for PhD students in Ecology, Evolution and Conservation at Department of Biology, Padua University, is open: apply by May 12, 2021

Start date: Oct 2021

Information about the available topics, the training program and the application procedure can be found at https://dottorato.biologia.unipd.it/ The board of the curriculum EVOLUTION, ECOLOGY and CONSERVATION of the BIOSCIENCES PhD program at Padua University invites applications from highly motivated and outstanding students with specific interest for evolutionary and ecological research.

Padua University is top ranked in Italy and among world Universities. The Department of Biology is rated as excellent by the Italian Ministry of Education, Universities and Research (MIUR).

Our PhD students have access to first-class facilities at the Biology Department and work within a friendly and strong international research community under the supervision of experts of the field. Research opportunities are multi-disciplinary, spanning the whole range of biological research. Interdisciplinary approaches are encouraged as well as the interaction among PhD students (approx. 40 PhD students are enrolled at the Bioscience PhD program), post-docs and the over 70 faculty members of the Department.

Proposed research topics for 2021 include: - Exploring species interactions in wetland restoration and their effects on ecosystem processes and services - Unveiling fine-scale patterns of biodiversity above and below the ground in a terrestrial European hotspot - ABC: microAlgae, Bivalves and Crustaceans as model organisms to assess transfer and effects of emerging contaminants through a marine food chain - Estimating survival rates of juveniles of sharks, skates and rays to develop effective management strategies for fishery - Mitochondrial genes and the pace of life in fish - Social, environmental, and evolutionary dynamics of replicated hybrid zones in swordtails (Teleostei: Xiphophorus) of Mexico's Sierra Madre Oriental

Based on excellence of applications 2-4 research projects can be funded. Details on the potential research projects and contact persons are reported in https:/-/dottorato.biologia.unipd.it/fileadmin/dottorato/-

Evolution_Ecology_and_Conservation_2021.pdf Candidates are encouraged to carefully read the potential research projects and to email the reference persons indicated therein for further details.

On behalf of the Evolution, Ecology and Conservation board

Lorenzo Zane (lorenzo.zane@unipd.it) Professor of Ecology Department of Biology Padua University (IT)

"lorenzo.zane@unipd.it" <lorenzo.zane@unipd.it>

UPrague AndeanEvolution

A *master's thesis* project is available!

Title of the thesis: Evolution of the high Andean genus /Loricaria/ (Asteraceae)

Starting date: *October 2021*

Project summary: The tropical high Andes, one of the fastest evolving *biodiversity* hotspots, are known for extreme habitats, unique climatic conditions, and spectacular evolutionary radiations. Diversification of lineages in these *heterogeneous landscapes* is triggered by various effects and differs between lineages.

This master's project will concentrate on the high Andean genus /Loricaria/, using *state-of-the-art methods in genomics and ecological modeling*. Is diversification in /Loricaria/ related to climatic changes in the past? Is speciation driven by valleys that act as barriers or by climatic niche differentiation?

Tasks will include wet-lab work, phylogenomics, and climatic modeling.

Requirements: You should bring a strong interest in evolution. No bioinformatic knowledge is required, but depending on interest can be learned. Good communication skills are needed for this position, as you will become part of an international team.

Why you should join us: We offer a creative and supportive scientific atmosphere, which will give you the opportunity to develop your scientific career.

Questions and applications (CV, including an outline of relevant courses + half-page motivation letter) should be sent to Roswitha Schmickl (roswitha.schmickl [a] natur.cuni.cz) or Martha Kandziora (kandziom [a] natur.cuni.cz). Please send your application until *30th April 2021*.

Dr. Martha Kandziora Independent Researcher Department of Botany Faculty of Science Charles University

Martha Kandziora <kandziom@natur.cuni.cz>

URennes ClimateAdaptation

Dear all

Sorry for possible cross posting. Please distribute as appropriate.

This is to inform you about a PhD project on "Resisting climatic stress due to genetically or phylogenetically distant neighbours: from the tree to the forest". The project is one out of 4 for in our research unit competing for 2 fundings. The project is supervised by Andreas Prinzing (links below), Matthew Potts (https://nature.berkeley.edu/pottslab/) and Freerk Molleman (https://www.researchgate.net/profile/Freerk-Molleman). Note the multiple-step application procedure indicated below.

The project: The climate is becoming increasingly hot and dry in most of Europe, which threatens forest trees: the plasticity or resistance of their seasonal phenology is insufficient in the face of climate change. As a consequence, the forest ecosystem is neither resistant nor resilient to current climate change. To deal with this problem, foresters are trying to adapt forests by planting tree species or genotypes that are more resistant to future climatic conditions. These species and genotypes are introduced from warmer and drier regions. However, introductions of new species or genotypes risk to trigger biological invasions. Management strategies favoring the resistance or resilience of native genotypes and species are needed. We propose such strategies, taking into account the interactions between trees via the natural enemies shared among trees, in particular among evolutionarily closely related trees. The work therefore contributes to an evolutionary ecology of the forest ecosystem, applied to management under climate change. The work will profit from the analysis of major databases of long-term observations and common garden experiments.

Scientific and technical skills required by the candidate: Knowledge of ecology, evolutionary biology, plant-animal interactions, or forestry. Knowledge of data processing and quantitative analysis. Driving license.

Net salary ca. 1400 Euros/month for three years. Contract as employee, i.e. with health insurance etc..

The host lab here is the Research Unit ECOBIO - Ecosystems, Biodiversity, Evolution, co-funded by University of Rennes 1 and Centre National de la Recherche Scientifique. See

http://ecobio.univ-rennes1.fr/ . Ecobio was ranked A in the national evaluation of research institutions. Several further research institutions in ecology and evolutionary biology exist at Rennes.

The location: Rennes has approximately 200 000 inhabitants and is the capitol of the Bretagne region with exceptional coastal and mainland landscapes, and a french-celtic heritage (https://www.brittanytourism.com/). It is situated some 1.5 hours by train from Paris. English is spoken everywhere in academia, but not necessarily by everybody outside. Like in any French city, child care is excellent (almost for free, no waiting list, nearby). Several bilingual French-English schools are available at all levels of education, as well as one French-German grammar school. Living costs at Rennes are indicated here: https://www.crous-rennes.fr/international/prevoir-son-budget/ (- budget à prévoir à Rennes 2020).

More information on the project and the application procedure at

https://theses.doctorat-bretagneloire.fr/egaal/copy_of_theses-2020 - Ecologie - Ãcosystèmes - Biodiversité - Ãvolution - UMR 6553 UR1 CNRS [ECOBIO] / 7. Formal deadline is May/27 **If interested, please directly contact me directly (andreas.prinzing@univ-rennes1.fr) at least a week before, i.e. latest May/20 **

Best regards Andreas Prinzing

Andreas Prinzing, Prof.

Ecology of Diversification Research Unit "Ecobio: Ecosystems - Biodiversity - Evolution";

Université de Rennes 1 / Centre National de la Recherche Scientifique

Campus de Beaulieu, Bâtiment 14 A ; 35042 Rennes, France Tél. +(33) 02 23 23 67 12- Fax: +(33) 02 99 28 50 26 - E-Mail: andreas.prinzing@univ-rennes1.fr https://www.researchgate.net/profile/Andreas-Prinzing-2 https://scholar.google.com/citations?user=w5Ogsc0AAAAJ&hl=en "andreas.prinzing@univ-rennes1.fr" <andreas.prinzing@univ-rennes1.fr>

USGS Colorado PtarmiganPopulations

Two (2) PhD or MS Assistantships in Ecology to Study White-tailed Ptarmigan Population Processes (Demographics and Genomics)

We are recruiting two graduate students to study white-tailed ptarmigan population dynamics in the southern Rocky Mountains of Colorado. This research is part of a continuing long-term study of two ptarmigan populations (Mt. Evans and Trail Ridge [Rocky Mountain NP]) that began in 1966. The first student (Demographic) will investigate habitat relationships by combining newly collected VHF-telemetry data with an existing location database and applying resource selection functions to model quality habitats, and predict likely future changes to habitat under various climate scenarios. This student will also conduct field work to monitor breeding activities during the spring and summer, and construct population models used to estimate various demographic rates and processes. The second student (Genomic) will have access to a full genetic catalog of biological samples collected from every banded white-tailed ptarmigan captured within the past 15 years, with associated repeated measurement data on timing of breeding events (for females) and demographic data. This student will potentially conduct paternity analyses, and relatedness matrices for use in animal models to evaluate the adaptive nature and evolvability of timing of breeding and molt. This student will also participate in the collection of field data. There will be considerable freedom for both students to develop their own research program, so long as they align at least somewhat with these research topics.

Those interested in applying for a PhD assistantship must have a MS degree in wildlife biology, ecology, statistics, or a closely related field. We prefer to hire PhD students for both positions, but will also consider outstanding students with a bachelor's degree given they have demonstrated field and research/quantitative experience. Please make sure to highlight such experience in your cover letter. Ideally, students will be available to begin field work in late-May or June of 2021, and begin taking classes in the fall (mid-August) of 2021. There may be some flexibility in this start date, but coursework must begin in August. Please specify which position you are applying for in your cover letter, what skills you have that would make you ideal for this position, and why you could be a good candidate.

Required Qualifications:

* MS (PhD applicants) or BS (MS applicants) in wildlife biology, statistics, or related field * Excellent written and oral communication skills * Excellent organizational skills * Ability to work independently in rugged and sometimes isolated wilderness * Demonstrated coursework in statistics, population genetics, or demographic modeling (MS) * Demonstrated research thesis or publications (PhD)

Desired Qualifications:

* Strong quantitative skills, including Bayesian hierarchical modeling, mark-recapture analyses, or generalized linear models * Experience coding in R or Python, including GIS spatial processing * Knowledge of avian biology or alpine ecosystems

Students would be enrolled in the Graduate Degree Program in Ecology at Colorado State University and directly advised by Dr Cameron Aldridge who is a Research Ecologist at the USGS Fort Collins Science Center and an Affiliate Faculty at CSU; Dr. Sara Oyler-McCance who is a Research Geneticist with USGS and runs the Molecular Ecology lab at FORT; and Dr. Greg Wann, who is also an Ecologist at USGS-FORT. This is a unique team of wildlife ecologists, who are experts in the fields of ecology, population demography, resource selection, grouse and ptarmigan ecology, quantitative modeling, and applied genetics and genomics.

Colorado State University (http://admissions.colostate.edu/) has prolific research in natural resources (http://warnercnr.colostate.edu/) and a world class Graduate Degree Program in Ecology (http://ecology.colostate.edu/). CSU is located in beautiful Fort Collins, on the foothills of the Rocky Mountains, and has been voted as one of the best places in the United Sates to live.

Compensation includes annual stipend of ˜$26,000 (MS) or ˜$27,000 (PhD), plus tuition and benefits.

Individuals interesting in applying for this position should contact Dr. Cameron Aldridge (aldridgec@usgs.gov), with the subject Title: "Ptarmigan Positions". Please send 1) a cover letter explaining your long-term career/research goals and academic interests, 2) a copy of your current CV (resume), 3) GRE scores and unofficial transcripts, 4) names, addresses, and e-mail contacts for three references. Applications will be evaluated upon receipt. Deadline to apply: May 02, 2021

"Fike, Jennifer" <fikej@usgs.gov>

UToulouse
ModelingHostPathogenInteraction

PhD student position in modeling of host-pathogen interaction

Job description

Applications are invited for a 3 year position as a PhD Research Fellow in Evolutionary Biology at the Evolution and Biodiversity lab in the University of Toulouse, France. The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD program at the SEVAB Doctoral School.

Starting date

01/10/2021

Description of the project: Intra-host dynamics of a bacterial pathogen: mathematical modeling and statistical inference.

Most of the interactions between a pathogen and its host arise during the infection, when pathogens proliferate inside the host. These interactions have shaped both the evolution of our immune system and that of the pathogens which infect us. The main goal of the project is to study the within host dynamics of a pathogen to better understand these selective pressures.

It may seem relatively easy to measure the immune response of a host: immune cells can be counted, antibodies can be quantified, the expression of immunity genes can be assessed, etc. But all these molecular measurements are usually restricted to a part of the immune response (e.g. the expression of a small number of immunity genes are measured) and do not really tell what effect it has on pathogens. As such, these measurements do not describe the interaction we are interested in.

If we are to really understand how immunity works, we rather need to describe its effect on pathogens, while taking into account all possible types of immune responses and their respective regulation. Recent experimental work has shown that it is possible to study in details the dynamics of bacterial pathogens inside the experimental host Drosophila melanogaster, and that this dynamics reveals some aspects of the global immune response of the host.

The aim of the PhD is:

1/ to design and study mathematical models that describe the intra-host dynamics of a pathogen in order to better understand what it reveals of its interaction with the immune system of its host;

2/ to develop methods (e.g. maximum likelihood) that will allow to adjust the model on experimental measurements of within-host pathogen dynamics;

3/ to use these tools to study how the host resists or tolerates infectious diseases;

4/ to integrate the models in an evolutionary perspective, with the possibility for example to study how pathogens will evolve depending on the defense strategy the host uses.

Qualification requirements:

- Applicants must hold a Master's degree or equivalent in evolutionary biology or in applied mathematics.

Good programming skills (e.g. in C++ or R) will be appreciated, the wish to learn will be required!

Experience in advanced statistical analysis

- Good communication skills (including written and spoken English)

Preferred experience (experience with one or more of these would be

beneficial):

Experience in basic microbiology

- Experience in insect rearing, especially with Drosophila melanogaster

We offer:

- Net salary is 1500 euros per month

- Challenging research questions and a friendly working environment

- The campus of University Paul Sabatier is close to the city center of Toulouse. The Pyrénées are only 150km away and accessible by railway!

How to apply:

Candidates should send their application to jean-baptiste.ferdy@univ-tlse3.fr. The selected candidate will be interviewed by the SEVAB Doctoral School the 5th or 6th of July 2021.

The application must include:

Application letter including a one-page statement explaining how a PhD in the actual research field will fit into the applicant's career plan

- CV (summarizing education, positions and academic work, scientific publications and other relevant experi-

ence)

List of publications and academic work that the applicant wishes to be considered by the evaluating committee

Names and contact details of 2-3 references (name, affiliation, relation to candidate, e-mail). The references will be contacted if necessary. Letters of recommendation are therefore not required for the initial application.

Jean-Baptiste Ferdy jean-baptiste.ferdy@univ-tlse3.fr
Jean-Baptiste Ferdy jean-baptiste.ferdy@univ-tlse3.fr

Vienna MolecularEvolution

Ph.D. student position in molecular evolution

Are you intrigued by the still elusive link between genome evolution, natural selection, and species adaptation? Then, this Ph.D. position and excellent Ph.D. program might be a good fit for you:

Topic: Molecular evolution of coding sequences

Advisors: Rui Borges (Vetmeduni Vienna) and Carolin Kosiol (University of St. Andrews)

Description: A major goal in evolutionary biology is to understand the forces that operate in the genomic sequences and are responsible for the adaptation of species to different environments. Codon models are one of the main tools used to infer selection on protein-coding genes. These have been popularized in comparative genomic studies by their extensive use in genome-wide scans of natural selection. However, current models of codon evolution have significant limitations that are increasingly being recognized. The main one being that current codon models make simplistic assumptions about the evolutionary process: e.g., fluctuating demography and GC-biased gene conversion. This Ph.D. project seeks to develop a new codon evolution model to detect signatures of natural selection on protein-coding sequences. By properly reconciling the neutral and adaptive processes by which coding sequences evolve, the models and methods developed in this project will allow us to tell apart the sole action of natural selection from known confounding forces. This project will ultimately contribute to better understanding the dynamics of adaptation during species divergence. More info: https://mrborges23.github.io/mypage/pomocod
Profile: The project is particularly well-suited for students with a keen interest in computational biology,

phylogenetics, or population genetics. Prior experience in programming or statistics would be a plus.

Doctoral program: The successful candidate will integrate the Vienna Graduate School of Population Genetics, which comprises an extensive network of evolutionary biologists in Vienna. Depending on the project, Ph.D. degrees will be awarded either in genetics, mathematics, or statistics. More info: https://www.popgen-vienna.at/ Duration: Three years

Starting date: Ideally, September 2021 or earlier

Application: https://www.popgen-vienna.at/-application/procedure/ Place: Institute of Population Genetics, Vetmeduni Vienna (https://-www.vetmeduni.ac.at/en/population-genetics/)

Salary: 2,237.60Â (before tax) times 14 months, which represents a fairly good salary for the standard living conditions in Vienna.

Funding agency: FWF (Austrian Science Fund) through the project P34524-B.

Application deadline: May 16, 2021

Questions about the project: Rui Borges (ruiborges23_at_gmail.com)

Questions about the doctoral program: Julia Hosp (julia.hosp_at_vetmeduni.ac.at)

Rui Borges <ruiborges23@gmail.com>

Vienna PopulationGenetics

Reminder: Call for PhD students closes May 16th

Start date: Sept 2021 (or earlier)

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

We invite applications from highly motivated and outstanding students with a love for evolutionary research and a background in one of the following disciplines: evolutionary genetics, functional genetics, theoretical or experimental population genetics, bioinformatics, mathematics, statistics.

Topics include:

- Evolution from de novo mutations - influence of ele-

vated mutation rates. - Evolution of sex-specific neuronal signaling. - Genome evolution in columbines. - Inference of selection signatures from time-series data. - Long-term dynamics of local *Drosophila *populations. - Molecular evolution of coding sequences. - Molecular genetics of epigenetics. - PoPoolation3 - Seed ecology. - Structural variation and genome evolution. - Temperature adaptation in *Drosophila*: phenotypic adaptation. - The sources of diversity shaping adaptive radiation. - Understanding polygenic adaptation.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 16, 2021 will be considered. Two letters of recommendation need to be sent directly by the referees.

Depending on the project, PhD degrees will be awarded either in genetics, mathematics or statistics. PhD students will receive a monthly salary based on currently 2.237,60 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator

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

Current home office contact via Skype: julia.hosp Office: +43 1 25077 4338 (currently unavailable)

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

Jobs

BournemouthU ComputationalGenomics

The department of life and environmental sciences at Bournemouth University is currently hiring 4 lecturers (permanent position) in :

- Computational genomics (https://-www.bournemouth.ac.uk/lecturer-academic-computational-genomics) - Systems biology (https://www.bournemouth.ac.uk/lecturer-academic-systems-biology-0) - Biomedical science (https:-//www.bournemouth.ac.uk/lecturer-academic-biomedical-science) - Environmental forensics (https://www.bournemouth.ac.uk/lecturer-academic-environmental-forensics)

The detailed job description and information on how to apply can be found on our website : https://www.bournemouth.ac.uk/about/jobs/all-vacancies/academic-roles Best regards

Emilie

Dr. Emilie Hardouin Principal Academic in conservation genetics Deputy head of Departement of Life and Environmental sciences Bournemouth University Faculty of Science and Technology Christchurch House Talbot Campus Poole, Dorset BH12 5BB United Kingdom

Tel: +0044 (0)1202 962402

Emilie Hardouin <ehardouin@bournemouth.ac.uk>

CaliforniaAcademySciences LabTech ComparativeGenomics

Lab Technician, Center for Comparative GenomicsCalifornia Academy of Sciences

We hope you are inspired by what we do and are excited to contribute to our mission. The Academy is looking for candidates who do great work, and we know they may come from a number of different backgrounds and experiences. We encourage you to apply even if you don't believe you meet every Â'one of the qualifications for the position.

POSITION SUMMARY: Under the supervision of the Assistant Director of the Center for Comparative Ge-

nomics, the Lab Technician will: 1) Serve as CCG HAZMAT Monitor; 2) Support California Academy of Sciences' researchers with molecular work; 3) Assist in the development of new lab protocols; 4) Support the training of students, visitors, and staff in molecular techniques; and 5) Assist with lab equipment maintenance. This is a temporary 30 hours/week position with the strong possibility of extending to a regular full-time position.

POSITION DUTIES AND RESPONSIBILITIES: Reasonable accommodations may be made to enable persons with disabilities to perform the essential functions.

LAB MAINTENANCE

- Prepare aliquots of reagents for general lab use - Prepare stock solutions for use in the lab - Stock lab consumables (tubes, tips, etc.) for general lab use - Inventory frozen DNA collection - Assist with chemical inventory - Assist with accounting, billing, budgeting

LAB SAFETY

- Handle HAZMAT Monitor duties for the CCG - Handle Health & Safety Monitor duties for the CCG

MOLECULAR WORK

- DNA and RNA extraction - Assist with operation maintenance of DNA sequencers (ABI3130 & MiSeq) - DNA Sequencing (Sanger, NGS, long read sequencing, Hi-C etc.) - Training students, visitors, and staff in the above techniques - Assist with new user orientation

COMPUTER WORK

- Assist with cryogenic database management - Assist with cryogenic collection duties - Assist with public database submission (Genbank, Dryad, etc.)

OTHER

- Follow all Academy safety regulations - Other duties as assigned

MINIMUM QUALIFICATIONS: The qualifications listed below are representative of the knowledge, skill, and/or ability required or preferred.

EXPERIENCE:

- Bachelor's degree in biological sciences or equivalent - Minimum two years' experience in standard PCR/Sanger sequencing-based laboratory protocols - Experience in second and third generation sequencing techniques and protocols preferred (but not required)

KNOWLEDGE, SKILLS AND ABILITIES:

- Good communication and organizational skills - Ability to work as a member of a team - Ability to perform repetitive work - Perform standard PCR and DNA se-

quencing lab work - Familiarity with second and third generation sequencing techniques - Experience using relevant DNA analyses programs, MS Office and FileMaker Pro - Ability to read and interpret documents such as safety rules, operating and maintenance instructions, and procedure manuals - Ability to write routine reports and correspondence - Ability to lift 10 lbs. - Ability to perform repetitive motions 20% of the time

WORK ENVIRONMENT: The physical expectations described here are representative of those that must be met by an employee to successfully perform the position duties and responsibilities. This position spends about 30% of the day working in a fixed location at a desk at a computer. The reminder the time will be spent on general upkeep of the lab.

APPLICATION DEADLINE: May 10, 2021 5:00 PM PST. Applications will be accepted and reviewed on a rolling basis.

HOW TO APPLY: Please submit a resume and complete a brief online application at https://-/californiaacademyofsciences.applytojob.com/-apply/MHLC2Ba3nx/Lab-Technician-Center-For-Comparative-Genomics –

Paula Duarte HR Assistant Pronouns: she/her/hers

California Academy of Sciences T 415.379.5875

pduarte@calacademy.org

55 Music Concourse Drive Golden Gate Park San Francisco, CA 94118 www.calacademy.org Facebook < http://www.facebook.com/calacademy > | Twitter < https://twitter.com/calacademy > | Instagram

< https://www.instagram.com/calacademy/ >

The California Academy of Sciences is now open! Learn how we're keeping guests safe-and make reservations < https://www.calacademy.org/reopening > for your next visit today.

pduarte@calacademy.org

Chicago
ComputationalSpeciesConservation

The Species Conservation Toolkit Initiative (SCTI), hosted by the Chicago Zoological Society (CZS), has an opening for a Computational Biologist who will work as part of the small team of conservation scientists to design, build, and support software that is used globally by wildlife managers, researchers, and students. SCTI is a multi-institutional, international partnership to ensure that the new innovations and tools needed for species risk assessment, conservation planning, and managing populations are developed, are globally available, and are used effectively. The initiative leverages expertise in population biology, computer programming, and species conservation planning. You may learn more by visiting https://scti.tools/ More details regarding this position are available on the CZS career site (https://sjobs.brassring.com/TGnewUI/-Search/Home/Home?partnerid=3D25814&siteid=-5163#jobDetails=662003_5163). Anyone who is interested in being considered for this opening is encouraged to visit the CZS Career Center to obtain more details about the position and to apply by submitting a profile as soon as possible. Please visit our website at www.czs.org/careers and look for requisition number 2149BR.

Primary duties and responsibilities: Professionally represent the Species Conservation Toolkit Initiative (SCTI) and CZS externally to organizations, groups and individuals including, but not limited to, local, national, and international conservation groups, zoological associations, and the academic community.

Participate in the creation of novel software solutions and enhancement of existing software packages to both solve immediate conservation needs and improve the state-of-the-art for conservation software tools. Plan and execute all aspects of the software development life cycle as needed.

Remain current with changes in the scientific software ecosystem, software development trends, and computational biology advances and integrate emerging tools and protocols into SCTI common practices. Improve SCTI operations by conducting systems analysis and collaborating with peers to implement changes in policies and procedures.

Remain connected with the conservation community to understand current and emerging software needs. Confer with SCTI tool users and analyze work processes, dataflow logic, and information needs.

Work with SCTI, CZS, and external scientists to write, develop, and coordinate grant applications to fund SCTI activities and needs.

Coordinate and conduct research that furthers our understanding of population management and sustainability. Monitor the professional literature in conservation biology to remain current on science related to in situ and ex situ population management and population viability monitoring. Work collaboratively with other

scientists within SCTI, CZS, and the greater conservation community.

Prepare reports for scientific peer-reviewed publication and presentation at professional meetings. Communicate progress and advances in software tools to the conservation community.

Coordinate or assist in educational, outreach, and other special programs (modeling training, conservation workshops, etc.) to meet the needs of the conservation community. Provide technical support and help to provide training to conservation professionals and graduate students using modeling methods and tools.

Manage SCTI cloud resources including the team website and communication suite. Other related duties as assigned.

The requirements for this position include the following: * Ph.D. degree in conservation biology, evolutionary biology, population biology, or related field. * Three years of experience in conservation biology research or species management required. * Experience with object-oriented programming languages, CMS administration, and modern software architecture patterns. * Excellent verbal and written communication skills, including proven ability in writing of reports and scientific papers, grant proposal preparation, and oral presentations. * Excellent critical thinking and problem-solving skills. * English fluency at a full professional proficiency required. * Ability to work independently and collaboratively as part of a team. * Ability to maintain the confidentiality of privileged information is essential. * Cultural competency; experience and/or ability to work and interact effectively with a diverse, multicultural audience.

The preferred qualifications: * Broad research and conservation interests. * Experience using SCTI software (Vortex, PMx, Outbreak, or MetaModelManager) or other modeling software (i.e., RAMAS, ST-Sim, PML & StudbookR, HexSim, etc.). * Experience in population viability analysis and/or management of in

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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

ColumbiaU ResTech
TickDiseaseEvoEco

Part time lab technician:

Overview: The Diuk-Wasser in the Department of Ecology, Evolution and Environmental Biology

is looking to hire a part time lab technician for molecular and field work to study tick-borne disease pathogens. This is a 12-month term appointment with the possibility of extension contingent on successful performance and continued funding.

Responsibilities: The lab's work focuses on studying the evolution and ecology of tick- borne pathogens by collecting field samples during the summer months, conducting quantitative PCR and tissue culture, and animal-tick transmission experiments to study evolutionary mechanisms during the academic year (see https://ecoepidemiologylab.e3b.columbia.edu). The technician would assist in all these activities, help order reagents for the lab as well as help coordinate and prepare for the field sampling season.

Expected breakdown of work hours: Conduct DNA extractions and quantitative PCR. 30% Project management for the Diuk-Wasser Lab. 25% Collect field samples during the summer months. 20% Coordinate and prepare for the field sampling season. 15% Help order reagents for the lab. 10%

The ideal candidate will have experience with DNA extractions and quantitative PCR, will have previous field experience (not necessarily collecting ticks) and have experience working with laboratory animals (optional). The candidate should have a strong interest in disease ecology and will participate in providing support to students and postdocs in the lab. The candidate should have excellent communication skills, have meticulous attention to detail, and exhibit strong project management skills.

Minimum Qualifications: - Bachelor's Degree in the biological sciences - Two years of experience in a research environment. - Experience working in a molecular laboratory and some field experience.

Preferred Qualifications: - A graduate degree in Ecology/Biology/Evolution and experience in pathogen screening. - Strong dedication and organizational skills evidenced in recommendation letters (2 letters required) - Molecular experience: DNA extraction, quantitative PCR. - Field experience (tick sampling, mammal trapping) - Laboratory animal experience

Other information: Location: Columbia University, Morningside Campus, New York City, NY Job Type: Support staff, non-union Hours per week: 20 Salary range: $23,202.40 Minimum

Equal Opportunity Employer / Disability / Veteran

Columbia University is committed to the hiring of qualified local residents.

To apply, visit: https://opportunities.columbia.edu/-en-us/job/513430/lab-technician# Matthew Combs <matthewcombs2@gmail.com>

Guam ResAssoc 2 MarineConservation

Marine Microbiology and Marine Ecophysiology - Guam EPSCoR at the University of Guam

Marine Microbiologist (JOB# RC-21-45) https://www.uog.edu/_resources/files/rcuog/-_job_announcements/ja_2021/pt_ft_positions/RC-21-45_SENIOR_RESEARCH_ASSOCIATE_MICROBIOLOGIST.pdf Marine Ecophysiologist (JOB# RC-21-45) https://www.uog.edu/_resources/files/rcuog/-_job_announcements/ja_2021/pt_ft_positions/RC-21-46_SENIOR_RESEARCH_ASSOCIATE_ECOPHYSIOLOGIST.pdf Guam EPSCoR is recruiting two senior research associates to develop and implement a competitive research program under the umbrella of the Guam Ecosystems Collaboratorium for Corals and Oceans. The focus of this $20,000,000 project is understanding the genetic and phenotypic traits that confer resilience to reef-building corals and their associated communities in a changing climate. For more information about the project and the team of researchers please visit our website and consult Guam EPSCoR's strategic plan (https://guamepscor.uog.edu/about-guam-epscor/).

Both positions are open until filled, with initial review of applications to begin on May 10, 2021. The positions are currently funded for the duration of the project until June 30, 2025. Compensation is commensurate with experience ($55,488 to $76,164 per year plus benefits).

The successful candidate will have access to a state-of-the art genetics laboratory, flow-through water systems for experimental work, and field sites in close proximity to conduct in situ experiments. Guam hosts a variety of near-shore reef systems, including several sites that cover environmental gradients (eg, sedimentation) that lend themselves to conducting experiments on corals and other reef organisms under natural conditions. Additional infrastructure developments, including the outfitting of ecophysiology and microbiology lab facilities will be funded through Guam EPSCoR and implemented with the input of the successful hire. The successful candidate will have the opportunity to use Guam's strategic location to develop a program conducting coral reef research across the broader Micronesian region.

Funding is available for the successful candidate to conduct research immediately upon arrival at the University of Guam. Applicants will receive support from the Guam EPSCoR leadership team to leverage these funds in seeking additional grant support to develop a strong research portfolio.

Financial support will be provided for the successful candidate to attend conferences, workshops, and develop collaborations that further the candidate's professional development and the goals of the overall project. The successful candidate will also receive support for graduate students through the University of Guam MS programs.

Qualifications: - PhD degree in a relevant field - at least five (5) years of relevant research experience - at least two (2) years of postdoctoral experience are preferred

Character of Duties: - Project design - Project implementation - Laboratory and field work - Data collection and analysis - Manuscript and report preparation - Present research at relevant scientific conferences - Grant writing - Student mentoring - Resident Instruction - Other duties as assigned

Application Materials: - Cover Letter (Research Statement) - CV - Contact details for three (3) professional references - Transcripts (or foreign equivalent)

Please submit your application online to the Research Corporation of the University of Guam: https://-www.uog.edu/rcuog/job-announcements.php For inquiries please contact the chair of the search committee, Dr. Bastian Bentlage (bentlageb@triton.uog.edu).

Bastian Bentlage <bentlageb@triton.uog.edu>

HarvardU ResAssist AntEvoDevo

The job is for an RA IV to help with establishing and maintaining a wet lab studying the evo-devo of ants.

https://sjobs.brassring.com/TGnewUI/Search/home/-HomeWithPreLoad?PageType=JobDetails&partnerid=25240&siteid=5341&Areq=53577BR#jobDetails=-1561995_5341 or

https://bit.ly/3w8pRtM "Research Assistant IV: Evolutionary developmental biology of ant castes, Harvard University, Cambridge, MA

The Trible lab at Harvard University is recruiting an RA IV to help establish and maintaina wet lab in ant evo-devo. The lab is a dynamic group focusing on ant castes using techniqueslike genome editing, larval rearing, in-situ hybridization, and single cell genomics. We are looking for a dynamic and enthusiastic researcher who can work both independently and as part of a larger group. The lab provides a supportive educational environment, and is part of the diverse Quantitative Biology Initiative, which provides access to researchers and ideas from all areas of modern biology."

Buck Trible <bucktrible@g.harvard.edu>

JohnInnesCentre ResAssist Entomology

Research Assistant (Entomology)

Location: John Innes Centre, Norwich, UK

Salary: 25,315 - 30,875 per year, depending on qualifications and experience

Contract:— Fulltime, Permanent

Closing date: 9 May 2021

Reference: 1004038

An exciting opportunity has arisen for a Research Assistant to join the Entomology and Insectary team. This role involves working with the Platform's Entomology Team to design, undertake, and support a range of assays working closely with academic and commercial partners. You will also assist with the day to day maintenance of insect colonies for research purposes, and the basic duties associated with maintaining an entomology facility to the high standards of hygiene and strict operational procedures required for operating under a Defra licence, including assisting in horticultural tasks associated with producing insect food plants.

The Entomology and Insectary Platform:

The John Innes Centre is an independent, international centre of excellence in plant science, genetics and microbiology. The Entomology and Insectary Platform is a unique and specialised service for supporting invertebrate-related studies. It is managed by a skilled team of entomologists with extensive experience in the husbandry of many different species of invertebrates, as well as in the design, undertaking and overseeing of a wide range of experiments. The Entomology team is currently working along with John Innes Centre group leaders to develop new ways of tackling emerging challenges in invertebrate pest research by generating invertebrate genomic resources and analysing large genomic datasets using evolutionary approaches. The Entomology and Insectary Platform not only support excellent research within the John Innes Centre, but also engage in national and international collaborations with academic and commercial partners. You can find more information here: https://www.jic.ac.uk/research-impact/technology-research-platforms/entomology-and-insectary/ The ideal candidate:

You will have a degree in Biology or a similar subject. You will have a keen interest in entomology, and demonstrable experience either working with live invertebrates or in a molecular biology laboratory. Knowledge of insect husbandry, experimental design with live invertebrates, molecular biology protocols, ecology, genetics and evolution of invertebrates, and plant-insect and plant-insect-pathogen is highly desirable. You will have a strong interest in pursuing a research career in entomology supporting research projects with both academic and commercial partners.

Additional information: Further information and details of how to apply can be found on https://-jobs.jic.ac.uk/Details.asp?vacancyID=16008, or contact the Human Resources team on 01603 450462 or nbi.recruitment@nbi.ac.uk quoting reference 1004038.

We are an equal opportunities employer, actively supporting inclusivity and diversity.— As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy. We are proud to hold a prestigious Gold Athena SWAN award in recognition of our inclu-

sive culture, commitment and good practices towards advancing of gender equality.— We offer an exciting, stimulating, diverse research environment and actively promote a family friendly workplace. The Institute is also a member of Stonewall's Diversity Champions programme.

– Dr Victor Soria-Carrasco Head of Entomology and Insectary John Innes Centre Norwich Research Park NR4 7UH, Norwich, UK Phone: +44 (0)1603 450 350

Victor.Soria-Carrasco@jic.ac.uk

LeibnizInst Hamburg MolecularLabHead

The Leibniz Institute for the Analysis of Biodiversity Change (LIB) seeks to hire a Head of Molecular Laboratory, at Hamburg

The Leibniz Institute for the Analysis of Biodiversity Change (LIB) will be established as an integration of the Centre of Natural History of the University of Hamburg (CeNak), Hamburg, into the Zoological Research Museum Alexander Koenig - Leibniz Institute for Animal Biodiversity (ZFMK), Bonn. As such, the LIB will be a foundation under public law and a research museum of the Leibniz Association. The LIB will contribute to biodiversity research with its extensive collections and through its research fields of taxonomy, morphology and molecular science. LIB will further contribute to the conservation of global biodiversity, to documenting and analyzing evolutionary and ecological biodiversity change, and engage in science transfer activities on biodiversity change and its potential causes.

The LIB is looking for a scientist for a tenure track position as Head of the Molecular Laboratory at the branch Hamburg, representing research at an internationally competitive level. The head of the molecular laboratory Hamburg will play a leading role in advancing molecular research at highest scientific standards at the LIB.

The successful candidate will closely collaborate with the LIB research sections covering the entire animal diversity, apply and develop advanced molecular methods and research approaches and will coordinate all operations of the central infrastructure of the Hamburg molecular lab, providing services to a broad range of projects at the LIB.

We expect the candidate to

*_____ hold a PhD in Ecology, Evolution or Molecular Biology or a closely related field with strong emphasis on empirical molecular work and computational skills in these subjects;

*_____ have experience in working with non-model organisms (animals);

*_____ have expertise in molecular genetics, including DNA extractions, PCR, next-generation sequencing, roboting, establishing lab setups;

*_____ have strong experience in data management and analysing DNA sequence and genome data (computational skills) in compliance with the FAIR principles;

*_____ have experience in team management and student supervision;

*_____ have experience in developing long-term strategies for the lab, meeting the goals of a state of the art central molecular lab service;

*_____ have motivation to work in a team and take responsibility;

*_____ closely collaborate with the Bonn molecular lab, promote novel ideas for methods and techniques and apply them in research projects tailored to requirements of museomics ;

*_____ excellent communication skills.

acquire substantial third-party funding with other LIB researchers of both localities.

It is desirable that the applicant has/is:

*_____ a good knowledge of the software R for programming, statistical analyses or graphical visualization of data;

*_____ experience with soft money acquisition, in particular concerning infrastructure development;

*_____ fluent in English; a good understanding of German is advantageous.

The Molecular Laboratory is a centralized facility, with its branches in Bonn and Hamburg providing knowledge and infrastructure to all LIB researchers. The Molecular Labs of both branches are part of the Centre for Molecular Biodiversity Research, and contribute to the ongoing development of the LIB as a globally leading institute for the study of biodiversity change. The labs of both localities are independent but closely collaborate in developing future strategic developments and perspectives and in making their particular experiences available to all researchers in the LIB. As Head of the Hamburg Molecular Lab, the successful candidate will

take full responsibility for the lab's operations, coordination and training of users, maintenance of equipment, documentation (protocols), and compliance with security guidelines.

Applicants are evaluated based on how well they fulfil the requirements detailed above. Such evidence may include documentation of completed course work, scientific publications, technical and analytical know-how, evidence of organisational skills, and prior experience in lab management. Whenever possible, statements to these effects should be accompanied by objective or independent assessment of the candidate's track record and potential. These may include links to access published or unpublished material or letters of support from supervisors or

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LeibnizInst Hamburg Phylogenetics

The Leibniz Institute for the Analysis of Biodiversity Change (LIB) seeks to hire a scientist in phylogenetics (w/m/d), at Hamburg

The Leibniz Institute for the Analysis of Biodiversity Change (LIB) will be established in July 2021 as an integration of the Center of Natural History of the University of Hamburg (CeNak), Hamburg, into the Zoological Research Museum Alexander Koenig - Leibniz Institute for Animal Biodiversity (ZFMK), Bonn. As such, the LIB will be a foundation under public law and a research museum of the Leibniz Association. The LIB will contribute to biodiversity research with its extensive collections and through its research fields of taxonomy, morphology and molecular science. LIB will further contribute to the conservation of global biodiversity, to documenting and analyzing evolutionary and ecological biodiversity change, and engage in science transfer activities on biodiversity change and its potential causes.

The LIB is looking for a scientist for a tenure track position in phylogenetics, representing this field of research at an internationally competitive level. The position holder will play a leading role in advancing molecular research at highest scientific standards at the LIB.

The successful candidate will closely collaborate with the LIB research sections covering the entire animal diversity, apply and develop advanced phylogenetic including genomic methods providing services and collaboration to a broad range of projects at the LIB.

We expect the candidate to * hold a PhD in Zoology, Molecular Genetics or a closely related field with strong emphasis on phylogenetics and phylogenomic methods; * have advanced knowledge in the application and development of phylogenetic methods for the analyses of molecular genetic and genomic data for evolutionary and population genetic research; * have relevant/extensive experience in the application of phylogenetic approaches in biological systematics and related fields; * have strong experience in data management and analysing DNA sequence including also genome data; * have experience in developing independent research projects and the development of new methodological approaches; have experience in team management and student supervision; * have motivation to work in a team and take responsibility; * closely collaborate within the LIB; * instruct users in the usage of hardware and software for molecular genetic data analyses * excellent communication skills; * acquire substantial third-party funding with other LIB researchers of both localities.

It is desirable that the applicant has/is:

* a good knowledge of the software R for programming, statistical analyses or graphical visualization of data; * experience with soft money acquisition; * fluent in English; a good understanding of German is advantageous.

The section of phylogenetics is part of the Centre of Molecular Biodiversity Research with its branches in Bonn and Hamburg providing knowledge and infrastructure to all LIB researchers. The Centre for Molecular Biodiversity Research contributes to the ongoing development of the LIB as a globally leading institute for the study of biodiversity change. The work groups of both localities closely collaborate in developing future strategic developments and perspectives and in making their particular experiences available to all researchers in the LIB. Applicants are evaluated based on how well they fulfil the requirements detailed above. Such evidence may include documentation of completed course work, scientific publications, technical and analytical knowhow, and evidence of organisational skills. Whenever possible, statements to these effects should be accompanied by objective or independent assessment of the candidate's track record and potential. These may include links to access published or unpublished material or letters of support from supervisors or previous employers. The tenure procedure will evaluate the above listed essential criteria. Working language is English,

German language skills should be acquired on long term. The Leibniz Association is committed to diversity and gender equity. The LIB is certified as a family-friendly institution. We aim to increase the proportion of women in areas, where women are under-represented and to promote their careers in particular. We therefore strongly encourage women with relevant qualifications to apply. Applications will be handled in accordance with the Landesgleichstellungsgesetz NRW (State Equality Act). Applications from suitable individuals with a certified serious

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MissouriStateU TeachingEvolution

The Biology Department at Missouri State University invites applications for a nontenure-track Visiting Assistant Professor with a commitment to inclusive teaching practices and increasing student diversity and retention. Requirements include a PhD in any area of biology and excellent communication skills. Primary duties include teaching introductory biology, general physiology (including labs), undergraduate academic advising, and service. Salary is $55,000. A letter of application, CV, names and contact information for 3 references, a statement of teaching experience and interests, and copies of all university transcripts should be submitted online at: https://jobs.missouristate.edu/postings/53676. The University is committed to building a culturally diverse educational environment. Applicants should include in their materials how their background and experience will further this goal. We encourage applications from members of all underrepresented groups. Direct questions to SPMaher@MissouriState.edu. Review of applications begins 5 May 2021. The starting date is 16 August 2021. EO/AA/M/F/Veterans/Disability/Sexual Orientation/Gender Identity

Sean P. Maher Associate Professor Department of Biology Missouri State University 417-836-6916 | 269 Temple Hall

"Maher, Sean P" <SPMaher@MissouriState.edu>

NatlMicroLab Canada BioinformaticsGenomics

Who: Public Health Agency of Canada - National Microbiology Laboratory Where: Various Locations Classification and Salary: BI-03; $81,359 to $104,748 Closing date: 30 June 2021 - 23:59, Pacific Time

The National Microbiology Laboratory is committed to providing exciting opportunities in an open and collaborative environment. You'll be at the forefront of scientific computing for use in investigating the world's most important infectious diseases.

We are seeking highly motivated individuals to lead the application and development of genomic and bioinformatics tools, algorithms, and analytical methods to support the Agency's programs for public health research, surveillance, diagnostics and outbreak response.

The incumbent will support science leads in collaboratively designing, developing and conducting computational data analytics for large data sets in the "omics" fields (genomics, transcriptomics, proteomics), provide expert advice, drive technology adoption in science programs, and manage projects and/or supervise multidisciplinary teams.

To build national capacity to address the COVID-19 pandemic, we are immediately seeking individuals for bioinformatics analysis of complex genomics data. This important work will help to identify and track transmission trends and inform critical decision making relevant to health authorities across Canada during the pandemic.

Who can apply: Persons residing in Canada and Canadian citizens residing abroad.

Full Job Poster https://emploisfp-psjobs.cfp-psc.gc.ca/psrs-srfp/applicant/page1800?poster=1567079 v Reference number: AHS21J-019669-000027 Selection process number: 21-AHS-IDPC-EA-NCR-308732

Contact information PHAC HR Recruit phac.hrrecruit-recruterrh.aspc@canada.ca Apply online < https://emploisfp-psjobs.cfp-psc.gc.ca/psrs-srfp/applicant/page1710?careerChoiceId=1567079&psrsMode=1 >

NAU Mexico AssocRes FloraConservation

Job

Announcement

Institute of Biology, National Autonomous University of Mexico

Full Time Associate Researcher "C"

The Botanical Garden of the Institute of Biology, UNAM (IBUNAM) has the mission of conducting research on the diversity, sustainable use, in situ and ex situ conservation, management and cultural relevance of Mexican flora, as well as the dissemination of this knowledge. To fulfill this mission, this announcement is issued.

The Institute of Biology of the National Autonomous University of Mexico, through its Academic Secretariat, calls upon those interested in occupying a full-time position as Associate Researcher "C" with a monthly salary of $ 20,329.60 MXN, in the area of Ethnobotany within the Botanical Garden, to submit their documentation under the following specifications.

Candidate profile.

An academic person is required to consolidate the area of research in agrobiodiversity, which integrates the knowledge and sustainable management of biodiversity, considering the plant genetic resources and the socioecosystems used by the people of various cultures in Mexico. Three core characteristics are required:

- Knowledge of cultivated or wild plants, whether native to Mexico or naturalized. - Knowledge to implement current or innovative technologies for the generation of models for the sustainable management of plant resources. - Botanical experience to complement the research line described above in coordination, consolidation and projection with the Ethnobotanical Collection that is part of the Botanical Garden, including the management of funds, outreach activities, etc.

Requirements.

- Degree of Doctor in Sciences or equivalent (Ph.D.) in the areas of Botany, Plant Ecology, Agrobiodiversity, Ethnobotany, Agroforestry or another related discipline. - Knowledge and professional experience of at least 3 years in research in the sustainable management of plant resources, applying current and interdisciplinary tech-

nological tools, allowing the generation of knowledge of plant genetic resources, as well as in the development of productive and conservation projects in communities of Mexico. - Experience and commitment in the curation of biological collections, to coordinate the Ethnobotanical Collection of the Botanical Garden. - Vocation to develop complementary activities to research, including the training of high-level human resources through teaching in the educational programs of the UNAM, supervision of undergraduate and graduate students, as well as collaborating in activities to disseminate botany and institutional participation. - Be able to immediately join the academic activities of the IB-UNAM Botanical Garden, exercise leadership in this line of research and possess the ability to obtain external funds and are able to form and join research groups. - In the case of foreign candidates, they must be proficient in the Spanish language.

Guide for application submission.

The following documentation should be sent to sacademica@ib.unam.mx, with a copy to secacad_vl@ib.unam.mx

1. Curriculum vitae (CV), including academic degrees, publication history, and experience in ethnobotany. 2. Description of the line of research (1-2 pages) 3. Work plan to be developed in one year, with a maximum length of 15 pages including:

(1) A research proposal for the sustainable management of plant resources, either at the population, species or community level; (2) methodological strategies for their conservation, which should be applicable in socioecological systems of Mexico and (3) a proposal for linking and projecting of the Ethnobotanical Collection with the aim of increasing and disseminating the scientific knowledge of this collection.

4. A cover letter addressed to the Director of IBUNAM (Dr. Susana Aurora MagallÂÂn Puebla), stating the motives and interest in developing an academic career at the IBUNAM (maximum 3 pages) 5. Names and contact details of at least two people who can provide academic references.

Applications, accompanied by documentation, will be received from April 12, 2021 until the close of this call, which will be on May 21, 2021 at 6:00 p.m. Pre-selected candidates will be contacted for a personal interview.

Contact.

For any questions regarding this announcement, contact the Academic Secretary of IBUNAM at the emails: sacademica@ib.unam.mx and / or secacad_vl@ib.unam.mx

Dra. Virginia LeÂÂn RÂÂgagnon Secretaria Académica

Instituto de BiologÂÂa, UNAM

Tels. 56229067 y 68

secacad_vl@ib.unam.mx;http://www.ib.unam.mx/ Secretar ÂÂa Académica IB <secacad_vl@ib.unam.mx>

NovaSoutheasternU FL ConservationBiol

The Department of Marine and Environmental Sciences (https://hcas.nova.edu/departments/marine-biology-environmental-sciences/index.html) at Nova Southeastern University's Halmos College of Arts and Sciences seeks a new faculty member at the Assistant Professor level. We are looking for a researcher-teacher with postdoctoral experience, a strong publication and external funding track record, expertise in quantitative fisheries and/or conservation modeling and sustainability, and interest in conducting research locally. The department's research focuses on fish and fisheries, freshwater ecology, deep sea science, and coral reef ecology. Candidates will be required to contribute to undergraduate and graduate education in both environmental sciences and marine biology, with a goal towards incorporating research knowledge and expertise into their curriculum. The successful candidate's effort will be split between teaching, mentoring, research, and university service. The selected candidate is expected to teach within the first year. Nova Southeastern University is a private, not-for-profit university in Fort Lauderdale, Florida with over 20,000 students of whom over 5,000 are undergraduates. Members of the NSU community have a shared vision, summarized here: https://www.nova.edu/about/mission.html. The position will be based at the Ocean Campus in Dania Beach: https://www.nova.edu/ghoc/map-directions.html . Candidates should submit a cover letter, CV, research statement, teaching statement, and list of 3 references. Apply for position 998833 at: https://nsucareers.nova.edu/en-us/job/498306/faculty-rank-tbd-mrn-bio-998833 .For questions relative to this position, contact the Chair of the Faculty Search Committee, Dr. Joana Figueiredo, at jfigueiredo@nova.edu including "DOMES Faculty Hire" on the Subject line. We encourage candidates of all backgrounds to apply, as NSU is committed to enhancing diversity, equity, and inclusion. Review of applications will begin June 15, 2021.

Jeffrey Hoch <jhoch@nova.edu>

OhioStateU ViralEvolution

The Ohio State University College of Veterinary Medicine invites applications for multiple research-intensive tenure-track faculty positions at the Assistant or Associate Professor level in emerging and re-emerging viruses. Areas of interest include, but are not limited to genetics and evolution, ecology, zoonotic transmission, animal models, immunology, structural biology, and virus-host interactions. Successful candidates will join a highly interactive virology and infectious disease research community on campus that is an integral part of the university's Infectious Disease Institute, including the Center for Retrovirus Research, Center of Microbiome Science, and a newly NIH-funded center, STOP-COVID. Applicants should have a doctoral degree (PhD, DVM, MD or equivalent) with advanced training in virology, viral evolution, or related fields. Academic rank and salary are commensurate with experience. Candidates at the rank of Associate Professor should have demonstrated research productivity and evidence of an independently funded and sustainable research program, as well as experience working with interdisciplinary research teams. Candidates at the rank of Assistant Professor should have training, experience, excellent scholarship, and demonstrated evidence of the likelihood of obtaining and maintaining an independently funded and sustainable research program. All candidates should have interest in programmatic synergy with existing members of the Ohio State faculty.

Columbus, Ohio's capital and largest city and the 14th largest city in the US, offers many cultural and recreational opportunities, excellent schools, easy commute and a strong economy with growing industries in biomedical science, finance, insurance, healthcare, retail and e-commerce and information technology. Columbus has consistently been rated as one of the top U.S. cities for quality of life and affordability and one of the best places for business and careers in part due to a strong multicultural population and efforts to foster and embrace diversity, equity and inclusion. Residents enjoy the many amenities of the city including professional sports teams, museums, Columbus Zoo and Aquarium, outstanding restaurants, performing arts, metro parks, and more.

Applications should be submitted via email as a single PDF including (1) a cover letter; (2) curriculum vitae; (3) a summary of past research accomplishments; (4)

a statement that addresses (i) your future research directions, (ii) your teaching and mentoring philosophy, and (iii) how you foresee integrating diversity and inclusion into your research, teaching and professional service; and (5) the names and contact information of four professional references.

Application materials should be submitted to Casey Hofmann (hofmann.75@osu.edu). Review of applications will begin June 1, 2021 and continue until positions are filled. Inquiries may be directed to the chair of the search committee, Dr. Shan-Lu Liu (liu.6244@osu.edu).

The Ohio State University is committed to establishing a culturally and intellectually diverse environment, encouraging all members of our learning community to reach their full potential. We are responsive to dual-career families and strongly promote work-life balance to support our community members through a suite of institutional policies. To build a diverse workforce, qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, or protected veteran status. EEO/AA employer.

"Nelson, Martha (NIH/NIAID) [C]" <nelsonma@mail.nih.gov>

PrincetonU ResTech MosquitoeEvolutionBehavior

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

Responsibilities

Research project activities may include - Mosquito behavioral experiments and breeding - Generation of trans-

genic strains using CRISPR/Cas9 - Odor collection and analysis using GC-Mass Spec - Molecular biology studies including DNA/RNA extraction, PCR, cloning - Preparation of high throughput sequencing libraries. - General maintenance and lab support.

Qualifications

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

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

Applications will be reviewed starting May 1st and continue on a rolling basis. Contact Lindy McBride at csm7@princeton.edu with questions. TO APPLY visit https://bit.ly/3uPVWVR csm7@princeton.edu

Lindy McBride <csm7@princeton.edu>

QMUL London 3 EvolutionaryBiology

The School of Biological and Chemical Sciences at Queen Mary University of London is seeking to appoint three senior lecturers in Genetics, Ecology and Organismal Biology. These are teaching and research positions with the successful candidate expected to carry out world-class research in their subject area.

For more info and application instructions:

Senior Lecturer in Genetics: https://webapps2.is.qmul.ac.uk/jobs/job.action?jobIDW74
    Senior Lecturer in Ecology: https://webapps2.is.qmul.ac.uk/jobs/job.action?jobIDW95
  Senior Lecturer in Organismal Biology: https://-

webapps2.is.qmul.ac.uk/jobs/job.action?jobIDW96
Best,

Mario dos Reis

Senior Lecturer @ QMUL dosreislab.github.io

Mario dos Reis <mariodosreis@gmail.com>

SangerInst UK Bioinformatician AquaticSymbiosis

We are seeking a talented bioinformatician or genomics data scientist to deliver genome data QC and high-throughput assembly for the Moore Foundation Aquatic Symbiosis project.

There are opportunities and challenges to design scalable and robust informatics solutions for the data tracking, storage, and analysis of this data. One of the most challenging aspects of this role will be to produce high-quality scientific results on a large scale while adapting to rapid developments in sequencing technology and software.

About Us:

The Tree of Life Programme at the Wellcome Sanger Institute is dedicated to the generation and analysis of high quality genome sequences from across eukaryotic biodiversity. The Tree of Life team is initiating a new, three-year project on the Genomics of Symbiosis in Aquatic Systems, funded by the Gordon and Betty Moore Foundation, where we will use advanced genomics toolkits to describe and decipher the biology of thousands of species that live in intimate association. The project will collaborate internationally to deliver exciting research outcomes and further understanding of the importance of symbiosis in generating diversity and maintaining function in aquatic ecosystems. To deliver this new project we are recruiting a team of molecular biologists, computing scientists and project management support.

About You:

You will contribute to the development of methods and software for genome data QC and assembly. Sequencing technologies are constantly evolving in terms of the type and volume of the sequence data they produce. The recent progress in long-read sequencing technologies means that we are now able to efficiently deliver high quality genome assemblies for species that did not previously have such a resource. We will produce thousands of genome assemblies for symbiotic organisms, and analyse these to understand their biology.

You will have previous experience with genome bioinformatics or other large-scale scientific data analysis, or a newly qualified graduate student with data science skills interested in assembling DNA sequence data. While desirable, previous experience with DNA sequencing data is not strictly necessary for the position. We have a strong publication record and culture of producing open data resources and open source software development. This role requires an investigative and solution-oriented mindset and excellent communication skills to work effectively within large national and international consortia.

Three year positions, closing date 26th May.

See   https://jobs.sanger.ac.uk/vacancy/senior-bioinformatician-bioinformatician-assembly-442464.html for more information and to apply.

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.

Sophie Potter <sp27@sanger.ac.uk>

SarsCentre Bergen FacilityTech NeuroEvolution

https://www.jobbnorge.no/en/available-jobs/job/204415/senior-facility-technician-seniorforskningsteknikar-code-1513   Senior Facility Technician

A 100% permanent position as Senior Facility Technician is available in the research group of Dr. Pawel Burkhardt at the Sars Centre. The Sars Centre belongs to the University of Bergen and is partner of the European Molecular Biology Laboratory (EMBL) (www.embl.de). The place of work will be at the Sars Centre. The starting date is 01 October 2021.

Work in the Burkhardt group focuses on the evolutionary origin of synapses and neurons, using choanoflagellates, sponges and ctenophores as marine model systems.

Tasks: The main responsibilities of the position will be the daily running of a ctenophore/sponge facility, including:

Culturing of algae and copepods for feeding animals Feeding and breeding of animals Operation and maintenance of the animal facility Maintenance of equipment and building of new equipment to improve functioning of the facility Periodic field collection of sponges and ctenophores Some weekend duties might be requested

Qualifications: Essential requirements for the successful candidate are to be able to demonstrate reliable working habits, independency, initiative, and the ability to interact in a productive manner with other group members Prior experience with building and/or maintaining animal facilities is required Prior experience working with ctenophores or other marine invertebrates is highly advantageous Experience maintaining algae and/or zooplankton cultures is highly desirable The applicant must be able to communicate (written and spoken) in English and/or Norwegian

We can offer: A challenging position with interesting tasks in an internationally acknowledged scientific environment.

Salary as Senior Research Technician ("seniorforskningsteknikar", code 1513) from grade level 43, based on a formal assessment of civil service seniority and qualifications. Currently equal to NOK 404.400.

Enrolment in the Norwegian Public Service Pension Fund (SPK). Good welfare benefits Application in English: Application must include:

Application letter stating your motivation for the position and why you feel you are a good candidate for this position Overview of your education and work experience (CV) Certified copies of educational transcripts and other relevant documents Two references (names and contact information)

Please send your application via the link "Søk stillingen/Apply for job" at https://www.jobbnorge.no/-en/available-jobs/job/204415/senior-facility-technician-seniorforskningsteknikar-code-1513referred to at the www.jobbNorge.no website and note that applications will be assessed only with the information available in JobbNorge when the deadline expires. It is the applicant's responsibility to ensure that all relevant attachments are submitted by the deadline.

Applications by e-mail will not be considered.

Application Deadline: 5 May 2021.

General information: For further information about the position please contact Group Leader Pawel Burkhardt, tel +47 55 58 43 57, email: pawel.burkhardt@uib.no.

Senior Facility Technician, (Seniorforskningsteknikar, code 1513) (204415) | University of Bergen

Job title: Senior Facility Technician, (Seniorforskningsteknikar, code 1513) (204415), Employer: University of Bergen, Deadline: Wednesday, May 5, 2021

www.jobbnorge.no DrPawel Burkhardt Group Leader Sars InternationalCentre for Marine Molecular Biology University of Bergen Thormohlensgate 55 5020 Bergen, Norway

Tel: +47 55 58 43 57 E-Mail:Pawel.Burkhardt@uib.no Webpage:https://www.uib.no/en/sarssenteret/-114773/burkhardt-group Twitter:https://-twitter.com/Pawel_Burkhardt Pawel Burkhardt <Pawel.Burkhardt@uib.no>

SGN Frankfurt VegetationModelling

Job announcement ref.#11-21005

The Senckenberg Gesellschaft für Naturforschung (SGN), a member institution of the Leibniz Association, with almost 800 employees and its headquarters in Frankfurt am Main, is conducting integrative natural history research with leading research institutions in six federal states. The Senckenberg Biodiversity and Climate Research Centre (SBiK-F) explores interactions between biodiversity and climate.

The Senckenberg Gesellschaft für Naturforschung (SGN) seeks in the scope of the EU-funded integrated project Horizon2020 FirEUrisk (Developing a holistic, risk-wise strategy for European wildfire management), at SBiK-F in Frankfurt am Main a

Research Associate (m/f/d) in Vegetation Modelling

(full time position)

This position will combine mechanistic fire modelling with machine learning calibration and downscaling to produce policy-relevant fire predictions at the European scale within the FirEUrisk project. FirEUrisk will develop, evaluate and disseminate a science-based integrated strategy to: 1) advance current wildfire risk assessment systems, 2) to produce effective measures to reduce current fire risk conditions, and 3) to adapt management strategies to expected future climate and socio-economic changes.

The project with more than 30 partners builds upon close collaboration between researchers, stakeholders and citizens, aiming at developing guidelines and policy recommendations to improve current systems and practices from regional to EU scales. FireEUrisk includes

experts and activities in remote sensing, forestry and ecology, and it is anticipated that data from these activities shall inform the modelling work done here. You will primarily contribute to the work package on adaptation to future fire regimes.

Your tasks

Adapt existing fire modules of the Lund-Potsdam-Jena General Ecosystem Simulator (LPJ-GUESS) to European conditions (most likely the SPITFIRE module)Improve the calibration of the model with new data sets, also using machine learning techniquesUse the model to develop scenarios of future impacts of climate change and socioeconomic drivers on ecosystems, fire and ecosystem servicesCo-lead the task to generate future scenarios (to which several experts in climate and climate scenario data, land use change scenarios and vegetation-fire modellers will contribute)Contribute to dissemination activities towards policy makers and stakeholdersDisseminate results in scientific journals and more stakeholder-oriented formatsParticipation in meeting/workshops in Germany and across the EU are expected

Your profile

Master or PhD degree in Biology, Ecology, Environmental Modelling, Geography, Environmental Physics or related fieldsStrong expertise in computer programming, preferably in C/C++ and RExperience in ecological or environmental modellingDocumented ability to publish scientific papers in international journalsResearch experience in interdisciplinary working environmentsExcellent written and oral communication skills in EnglishIdeally also experience in applied projects and stakeholder interaction

What is awaiting you?

An interesting and relevant task in a large interdisciplinary research teamBecoming a member of dynamic team at Senckenberg specialized in ecosystem modelling and climate impact researchThe possibility to build and extend your network with scientists at an international level and to attend national and international conferencesFlexible working hours - mobile working - leave of absence due to family reasons - parent-child-office (certified by the audit berufundfamilie) - annual special payment - company pension scheme - Senckenberg badge for free entry in the Senckenberg museums - leave of 30 days/year - discounted job ticket

Salary and benefits are according to a public service position in Germany (TV-H E 13, full time position). The position shall be filled as soon as possible, subject to the cooperation agreement and the grant agreement coming into force. The position is restricted to 31 months.

SGN supports equal opportunity of men and women and therefore strongly invites women to apply.

Equally qualified handicapped applicants will be given preference.

The place of employment will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung (SGN).

You would like to apply?

Please include the reference to this position (ref.#11-21005) in the subject line and include

a cover letter outlining your suitability and motivation to apply,a detailed CV,your full publication list (if available),your full academic credentials/certificates andcontact details of two academic references, as well as copies of your two most important publications.

Please submit your application (a single PDF file) using the online application form on our website, or hand it in by e-mail by 16th May 2021.

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

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SouthwesternOklahomaStateU OrganismalGenetics

The Department of Biological Sciences at Southwestern Oklahoma State University is searching for a faculty with expertise in organismal genetics. To learn more about the position visit https://swosu.csod.com/ux/ats/careersite/1/home/requisition/33?c=swosu . Rickey Cothran Associate Professor & Chair Department of Biological Sciences Southwestern Oklahoma State Univ. https://rdcothran.wixsite.com/hyalella rickey.cothran@swosu.edu

SwissOrnithologicalInst AvianConservation

The Swiss Ornithological Institute is a non-profit foundation for the study and conservation of birds, uniting basic research, applied research and implementation under the same roof. Due to an upcoming retirement, we are looking for a

Head of research division "Anthropogenic impact" (80-100%) as of 1 September 2021 or by arrangement.

Your tasks: You will build and direct a research unit to explore the effects on birds of anthropogenic influences with or without direct human involvement. You have in-depth knowledge in at least one of the following fields: disturbance ecology, ecotoxicology, or behavioural physiology. You will design and implement research projects, publish the results and raise funds. You will promote internal and external collaboration in your research division and contribute to the institute's general activities.

What we expect: You are respected in your discipline and passionate about research. You are an innovative and creative person interested in new ideas and methods who seeks to advance the research area "Anthropogenic impact". As an integrative researcher, you enjoy conceptual work, constructive and open communication as well as guiding your team members and supporting their development. You have a doctoral degree in biology as well as several years of experience carrying out your own research. Experience leading research teams and sound ornithological knowledge are desired. You regularly publish in high-ranking journals and are an experienced fundraiser and supervisor of academic theses. You speak one of Switzerland's national languages and have a very good command of English. Other requirements include team skills, excellent interpersonal skills and a detail-oriented and independent working style.

What we offer: We offer a varied and responsible position in an inspiring work environment. You can look forward to family-friendly and flexible working hours, plenty of opportunities for continuing education, and exemplary social security benefits. The place of work is Sempach.

Your application: The Swiss Ornithological Institute is committed to increasing the representation of women in leadership roles and research and specifically encourages applications from qualified women. For more details on the position, please contact Dr Michael Schaub (michael.schaub@vogelwarte.ch), head of the department for ecological research. We look forward to receiving your online application by 22 May 2021. Please send your application documents (cover letter, CV, list of publications, list of funds raised, copies of diplomas, three references with contact details) in a single PDF file. <michael.schaub@vogelwarte.ch>

Link for sending an application: my.jobalino.ch/de/jobpreview/1742

Schaub Michael <michael.schaub@vogelwarte.ch>

Taiwan FacultyPlantAndMicrobialBiology

MULTIPLE TENURE-TRACK FACULTY POSITIONS

The Institute of Plant and Microbial Biology (IPMB), Academia Sinica, Taipei, Taiwan (http://ipmb.sinica.edu.tw/) is inviting applications for tenure-track research-oriented faculty positions. Academia Sinica, the foremost academic institution in Taiwan, comprises 32 research institutes/centers and provides an active research environment. IPMB explores the functionality of plants and microbes to benefit science, agriculture, environmental sustainability and human well-being.

Candidates should hold a Ph.D. degree with postdoctoral training and are expected to have complementary or synergetic expertise to the current IPMB research capacities or have the potential to launch a new research direction for IPMB. Preference will be given to applicants at the Assistant Research Fellow level (equivalent to Assistant Professor). The successful candidates will receive generous startup and annual intramural funds in addition to external competitive grant opportunities. IPMB also maintains well-equipped core facilities for proteomics, genomics, metabolomics, bioinformatics, cell biology, and imaging that are managed by Research Specialists/Assistants to provide state-of-the-art resources and key technical expertise.

Application files should include 1) a cover letter, 2) a curriculum vitae, 3) a statement of research accomplishments (up to 2 pages), 4) a future research plan (up to 5 pages), and 5) up to five representative publications. These files in PDF should be uploaded to http://recruitment.ipmb.sinica.edu.tw. Please arrange

to have three letters of recommendation sent to: Dr. Erh-Min Lai, Chair of Search Committee c/o Ms. Hsiao-Yun Wang (email: ipmbsearch@gate.sinica.edu.tw).

The review of applications will begin on June 15, 2021 and continue until the positions are filled.

"chuanku@gate.sinica.edu.tw"
<chuanku@gate.sinica.edu.tw>

UBern FishConservation

A technician position in fish ecology and conservation is available (each 2-3 years) in the Aquatic Ecology & Evolution group of Ole Seehausen at the University of Bern, Switzerland

With the Wyss Academy for Nature, we are starting an ambitious freshwater conservation biology project with a focus on fish. Working initially at the scale of the largest Swiss catchment, the Aare, home to more than 60 different species of fish, we want to go all the way from field ecology, niche modelling and projections of range shifts under climate change to identifying priority areas for biodiversity conservation, and designing measures to mitigate predicted and recover past losses. As implementation partner, the Swiss Fisheries Competence Center will develop applications of such measures initially in a test region. The project is supported by the Wyss Academy for Nature at the University of Bern in partnership with the Canton of Bern and the Swiss Federal Office for the Environment (FOEN/Bafu). If successful, the project may continue for up to eight years, with the goals of upscaling projections to other catchments of Switzerland and a fully fledged mitigation program.

The Aare catchment contains several of the large perialpine lakes, each of which has endemic species of coldwater fish, several of which have already gone extinct. It also has many mountain rivers with environmental gradients stretching from the arctic-alpine to the temperate climate zone, including one of the most pristine braided rivers left on the North face of the Alps. We have an extensive data set on distribution records for most species of fish in Switzerland and many environmental variables. Our goal is to complement this data with additional dense sampling of fish and environmental variables across the entire Aare catchment. Our recent work has uncovered old cryptic species as well as postglacial ecological species within the broad category of taxonomic "species" currently in use in man-

agement. Whenever possible we will do niche modelling and change projections at the level of these evolutionary significant units (ESUs). We will work with and add to our large collection of voucher specimens and tissue samples covering many populations of most Swiss fish species. We will develop data rich niche models for all species/ESUs of fish and also for some key aquatic invertebrates. We will combine the niche models with locally resolved climate and land-use change projections to predict habitat gains and losses and identify hotspots of expected biodiversity loss. We will use the results to develop mitigation strategies, components of which will be explored initially in a test region, in close collaboration with the Swiss Fisheries Competence Centre, the Wyss Academy for Nature, the Canton Bern office for the environment (LANAT) and the Federal Office for the Environment (FOEN).

We are hiring a technician to support a team of Postdoctoral scientists. You are in charge of the sampling. This includes electrofishing and snorkelling in streams, netfishing, diving and ROV operations in lakes, processing of samples and genetic lab work (barcoding and RAD sequencing). You are also in charge of obtaining sampling permits. Employment as technician/senior technician depending on experience.

Qualifications: MSc or PhD in fish biology with relevant field experience and strong technical skills. Social skills and proficiency in German/Swiss-German are required for interactions with fisheries administrations and stakeholders.

The project is part of the Hub Bern of the Wyss Academy for Nature (https://www.wyssacademy.org/). It will be implemented in close collaboration between the Institute of Ecology & Evolution's division of Aquatic Ecology & Evolution (https://www.iee.unibe.ch/), the Swiss Fisheries Competence Centre, the Canton Bern office for the environment (LANAT), the Federal Office for the Environment (FOEN), and the Eawag Department of Fish Ecology & Evolution.

The group of Seehausen is based at the Institute of Ecology & Evolution of the University of Bern and at the Eawag Centre for Ecology, Evolution & Biogeochemistry in Kastanienbaum (Lucerne). The group works on the ecology, evolution and conservation of freshwater fish with a strong focus on the fish of the Alpine region and the African Great Lakes. The Postdocs and the Technician in this project will function as a project team within a much larger team of ecologists, evolutionary biologists and conservationists. The group's working language is English and fluency in speaking and writing is required. Knowledge of German is also required for the field technician. Salary will be according to

University of Bern salary scheme and commensurate with experience and job profile (e.g. responsibilities as project manager). Supervisor: Prof. Dr. Ole Seehausen, Institute of Ecology and Evolution

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UEdinburgh ResearchFellowship EvolBiology

The Institute of Evolutionary Biology at the University of Edinburgh IEB is keen to support applicants for URF and NERC fellowship schemes.

Independent Fellows play a key role within the Institute of Evolutionary Biology. Fellows are considered as PI level, eligible (and encouraged) to supervise research students and fully involved in all aspects of Institute decision making. Many of our current staff are on fellowships, and the record of our Fellows transferring to permanent positions at the end of their Fellowships is exceptional. We provide an excellent intellectual environment, with state of the art facilities where Fellows are supported to achieve their potential.

We are looking to identify candidates whose research interests complement the existing research strengths of IEB to support in applying for these schemes. In our experience, putting together a high-quality, competitive application requires several months, and so if you are interested in being considered for support for either scheme, please send a copy of your CV, and a two page research pitch to r.shields@ed.ac.uk by May 17 2021. The research pitch should outline your research plans, your longer-term goals and how your research will add to our Institute and fit with the School of Biological Sciences strategic research themes (see below).

If it looks like there could be a good match, we will invite you to speak to us online in early June and tell us more about your plans. We will then give you a final decision on whether we can support you in early July.

For informal enquiries (including questions about other fellowship programs), please e-mail n.colegrave@ed.ac.uk.

For information about IEB research themes: https://www.ed.ac.uk/biology/evolutionary-biology/research-themes For links to staff research interests: https://www.ed.ac.uk/biology/evolutionary-biology/staff-profiles For information about IEB Fellowship development: https://www.ed.ac.uk/biology/evolutionary-biology/fellowship-development For information about biological Sciences research themes: https://www.ed.ac.uk/biology/research/themes 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 katerina.guschanski@ebc.uu.se

UFlorida ArbovirusGenomics

" The University of Florida Institute of Food and Agricultural Sciences is hiring a faculty specialized in Arbovirus Systems Genetics, Genomics, or Engineering who will be stationed at Florida Medical Entomology Laboratory at Vero Beach, FL.

One position is a 9-month tenure-accruing position that will be 85% research and 15% teaching. Research duties focus on arthropod vectors of disease, particularly mosquitoes and ticks, and the pathogens they transmit with emphasis on using modern genetic engineering tools and procedures (e.g. CRISPR-Cas9 mediated transgenesis) for developing and evaluating new information and tools relevant to arbovirus system management. The detailed job description can be found at UF Jobs listing: https://facultyjobs.hr.ufl.edu/posting/84958 ."

I was not sure how to handle the link to the posting. Please make appropriate changes if the webpage link should be handled differently.

"Lee, Yoosook" <yoosook.lee@ufl.edu>

c.m.eising@rug.nl

UGroningen 5 EvolutionaryBiology

The Groningen Institute for Evolutionary Life Sciences (GELIFES, University of Groningen, The Netherlands) is currently hiring 5 Tenure Track Assistant Professors with an Education profile in the fields of:

* Behavioural Neurosciences * Bioinformatics * Datascience & Biostatistics * Ecology & Evolution * Functional Genetics & Genomics

We are looking for (early-)career academics who are interested to start a tenure-track that focuses on education. We offer 5 diverse positions to further teaching and teaching innovation in our Bachelor Biology and various Master programs while offering successful candidates to pursue their research at the same time.

Recognition and rewards

These positions are inspired by the national initiative recognition and rewards. One of the core aims of this initiative is to create a more diverse and dynamic career system at Dutch universities, so that excellence in education, research and societal impact is promoted. At the Faculty of Science and Engineering where GELIFES is embedded we embrace these ideas and have therefore introduced this new career path.

The positions we offer will be embedded in < https://-www.rug.nl/research/gelifes/ > the Groningen Institute for Evolutionary Life Sciences. GELIFES aims to enhance the understanding of adaptive processes and the maladaptive consequences of their limitations, across all levels of biological organization (from molecules and genes to individuals and ecosystems), to inform the society and contribute solutions to societal problems. GELIFES specifically aims at the integration of mechanistic, evolutionary and ecological approaches. The institute is coordinating one of the four Faculty strategic themes called < https://www.rug.nl/research/fmns/-themes/adaptive-life/ > Adaptive Life. The institute further has tight connections with the Faculty of Medical Sciences (FMS) and University Medical Centre Groningen (UMCG).

For more information on these positions, qualifications and conditions of employment, please check the vacancy texts and accompanying Profile reports, which can be found here: https://www.rug.nl/research/gelifes/-organisation/vacancies   Closing deadline is May 16th .

UHouston ResTech DrosophilaEvolution

Dear Evol-Dir,

I am seeking a lab/manager technician to support our research on the impact of transposable elements on Drosophila oogenesis. Read more about our research here: http://nsmn1.uh.edu/eskelleh/. Skills in Drosophila husbandry and molecular biology are a plus. General organizational skills and a being a good team player is a must. Start date is flexible and upcoming graduates are encouraged to apply. Houston remains an affordable, diverse and culturally-rich city for people of all ages.

Please forward this along to any trainees you are aware of who might be interested. Applicants should contact me directly (eskelleher@uh.edu). Thank you!

best wishes,

Erin

Erin Kelleher Associate Professor Biology and Biochemistry University of Houston eskelleher@uh.edu

Office: Science and Research 2 Rm 421D Lab: Science and Research 2 Rm 428 Office Phone: (713) 743-3640 http://nsmn1.uh.edu/eskelleh/   "Kelleher, Erin S" <eskelleh@Central.UH.EDU>

UMainz EvolutionaryEcology

Johannes Gutenberg University Mainz (JGU) is one of the largest universities in Germany. Thanks to its location in the Rhine-Main science region, the university can unfold to its full potential and showcase its innovative power and dynamism. Its status as a comprehensive university allows for multidisciplinary learning and teaching and has great potential for internationally renowned, interdisciplinary research. Almost all of its institutes are located on a single campus close to the Mainz city center creating a lively academic culture for researchers, teaching staff, and students from every continent.

The Institute of Organismic and Molecular Evolution

(iomE) at the Faculty of Biology invites applications for the position of a University Professor of Evolutionary Ecology

beginning at the earliest possible date.

Salary grade W 3 LBesG | Civil servant (tenured)

Tasks and expectations:

We are seeking an internationally renowned scientist in the field of animal evolutionary ecology. The research should focus on how animals adapt to global change and / or address intra- or interspecific interactions. We are interested in a candidate who combines studies of organismic and molecular evolution, covering the phenotype as well as the underlying genotype and epigenetic processes. Topics could include coevolution, phenotypic plasticity (epigenetics), animal-microbe interactions, niche construction, life history evolution (e.g. evolution of aging) or resilience.

The successful candidate is expected to develop an independent and internationally visible research program, supported by sustained extramural funding. We strongly encourage local and regional networking on campus within the Faculty of Biology, with other faculties in the natural and life sciences at Johannes Guten-berg University as well as with research institutes such as the Institute for Biotechnology and Drug Research (IBWF), the Institute of Molecular Biology (IMB), the Max Planck Institutes for Polymer Research and for Chemistry, and the Rhine-Main Universities alliance (RMU). Shaping of and active contribution to local research clusters such as collaborative research centers, graduate schools and profile areas like GenEvo (Gene regulation in Evolution) and ReALity (Resilience - Adaptation - Longevity) is desired (for further details see: https://www.bio.uni-mainz.de/-forschung). The future holder of the position is expected to teach courses in the field of ecology, evolutionary biology, zoology and biostatistics / bioinformatics in the Bachelor and Master programs.

Requirements:

In addition to the general requirements according to public services law, applicants must meet the recruitment requirements stipulated in Section 49 of the Hochschulgesetz of Rhineland-Palatinate.In addition to the doctorate, proof of excellent academic achievements is required.

The state of Rhineland-Palatinate and JGU are committed to close personal mentoring of students and therefore expect teaching staff to have a strong presence at the university. A cooperative, team-oriented and proactive work attitude, strong communication skills, and the willingness to assume responsibility including further professional development in accordance with JGUs

leadership guidelines is also expected.

What we have to offer:

JGU firmly supports making family and career compatible and promotes its employees further professional development with an extensive human resources development offer.

JGU is diverse and welcomes qualified applications from people with varied backgrounds.

JGU aims to increase the quota of women in research and teaching, and therefore encourages female scientists to apply.

Disabled candidates with adequate qualification will be given priority.

The interview symposium is tentatively planned for July 2021.

Please submit your complete application including the usual documents (CV; certificates; lists of publications and teaching activities; funding record; current research and future research plans; teaching concept etc.) no later than May 31th, 2021 via the Apply now button.

For questions and further information, please contact the chairperson of the search committee Prof. Dr. Susanne Foitzik (foitzik@uni-mainz.de).

https://stellenboerse.uni-mainz.de/HPv3.Jobs/-jgu/stellenangebot/17102/University-Professor-of-Evolutionary-Ecology "Foitzik, Susanne" <foitzik@uni-mainz.de>

UMassachusetts Lowell DiseaseEvolution

Job: Assistant/Associate Professor - Infectious Disease Biology The Department of Biological Sciences at the University of Massachusetts Lowell invites applications to fill a full-time tenure-track faculty position at the Assistant or Associate Professor level. We seek an individual who studies the biology of pathogens, including in the areas of disease ecology and/or evolution, interactions between microbes and the host immune system, interactions with vectors, the effects of global change and urbanization on disease systems, disease spillover,andpathogen population biology. The successful candidate will be expected to establish a vigorous, externally funded research program, and contribute to the department's teaching mission. Teaching responsibilities may include the development of undergraduate

courses, in addition to upper-level and graduate courses. The start date is September 2021, and we start reviewing applications on May 1st.

For more information and to apply, see:

https://explorejobs.uml.edu/en-us/job/507656/-assistantassociate-professor-infectious-disease-biology Frédéric Chain frederic_chain@uml.edu

"Chain, Frederic J" <Frederic_Chain@uml.edu>

UppsalaU Bioinformatician

Dear all,

A position as bioinformatician is available in the research group for Rheumatology/systemic autoimmunity at the Department of Medical Sciences, Uppsala University, Sweden. The group studies inflammatory autoimmune diseases, such as systemic lupus erythematosus (SLE) and Sjögren's syndrome, which are caused by the immune system attacking the body's own tissues. We perform translational research with molecular, genetic and cellular tools with the aim to understand the underlying mechanisms behind the diseases.

As a bioinformatician in the Rheumatology group you would be directly involved in the analytical part of our projects, participate in planning our studies and the work towards publication. Our research group offers a flexible working environment and good opportunities for further competence development. For more information about the research group, please see: http://-www.medsci.uu.se/forskning/reumatologi/ . For more details on the position and to apply please use: https:-/uu.varbi.com/en/what:job/jobID:392569/ Please submit your application by 29 April 2021.

Best regards, Pascal Pucholt

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 Pascal Pucholt <pascal.pucholt@medsci.uu.se>

Other

Apply For EuropeanResearchVisits

Dear EvolDir community,

please be informed that the deadlines for SYNTHESYS+ transnational as well as virtual access calls have been extended. Within the Transnational Access program (TA) you can apply for short research visits in the participating European institutions. Virtual Access (VA) is a program for digitization-on-demand of selected collection assets within the participating institutions for research purposes.

The new deadline for TA is May 7th 2021, for VA June 11, 2021. The portal closes at 5 pm UK time.

You'll find more information under https://-www.synthesys.info/access.html . Dr. Eva Häffner Freie Universität Berlin Science Policy Coordinator Botanischer Garten und Botanisches Museum Berlin Königin-Luise-Str. 6-8 14195 Berlin Tel.: (030) 838 59964 Fax: (030) 838 4 59964 E-Mail: e.haeffner@bgbm.org www.botanischer-garten-berlin.de E.Haeffner@bgbm.org

DataRequest PollutionAndBirdColouration

Data request - Influence of anthropogenic pollution on bird colouration.

Dear colleagues,

We are conducting a research on the influence of anthropogenic pollution on different types of bird colouration, including both feathers and bare-parts of skin. In this study, we aim to estimate the scale of the problem and to identify significant knowledge gaps for better targeting of future research. Specifically, we would like to focus on two aspects:

- the impact of specific types of pollution (e.g. heavy metals, *polychlorinated biphenyls* or radiation), preferably with a known concentration in the studied habitat or bird's tissues, on the expression of colour traits.

- the influence of urban environments on the expression of colour traits, preferably in studies comparing birds from urban vs rural/natural habitats.

We are seeking the data from both correlative and experimental studies. Whenever possible, we would like to request the raw data, with means, SE and sample size, otherwise we also request for correlation and other statistics from the models, together with sample sizes.

Examples of data we prefer are:

Differences in colouration between control and polluted/anthropogenic pressure treated groups

Correlation between pollution/anthropogenic factor and colouration

We will consider all measures of colouration (spectrophotometric, photography-based, colour scoring).

If you have any kind of unpublished data, data from PhD thesis, or from the upcoming articles, we will be very thankful for possibility to include your findings in our study. We are waiting for the data until the 15th of May.

Contact: katarzyna.janas1@gmail.com

We will be very grateful for your contribution!

Best wishes,

Agnieszka Gudowska (Jagiellonian University, Kraków),

Katarzyna Janas (Jagiellonian University, Kraków),

Szymon Drobniak (Jagiellonian University, University of New South Wales, Sydney)

Katarzyna Janas <katarzyna.janas1@gmail.com>

Demystifying GraduateSchool EcolEvol Apr20

Dear colleagues,

The Rutgers Ecology & Evolution graduate program is hosting an online info session and Q&A for undergraduates who may be interested in graduate school in ecology and evolution but are either unaware of the opportunities or unfamiliar with the process. If you have students you think may be interested, I'd be grateful if you could forward our invitation. Or, if you could post this, that would be appreciated.

The session will be a 90-minute Zoom webinar and will include faculty and grad student panels with opportunities to ask questions. We'll focus on demystifying the graduate school experience, offer some brief descriptions of the kinds of research one can do, and give some advice

on finding and applying to a lab in the field.

The session will be Tuesday, April 20th, from 4:00 - 5:30 pm EDT. Participants must register in advance here < https://rutgers.zoom.us/webinar/register/-WN_fXYgjBQ6QeSklyg8L6fHYQ > , or follow the link in this flyer < https://drive.google.com/file/-d/1W2QlxQZQa9CpjOJbGAaSYUo6dqvn3hqU/-view?usp=sharing > .

If you have any questions about the event or our program, please feel free to reach out! Thanks so much for your help distributing this announcement.

Sincerely,

Malin Pinsky

Malin Pinsky (he/him/his)

Associate Professor Director, Graduate Program in Ecology & Evolution Department of Ecology, Evolution, and Natural Resources, Rutgers University 14 College Farm Rd., New Brunswick, NJ 08901 USA malin.pinsky@rutgers.edu | @pinskylab < https://twitter.com/pinskylab > http://pinsky.marine.rutgers.edu Malin Pinsky <malin.pinsky@gmail.com>

EvoltreeOnlineSeminar ClimateChangeAdaptation

EVOLTREE Online Seminar Series on Adaptation to Climate Change

After the success of our first series last year, it is our pleasure to announce the second EVOLTREE Online Seminar Series, which will focus on Adaptation to Climate Change.

These virtual seminars will feature experts in research on climate change adaptation ? both in forest trees and other organisms. The events will be an opportunity to hear the latest from leading scientists in the field, exchange ideas and discuss potential collaborations and projects.

Programme (Wednesday mornings or afternoons)

14th April 2021, 11:00-12:30 CEST: Ary Hoffmann: 'Building genetic resilience in a rapidly changing world'

21st April 2021, 16:30-18.00 CEST: Ophélie Ronce: ?Integrating niche evolution with life history theory can help us better understand the consequences of climate change?

5th May 2021, 16:30-18.00 CEST: Moisés Expósito-Alonso: ?Locally-adaptive mutations and their relevance for climate change ecology?

More information: http://www.evoltree.eu/-index.php/8-news/news-left/181-evoltree-online-seminar-series-2021-on-adaptation-to-climate Registration: https://www.eventbrite.co.uk/e/evoltree-online-seminar-series-on-adapting-to-climate-change-tickets-148236899557 Seats in the live sessions are limited to 150. All seminars will be recorded and available on the EVOLTREE YouTube channel afterwards (https://www.youtube.com/channel/-UCla0sRglK9UUPYp5Ks8hwFA).

Organizers: Stephen Cavers (UKCEH, UK), Christian Rellstab (WSL, Switzerland), Michele Bozzano, Lidwina Koop, Ewa Hermanowicz (European Forestry Institute, Finland), Santiago C. González-Martínez (INRAE, France)

christian.rellstab@wsl.ch

FieldStation Participation Survey

Good morning/afternoon/evening,

Field stations and marine labs play a critical role in enabling observations and experimental research to improve our understanding of biological processes and to monitor changing ecosystems. Field-based institutions are a unique resource that presents numerous opportunities for the communication of scientific discovery into education, public engagement, and policy. They also pose unique challenges, including their often-remote location, limited resources, and constrained communication. Through our anonymous survey, we aim to identify factors that contribute to positive and negative student experiences in order to create solutions that increase retainment and promote equity at field-based institutions and marine labs.

If you have ever worked or participated in research at a field station or marine laboratory environment, please consider filling out this anonymous survey HERE. The survey will take 20-30 minutes to complete. Information collected from this study will be kept confidential and no unique personal identifying information will be collected. The survey will be open until May 1st, 2021.

Please consider distributing widely students and STEM

professionals (both academic and non-academic).

If you have any questions or concerns about the research, you can contact Dr. Amy May at armay@ship.edu or Victoria McDermott at vmmmcdermott@alaska.edu.

Our survey has been approved by Shippensburg University under IRB number 2373 for the involvement of human subjects in our research.

SURVEY LINK https://sdsu.co1.qualtrics.com/jfe/-form/SV_cMADVZzRgYhS0rb Thank you very much for your time. For those that have previously completed this survey, we appreciate your responses and they have been recorded. We also appreciate those that provided valued comments and suggestions for the survey, we have implemented suggestions.

Dr. Amy May and Victoria McDermott

(Shippensburg University #IRB2373)

Danielle Becker <danielle_becker@uri.edu>

JMolEvol ClassicPapers

EVOLDIR reported (March 4th) that for an issue celebrating the half century of the Journal of Molecular Evolution, ten members of its editorial board each gave their personal historical perspective on a classic paper from the journal and the research it subsequently spawned. These were made available at https://-/www.springer.com/journal/239/updates/18894136 together with links to the original paper referenced. One of these classics (JME 44:632-636) described the epic clash on the pages of the journal (1995) between the neutralist ideas of Naboru Sueoka and the selectionist ideas of Donald Forsdyke. The latter has now issued an update (see Genetica 149(2):81-88; https://rdcu.be/-cjAE0).

forsdyke@queensu.ca

Mediterranean SwordfishSamples

Dear EvolDir community,

In the context of my environmental DNA post-doc I'm looking for billfish tissues for a species-specificity test

with some probes we are going to use on our target species; the swordfish, Xiphias gladius, in the Mediterranean Sea. Specifically we are looking for the most relatives of the swordfish,which are the members of Istiophoridae:

Istiompax indica Istiophorus albicans Istiophorus platypterus Kajikia albida Kajikia audax Makaira mazara Makaira nigricans Tetrapturus angustirostris Tetrapturus belone Tetrapturus georgii Tetrapturus pfluegeri

These tissues will help us to conduct the species-specifity test of our probes, and they will serve also as an outgroup. We hope to find someone willing to share these samples with us. One of each species would be sufficient.

Together with Sophie Arnaud-Haond (Ifremer, University of Montpellier) we are ready to talk more about it, just in case.

Agostino Leone agostino.leone2@gmail.com Agostino.Leone@ifremer.fr Sophie Arnaud-Haond sophie.arnaud-haond@umontpellier.fr

Agostino Leone Postdoctoral Researcher Institut Français de Recherche pour l'Exploitation de la MER (IFREMER) MARine Biodiversity, Exploitation and Conservation (MARBEC) https://annuaire.ifremer.fr/-cv/28011/en/ Station de Sète - Avenue Jean Monnet - 171 - 34203, Sète Cedex, France

Agostino Leone <agostino.leone2@gmail.com>

MustReadPapers answers

Dear colleagues,

A while ago we posted a request for online resources on must-read papers in evolutionary biology, for a literature club. We received many answers in the meantime - thank you so much! Below is a summary of all answers that we received.

All the best,

Jana and Xiaoyan

1. *Nick Barton:*

- The textbook "Evolution" by Nick Barton, with resources for exploring the literature: Barton, N. H., Briggs, D. E. G., Eisen, J. A., Goldstein, D. B., & Patel, N. H. (2007). Evolution. Cold Spring Harbor Laboratory Press.

- Papers from a course named "Classics in Evolutionary Biology":

Evolutionary Synthesis 1. Haldane, J. B. S. 1932. The causes of evolution. Longmans. New York. (esp. Ch. IV). 2. Fisher, R. A. 1930. The genetical theory of natural selection. Oxford University Press, Oxford. Selected Sections - Fundamental Theorem.

Genetic Variation 1a. Lewontin, R. C., and J. L. Hubby. 1966. A molecular approach to the study of genic heterozygosity in natural populations. II. Amount of variation and degree of heterozygosity in natural populations of Drosophila pseudoobscura. Genetics. 54:595-609.

1b. Sachidandam et al. 2001. A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. 409: 928-33.

2. Wright S., Dobzhansky T., Hovanitz W. 1942 Genetics of natural populations VII The allelism of lethals in the third chromosome of Drosophila pseudoobscura. Genetics 27: 363-394.

Recombination and evolution 1. Hill, W. G., and A. Robertson. 1966. The effect of linkage on limits to artificial selection. Genet. Res. 8:269-294.

2. Maynard Smith and Haigh. 1974. The hitch-hiking effect of a favourable gene. Genet. Res. 23: 23-35.

Understanding sequence variation 1. Begun D. J., Aquadro C. F., 1992 Levels of naturally occurring DNA polymorphism correlate with recombination rate in Drosophila melanogaster. Nature 356: 519-520.

2. Green R. E., Reich D., Pääbo S., 2010 A draft sequence of the Neandertal genome. Science 328: 710-722.

Quantitative Genetics: variation in complex traits 1. Galton F., 1877 Typical laws of heredity. Nature 15: 492-495- 512-514- 532-533.

2. Turelli M., 1984 Heritable genetic variation via mutation-selection balance: Lerch's Zeta meets the abdominal bristle. Theor. Popul. Biol. 25: 138-193.

Quantitative Genetics: finding the genes 1. Shrimpton A. E., Robertson A., 1988 The Isolation of polygenic factors controlling bristle score in Drosophila melanogaster II Distribution of third chromosome bristle effects within chromosome sections. Genetics 118: 445-459.

2. Boyle E. A., Li Y. I., Pritchard J. K., 2017 An expanded view of complex traits: from polygenic to omnigenic. Cell 169: 1177-1186.

Neutral Evolution 1. Kimura, M. 1968. Evolutionary rate at the molecular level. Science. 217:624-626.

2a. Kern A. D., Hahn M. W., 2018 The Neutral Theory in Light of Natural Selection. Molecular Biology and Evolution 110: 21077-6.

2b. Jensen J. D., Payseur B. A., Stephan W., Aquadro C. F., Lynch M., Charlesworth D., Charlesworth B., 2018 The importance of the Neutral Theory in 1968 and 50 years on: a response to Kern and Hahn 2018. Evolution 112: 2109-4.

2c. Ellegren & Galtier. 2016. Determinants of genetic diversity. Nature Reviews Genetics.

Mutation and Genetic Variability 1. Luria, S. E., and M. Delbrück. 1943. Mutations of Bacteria from Virus Sensitivity to Virus Resistance. Genetics. 28(6):491-511.

2. Hill, W G. 1982. "Rates of Change in Quantitative Traits From Fixation of New Mutations." Proceedings of the National Academy of Sciences (U.S.A.) 79: 142-45.

Testing for selection 1. McDonald & Kreitman. 1991. Adaptive protein evolution at the Adh locus in Drosophila. Nature.

2. Begun, et al. Mol. Biol. Evol. 16, 1816-1819 (1999).

3. Siddiq et al. 2016. Experimental test and refutation of a classic case of molecular adaptation in Drosophila melanogaster. Nature Ecology & Evolution.

The shifting balance 1. Wright, S. 1932. The roles of mutation, inbreeding, crossbreeding and selection in evolution. Proceedings of the VI International Congress of Genetics: 1. pp 356-366.

2. Coyne, J.A., N.H. Barton, and M. Turelli. 1997. A critique of Wright's shifting balance theory of evolution. Evolution 51: 643-671.

3. Barton. 2016. Sewall Wright on Evolution in Mendelian Populations and the "Shifting Balance". Genetics.

Evolution of Sex 1. Muller, H.J. 1964. The relation of recombination to mutational advance. Mutation Res. 1(1):2-9

2. McDonald et al. 2016. Sex speeds adaptation by altering the dynamics of molecular evolution. Nature.

Kin Selection, Cooperation, and Conflict 1. Hamilton, W. D. 1964. The genetical evolution of social behaviour I. Journal of Theoretical Biology. 7:1-52.

2. Trivers, R. L. 1974 Parent-offspring conflict. American Zoologist. 14(1):249-264.

Sexual Selection 1. Zahavi, A. 1975. Mate selection - a selection of a handicap. J. Theor. Biol. 53:205-214.

— / —

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

vancement of Science and a member of the Institute of Medicine of the National Academy of Sciences.

rmnesse@gmail.com

OmennPrize BestEvolMedArticle DeadlineSoon

The $5000 Gilbert S. Omenn Prize is awarded by the International Society for Evolution, Medicine, and Public Health for best article published in the previous calendar year on a topic related to evolution in the context of medicine and public health. Nominations for articles published in 2020, including self-nominations, are welcome until April 30, 2021. Caleb Finch will chair the prize jury.

Full information here: https://isemph.org/Omenn-Prize Link for submission here: https://airtable.com/-shrFQfv2sKrCUevpA The International Society for Evolution, Medicine & Public Health invites nominations for the Omenn Prize of $5000 for the best article published in the previous calendar year in any scientific journal on a topic related to evolution in the context of medicine and public health.

The prize, provided by the generosity of Gilbert S. Omenn, will be awarded to the first author of the winning article. The Committee, chaired this year by Caleb Finch, may elect to recognize more than one article. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.Directions for NominationsPlease submit your nomination using this brief form. The form requests a reference for the nominated article, along with a brief statement in support of your nomination.

Peer-reviewed articles with a publication date of 2020 that use evolutionary principles to advance understanding of a disease or disease process are eligible. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications.

The prize is made possible by a generous donation by Gilbert Omenn, M.D., PhD. Director of the Center for Computational Medicine and Bioinformatics at the University of Michigan where he is a Professor of Internal Medicine, Human Genetics, and Public Health. Dr. Omenn served as Executive Vice President for Medical Affairs as Chief Executive Officer of the University of Michigan Health System from 1997-2002. He is a past president of the American Association for the Ad-

RoyalSocietyPublishing MolluscanGenomics

Royal Society Publishing has recently published a special issue of Philosophical Transactions B - Theo Murphy meeting entitled Molluscan genomics: broad insights and future directions for a neglected phylum organized and edited by Angus Davison and Maurine Neiman and the articles can be accessed directly www.bit.ly/PTB1825 A print version is also available at the special price of Â£35.00 per issue from Debbie.vaughan@royalsociety.org

Felicity Davie Royal Society Publishing

T +44 20 7451 2647

The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG http://royalsocietypublishing.org Registered Charity No 207043

Felicity Davie <Felicity.Davie@royalsociety.org> Felicity Davie <Felicity.Davie@royalsociety.org>

SexSpecific Fitness data

Dear Colleagues,

We are currently conducting a meta-analysis on sex-specific fitness responses to environmental stress. Specifically, we aim to test whether the effects of environmental stress (temperature, diet, pollution etc.) on fitness parameters (reproductive success, body mass and lifespan) differ between males and females. Because meta-analyses are often sensitive to publication bias, we are looking for unpublished datasets that quantified fitness responses to stress of both sexes within the same experimental setup or field population including a control. Ideally, the data should include sample size and mean estimates (or slopes) for both sexes. If you have, or know of, such unpublished data sets, we would love to hear about it. Please email suggestions or questions to: lennarthamburg@googlemail.com Many thanks in

advance!

Tim Janicke (CEFE-CNRS, Montpellier) and Lennart Winkler (TU Dresden)

lennarthamburg@googlemail.com

SMBE CallNominationsForFacultyAwards DeadlineMay15

Dear SMBE Members:

SMBE is now calling for nominations for recipients of the faculty awards for Early-Career Excellence, Mid-Career Excellence, Lifetime Contribution, and Community Service. Please consider nominating those of your colleagues you believe deserve to be rewarded for their extraordinary achievements and dedication to the field. Updated descriptions of the awards follow; please read them carefully.

Nominations require a nomination letter, which should clearly indicate the award under consideration and also serve as a recommendation letter; a separate one-page summary of the nominee's qualifications for the award; a CV of the nominee; and an additional letter of recommendation. Self-nomination is not allowed. The nominator need not be an SMBE member, but the nominee must be a member of SMBE to be considered for the award.

SMBE Early-Career Excellence Award

This award is intended for outstanding members of the SMBE community who are in the early stages of an independent research career (3-7 years post-Ph.D.). The primary signal of research excellence is a trajectory of innovative, creative research that is moving the field of Molecular Biology and Evolution forward. The ideal candidate will be one whose career embodies the values of the society, for example in mentoring, outreach, and teaching. The prize includes recognition at the annual SMBE banquet, a cash prize of $2000 and a travel award to attend the annual meeting. This award will be made annually.

SMBE Mid-Career Excellence Award

This award is intended for outstanding members of the SMBE community who are in the midst of their research careers (8-15 years post-Ph.D.). The primary criterion is a record of truly outstanding research that has contributed broadly to the field of Molecular Biology and Evolution. The ideal candidate will be one whose career embodies the values of the society, for example in mentoring, outreach, and teaching. The prize includes recognition at the annual SMBE banquet, a cash prize of $2000 and a travel award to attend the annual meeting. This award will be made annually.

SMBE Lifetime Contribution Award

This award is intended for outstanding senior members of the SMBE community (25 years post-Ph.D.). The primary criterion is a record of truly outstanding research that has contributed broadly to the field of Molecular Biology and Evolution. The ideal candidate will be one whose career embodies the values of the society, for example in mentoring, outreach, and teaching. The prize includes recognition at the annual SMBE banquet, a cash prize of $2000 and a travel award to attend the annual meeting. This award will be made annually and initiated by the SMBE council.

SMBE Community Service Award

This award will be awarded to members of SMBE who have provided exceptional service to SMBE and the broader scientific community. The term "service" applies broadly to include specific service to the community (such as to the SMBE journals, the Council or annual meetings) and also service that includes scientific outreach and education. The prize includes an award of $2000 as well as reimbursement to attend the annual meeting. This award will be made periodically and initiated by the SMBE council.

*The materials should be compiled into a single PDF file, and should be emailed to **smbe@allenpress.com* <smbe@allenpress.com>* before 15 May 2021.*

For more information on each award and the specific application details please see the links below:

Early-Career Excellence Award

https://www.smbe.org/smbe/-AWARDS/FacultyAwards/-SMBEEarlyCareerExcellenceAwards.aspx *Mid-Career Excellence Award*

https://www.smbe.org/smbe/AWARDS/-FacultyAwards/SMBEMidCareerExcellenceAward.aspx *Lifetime Contribution Award*

https://www.smbe.org/smbe/AWARDS/-FacultyAwards/SMBELifetimeContributionAward.aspx *Community   Service   Award   *   http://-www.smbe.org/smbe/AWARDS/FacultyAwards/-CommunityServiceAward.aspx Best Regards, Marta L. Wayne

SMBE Past President

smbe@allenpress.com

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

Software SpeciesRax InferringSpeciesTrees

Dear Community,

Today, we have released our new SpeciesRax tool for efficient Maximum Likelihood based inference of species trees from gene family trees under gene duplication, loss, and transfer.

For details, please see the respective preprint:

https://www.biorxiv.org/content/10.1101/-2021.03.29.437460v1 Alexis

– Alexandros (Alexis) Stamatakis

Research Group Leader, Heidelberg Institute for Theoretical Studies Full Professor, Dept. of Informatics, Karlsruhe Institute of Technology

www.exelixis-lab.org alexandros.stamatakis@gmail.com

Webinar DemystifyingGraduateSchoolInEvol

Dear colleagues,

Now four days away! The Rutgers Ecology & Evolution graduate program is hosting an online info session and Q&A for undergraduates who may be interested in graduate school in ecology and evolution but are either unaware of the opportunities or unfamiliar with the process. If you have students you think may be interested, I'd be grateful if you could forward our invitation. Or, if there is a site at your school to which you could post this, that would be appreciated.

The session will be a 90-minute Zoom webinar and will include faculty and grad student panels with opportunities to ask questions. We'll focus on demystifying the graduate school experience, offer some brief descriptions of the kinds of research one can do, and give some advice on finding and applying to a lab in the field.

The session will be Tuesday, April 20th, from 4:00 - 5:30 pm EDT. Participants must register in advance here (https://rutgers.zoom.us/webinar/register/-WN_fXYgjBQ6QeSklyg8L6fHYQ), or follow the link in this flyer (https://drive.google.com/file/-d/1W2QlxQZQa9CpjOJbGAaSYUo6dqvn3hqU/-view?usp=sharing).

If you have any questions about the event or our program, please feel free to reach out. Thanks so much for your help distributing this announcement.

Sincerely,

Malin Pinsky

malin.pinsky@gmail.com

WestarcticaInc ConservationResScholarship May3

Westarctica, Inc announces the second annual Westarctica Conservation Scholarship, a $500 graduate research grant for the study of climate change. The goal of this research scholarship is to invest in early-career researchers who are pursuing a career in climate-change science. The topic is intentionally vague, and can include research into range-changes, evolution of adaptive characteristics, etc. Be creative!

Who we are: Westarctica, Inc is a non-profit organization focused on advocating for global conservation, framing conversations around Western Antarctica, an uninhabited ecosystem with no political advocates. Conserving our polar ecosystems means many things reducing carbon use to halt warming and melting of polar ice, learning to talk to people who deny the problem, and researching better alternatives to virtually every aspect of modern living.

Qualification: This research scholarship is available to anyone who meets the following criteria: * pursuing a graduate (Master PhD) in any nationally accredited university or organization (i.e. zoo, field station) in the world. * researching a topic aligned with climate-change or global conservation issues. * planning a research project for the summer of 2020.

Application Procedure: Please fill out the application linked on the webpage (https://www.westarctica.org/-conservation-scholarship). You will be asked to answer five questions, each in 200 words or less (unless otherwise specified): * In 20 words or less, describe the research

question you are addressing. * What is the broad problem this question is addressing? * Why should the public care about your question/the problem/your research? * What possible solutions to climate-change might your work propose? * How will this money improve your research or the proposed solutions?

These applications will be reviewed by a panel of scientifically trained people from a variety of research and conservation backgrounds, as well as Westarctica, Inc board members. Finalists will be chosen, and the above answers will be submitted to the active members of the organization for a final vote.

Important Dates: May 3, 2021 (5pm EST): Applications Close May 10-14, 2021: Finalist selected and members vote May 17, 2021: Winner Announced

Requirements: In accepting the award, you agree to do one follow-up interview at the end of the research period, and complete one short, online course on talking about climate change to climate-deniers.

Last year's winner: Abena Dufie Wiredu Bremang, a doctoral student at the Kwame Nkrumah University of Science and Technology in Ghana was selected as the recipient of the 2020 Westarctica Conservation Scholarship. She was previously honored as a UNESCO Young Scientist in 2018 for her work on the effect of land use on water quality in the Lake Bosomtwe Biosphere Reserve.

Abena will used the grant to further her research on the hydrological impacts of climate change on water security of the White Volta Basin. The White Volta Basin is a transboundary region in West Africa shared between the countries of Burkina Faso, Ghana, and Togo. The Volta River and its tributaries provide water for many rural communities who depend on it to support their rural livelihoods.

If there are any questions, please feel free to email conserve@westarctica.info

"Sanders, Sheri" <ss93@iu.edu>

PostDocs

Arizona ComputationalPopulationGenomics

The Gutenkunst group at the University of Arizona has two open postdoc positions focused on computational population genomics. Both positions relate to our recent NIH grant to explore new models of natural selection within and between populations. We are seeking both candidates interested in developing novel inference methods and candidates interested in applying those methods to interesting data sets. Candidates interested in the application side should have some computational population genetics or molecular ecology experience, while candidates interested in methods development may have less specific biological experience but more statistical training. To learn more about our group, see http://gutengroup.mcb.arizona.edu/ . If interested, contact me at rgutenk@arizona.edu with your CV and any questions. Application review is ongoing and will continue until both positions are filled.

"rgutenk@arizona.edu" <rgutenk@arizona.edu>

BishopMuseumHawaii Biodiversity

The Bernice Pauahi Bishop Museum, the premier museum of Natural History and Culture of the Pacific, in collaboration with the Hawaii Department of Land and Natural Resources' Snail Extinction Prevention Program, is seeking highly qualified applicants for a Postdoctoral Fellowship. The successful applicant will join a team of passionate conservationists, taxonomists, and biodiversity researchers in Honolulu, Hawaii and help lead the development of genomic tools as part of the captive rearing program for Hawaiian land snails. The postdoc will primarily work in the Pacific Center for Molecular Biodiversity at the Bishop Museum where they will lead the development of genomic tools for parasite and pathogen detection in endangered and captive-reared land snails in Hawaii.

For details and to submit application materials visit https://www.bishopmuseum.org/careers/ Informal inquiries can be emailed to Dr. Kenneth A. Hayes (kenneth.hayes@bishopmuseum.org)

Kenneth A. Hayes

Director of Pacific Center for Molecular Biodiversity

Bishop Museum

T: 808.847.8217

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

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

About PCMB < https://www.bishopmuseum.org/pcmb/ >

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

hayes.ken@gmail.com

DanishTechU ComputationalPopulationGenetics

DTU Health Tech seeks qualified candidates for a vacant postdoc position in computational population genetics with a potential start date around September 1st 2021 (or according to mutual agreement).

In this position you will develop algorithms and computational methods to deal with the analysis of large datasets from modern and ancient sources. More specifically, these algorithms will be aimed at analyzing a large number of ancient genomes using population genetics methods. The bioinformatics section of DTU Health Tech performs research in the areas of different metagenomics, machine learning, cancer genomics and population genomics. Additional information should be obtained by contacting the potential main supervisor directly. The university is located in the greater Copenhagen area, which is acknowledged for its excellent standards of living, childcare and welfare system.

Current bioinformatics algorithms and software are often ill-equipped to deal with DNA extracted from ancient populations. This ancient DNA shows high levels of fragmentation and accumulated chemical damage. Furthermore, the number of individuals that can be sequences is often limited. Fortunately, several problems pertaining to ancient DNA and ancient paleogenetics can be described in a maximum-likelihood framework and computer science techniques can help us to solve such numerical problems efficiently via machine learning, numerical algorithms and data structures. You will work in collaboration with other partners including the University of Copenhagen in order to develop the next generation of algorithms and software applied to DNA from fossils which can then be used to reconstruct population history and infer selection.

Given the COVID19 pandemic, we will happily accommodate requests for remote work until in-person work is deemed safe.

Qualifications You must hold a PhD degree (or equivalent) ideally in biological science with a focus on quantitative and mathematical aspects, or in computer science or mathematics.

The candidate we are looking for should ideally have the following qualifications:

* Knowledge of a programming language like Python, Perl, C++ and/or Java * Ability to work in a UNIX environment, ideally in a high-performance computing environment * Ideally, proficiency in C/C++ or Java or similar is a plus (not required) * Thorough understanding of basic principles of population genetics * Knowledge of probabilities and statistics * Firm grasp of first-year university mathematics (differential calculus/linear algebra) * Knowledge of coalescence theory or diffusion theory is an advantage * Expertise in next-generation sequencing data generation and processing are also a plus

The language of communication at DTU is English.

We offer DTU is a leading technical university globally recognized for the excellence of its research, education, innovation and scientific advice. We offer a rewarding and challenging job in an international environment. We strive for academic excellence in an environment characterized by collegial respect and academic freedom tempered by responsibility.

Application Your complete online application must be submitted no later than 10 June 2021 (Danish time).

Apply at: https://www.dtu.dk/english/about/job-and-career/vacant-positions/job?id=3Db0566e4d-7261-467c-a05f-f8af13e040fa   Gabriel Renaud <gabriel.reno@gmail.com>

HeidelbergU Bioinformatics

BIOINFORMATICS POSTDOC IN EVOLUTIONARY GENOMICS

Center for Molecular Biology (ZMBH), Heidelberg University, Germany

A postdoctoral position (3 years with possible extensions) is available immediately in the evolutionary genomics group of Henrik Kaessmann.

We are seeking highly qualified and enthusiastic applicants with strong skills in computational biology/bioinformatics, ideally also with experience in data mining and comparative or evolutionary genome analyses.

We have been interested in a range of topics related to the origins and evolution of vertebrate organs. In the framework of our research, we generate and analyze comprehensive genomics (e.g., RNA-seq, ATAC-seq) datasets based on samples from our large organ collections. More recently, we have begun to bring the work

of our lab to the level of single cells using state-of-the-art single-cell genomics technologies and bioinformatics procedures.

The postdoctoral fellow will be funded by a recently awarded ERC Advanced Grant. In the framework of this grant, we seek to unravel the cellular and molecular origins and evolution of the vertebrate brain. The fellow will perform integrated evolutionary/bioinformatics analyses based on data produced in our lab and available genomic data. The precise project will be developed together with the candidate.

In our lab, we attach great importance to a highly collaborative and positive team spirit! And we are particularly fond of the diverse cultural backgrounds of our lab members, which contribute to a very enriching atmosphere.

The language of our institute is English and its members form a highly international group. The ZMBH is located in Heidelberg, a picturesque international city next to the large Odenwald forest and Neckar river. The city offers a very stimulating, diverse and collaborative research environment, with the European Molecular Biology Laboratory (EMBL), German Cancer Research Center (DKFZ), Heidelberg Institute of Theoretical Studies (HITS), and the Max Planck Institute for Medical Research located in close proximity to the University.

For more information on the group and our institute more generally, please refer to our website at the ZMBH (http://www.zmbh.uni-heidelberg.de/Kaessmann/).

Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (h.kaessmann@zmbh.uni-heidelberg.de).

– Selected publications:

Wang, Z.Y., Leushkin, E., Liechti, A., Ovchinnikova, S., Mößinger, K., Brüning, T., Rummel, C., Grützner, F., Cardoso-Moreira, M., Janich, P., Gatfield, D., Diagouraga, B., de Massy, B., Gill, M.E., Peters, A.H.F.M., Anders, S., and Kaessmann, H. (2020) Transcriptome and translatome co-evolution in mammals. Nature 588: 642-647.

Cardoso-Moreira M., Halbert, J., Valloton, D., Velten, B., Chen, C., Shao, Y., Liechti, A., Ascençāo, K., Rummel, C., Ovchinnikova, S., Mazin, P.V., Xenarios, I., Harshman, K., Mort, M., Cooper, D.N., Sandi, C., Soares, M.J., Ferreira, P.G., Afonso, S., Carneiro, M., Turner, J.M., VandeBerg, J.L., Fallahshahroudi, A., Jensen, P., Behr, R., Lisgo, S., Lindsay, S., Khaitovich, P., Huber, W., Baker, J., Anders, S., Zhang, Y.E., and Kaessmann H. (2019) Gene expression across mammalian organ development. Nature 571: 505-509.

Sarropoulos, I., Marin, R., Cardoso-Moreira, M., and Kaessmann, H. (2019) Developmental dynamics of lncRNAs across mammalian organs and species. Nature 571: 510-514.

Cortez, D., Marin, R., Toledo-Flores, D., Froidevaux, L., Liechti, A., Waters, P.D., Grutzner, F., and Kaessmann, H. (2014) Origins and functional evolution of Y chromosomes across mammals. Nature 508: 488-493.

Necsulea, A., Soumillon, M., Warnefors, M., Liechti, A., Daish, T., Zeller, U., Baker, J.C., Grutzner, F., and Kaessmann, H. (2014) The evolution of lncRNA repertoires and expression patterns in tetrapods. Nature 505: 635-640.

Brawand, D., Soumillon, M., Necsulea, A., Julien, P., Csardi, G., Harrigan, P., Weier, M., Liechti, A., Aximu-Petri, A., Kircher, M., Albert, F.W., Zeller, U., Khaitovich, P., Grutzner, F., Bergmann, S., Nielsen, R., Paabo, S., and Kaessmann, H. (2011) The evolution of gene expression levels in mammalian organs. Nature 478: 343-348.

Henrik　　　Kaessmann　　　<h.kaessmann@zmbh.uni-heidelberg.de>

HongKongU EvolutionaryGenomics

*** Postdoctoral Position in Evolutionary Genomics ***

We are looking for a Postdoctoral Researcher to work on genomics projects on non-model species. The lab has several study systems and active projects addressing population genomics, comparative genomics, genotype-phenotype association, and behavioural genetics. A key focus of the lab is to use genomic, epigenomic and transcriptomic data to understand the genetic basis and evolution of phenotypic traits. Collaborative international projects are already underway, ensuring a quick and productive start. The Postdoctoral Researcher will have extensive opportunities to interact with collaborators and be involved in different evolutionary and ecological genomics projects.

Duration: The initial appointment is for one year, with renewal based on performance. Funding is available for two years. This is a full time appointment.

Qualifications: Applicants must have completed a PhD (or will have completed a PhD before the position starts) in bioinformatics, genomics, evolutionary biology, population genetics, or a related discipline, with a demon-

strated record of research achievement (via publications). They will also be proficient with programming in a scripted language (e.g. Python, Perl, or R). Experience with shell scripting and computing cluster environments and/or experience working with whole genome datasets in population or comparative genomics will be beneficial.

Working Environment: The University of Hong Kong is an English-speaking institute and one of the most international universities in Asia. It has a rank of 39 according to the Times Higher Education World University Rankings 2021.

Start Date: Flexible in 2021.

Salary: A highly competitive salary plus annual leave and medical benefits will be offered.

How to apply: Please send a CV (with contact information for three references), cover letter describing research interests and skills, and copies of publications to Simon Sin (sinyw@hku.hk). Review of applications will begin immediately and continue until the position is filled.

Simon Sin

Assistant Professor School of Biological Sciences Kadoorie Biological Sciences Building The University of Hong Kong Pok Fu Lam Road, Hong Kong www.simonywsin.com <sinyw@hku.hk>

pskmmsin@gmail.com

ImperialC 3 ComputationalBiology

Job Summary: We are seeking three Postdoctoral Research Associate positions in computational ecology. The project is to create a virtual rainforest: a general ecosystem model replicating all physical and biotic components of the ecosystem and their interactions, with a view to understanding system-level emergent properties. We are particularly interested in finding applicants with an interest in systems ecology and experience in process-based modelling. However, this project requires team members who provide complementary and diverse technical skills and disciplinary knowledge, so applicants from any ecological background and/or with any relevant skillset are encouraged to apply. Positions are open to full or part-time applicants, and you will be given time, resources and encouragement to pursue your professional development.

Project Description: We are building a team to create a virtual rainforest: a general ecosystem model replicat-

ing all physical and biotic components of the ecosystem and their interactions, with a view to understanding system-level emergent properties. The virtual rainforest will link all of the biotic and abiotic system components through nutrient cycling, stoichiometric and metabolic processes. It will track the birth, growth and death of cohorts of plant, animal and soil microbial functional groups, and the movement of carbon, nitrogen, phosphorus, water and energy through the ecosystem. At its heart, the virtual rainforest will be an individual-based simulation of plants, animals, microbes and their interactions with the abiotic environment, and which rests upon the key individual-based processes of metabolism, respiration, reproduction and mortality. The virtual rainforest will be used to gain insight into the processes that govern three key, emergent properties of rainforests: their stability, resilience and sustainability.

Ecosystems cannot be understood through piecemeal studies of their individual components. The discipline of tropical forest ecology has at its disposal ever-accumulating datasets examining all aspects of rainforest ecosystems giving insight into everything from the population dynamics of plants through to the scavenging behaviour of ants. This knowledge allows us to understand much of how the ecosystem operates and the ecosystem services it generates, but in a disjointed fashion. As a Postdoctoral Research Associate in Computational Ecology, you will be part of an attempt to tie that knowledge into a single, comprehensive understanding of how the ecosystem operates in its entirety.

Duties and responsibilities:

The primary role of successful applicants will be to develop one of the four modules of the virtual rainforest: plant, animal, soil microbial or abiotic processes. You will be assisted in this by additional team members, including your peers, a separately appointed scientific programmer and postgraduate students. The project provides a generous budget for placements and secondments to give you the freedom to work with, and harness the expertise of, research groups beyond our own. The virtual rainforest will lean heavily on data collected from the SAFE Project (www.safeproject.net), and you will be required to help with the management of these datasets. All team members will be expected to help develop the skills and competencies of their peers through the sharing of tasks and knowledge. As part of a research group and environment that extends beyond the virtual rainforest team, you will contribute to the supervision of undergraduate and postgraduate student projects. You will be given time, resources and encouragement to pursue your professional development, along with opportunities to gain teaching experience in the form of tutorials, lectures, practical classes and field trips.

Essential requirements: We require team members who provide complementary technical skills and disciplinary knowledge, so applicants from any ecological background and with any relevant skillset are encouraged to apply. No individual team member is expected to have more than a small subset of this list of topics and skills, and we specifically encourage applicants to clearly identify the subset of skills that they could bring to the team. Among the team members, we will need understanding of plant, animal and microbial ecology, along with functional ecology, metabolic ecology, ecological stoichiometry, biogeochemistry, hydrology and microclimate processes. Candidates with an interest in systems ecology and the concepts of stability, resilience and sustainability are particularly encouraged to apply. Some programming experience - preferably in Python - is necessary for all applicants. Experience with either process-based or numeric simulation modelling is desirable, as is experience with error propagation and ecological statistics. We are also seeking experience with version

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ImperialCollegeLondon 3 ComputationalEvolution

Our research group is advertising three Postdoctoral Research Associate positions in computational ecology. The project is to create a virtual rainforest: a general ecosystem model replicating all physical and biotic components of the ecosystem and their interactions, with a view to understanding system-level emergent properties. I am particularly interested in finding applicants with an interest in systems ecology and experience in process-based modelling. However, this project requires team members who provide complementary and diverse technical skills and disciplinary knowledge, so applicants from any ecological background and with any relevant skillset are encouraged to apply. Positions are open to full or part-time applicants, and you will be given time, resources and encouragement to pursue your professional development.

More details and information about the application process can be found on Imperial College London's website (job reference NAT00878).

https://www.imperial.ac.uk/jobs/description/-NAT00878/research-associate-computational-ecology
Rob Ewers

Professor of Ecology

Imperial College London

https://www.imperial.ac.uk/people/r.ewers "Ewers, Robert M" <r.ewers@imperial.ac.uk>

Krakow PlasticityTranscriptomics

Institute of Nature Conservation PAS Krakow Poland.PlasticityTranscriptomics

Postdoc position in the project 'Integrating effects of anthropogenic and natural stressors: phenotypic and genetic expression approach' at the Institute of Nature Conservation PAS, Krakow, Poland in collaboration with the Jagiellonian U. U of Lodz, Norwegian Institute for Nature Research and Norwegian Veterinary Institute.

Cities as 'heat islands' are often hot spots for alien invasive species that can drastically alter population dynamics of native species. In addition, natural stressors such as seasonal time and thermal constraints at high latitudes can strongly affect organism fitness. The aim of the project is to understand how anthropogenic and natural stressors: urbanization, native and invasive alien predators, and latitudinal gradient affect traits linked to fitness down to gene expression level in a common bluetail damselfly.

Requirements: PhD in biology, ecology or related field (PhD defense not earlier than 7 years before the year of employment in the project); Experience in field and laboratory work on aquatic/semi-aquatic invertebrates; An experience in using molecular methods to address ecological or evolutionary questions, with an appropriate publication track record; Good working knowledge of R environment, including advanced skills in statistical modelling; Working knowledge of standard bioinformatics tools in the Linux environment; Publication record including articles in leading ecological and evolutionary journals; Involvement in work during irregular working hours (during field work); Strong motivation for work in the project; Fluency in English, written and spoken; Valid driving license; Experience in and enthusiasm for working in an international team would be an asset.

I have funding from Norway grants under the Norwegian

Financial Mechanism 2014-2021.

Principal investigator: Dr hab. inÂ¿. Szymon Âniegula, http://www.iop.krakow.pl/-pracownicy,102,szymon_sniegula.html Feel free to contact me at ecopond@iop.krakow.pl

The posting is here https://www.iop.krakow.pl/files/-327/jsz_call_2021_en_2.pdf Closing date: 21 May 2021

Starting date of employment: 1 June 2021

– Szymon Sniegula Institute of Nature Conservation Polish Academy of Sciences Mickiewicza 33 31-120 Krakow, POLAND

phone: +48 602 152996 e-mail: szymon.sniegula@gmail.com my personal website < http://www.iop.krakow.pl/-pracownicy,102,szymon_sniegula.html >

Szymon Sniegula <szymon.sniegula@gmail.com>

LausanneSwitzerland EvolNeuroGenomics

The Arguello Lab (http://arguellolab.org/) is looking for a postdoc that will lead the computational analyses of our work on the evolution of sensory organs using bulk RNA-seq and single-cell 'omic' datasets. This work will be carried out using ecologically diverse Drosophila species. The postdoc will work alongside a technician that will be involved in data generation.

We are a research group in the University of Lausanne's Department of Ecology and Evolution, and a member group of the Swiss Institute of Bioinformatics (https:-/www.sib.swiss/). Our interests are in the genomic and cellular bases of sensory differences and sensory-related behaviors, as well as other fundamental evolutionary genomic questions. We combine tools and approaches from evolutionary/population genomics, neurobiology/neurogenetics, developmental biology, behavioral biology, and large-scale genomics. Our team includes experimentalists and computational biologists (hybrid expertise always welcomed). Ecologically diverse Drosophila species provide our model system(s).

The Department of Ecology and Evolution is a lively, fun, productive, and highly diverse group. While UNIL is a French-speaking university, the working language of the Department and the lab is English. For more information about the Department of Ecology and Evolution please follow this link: https://www.unil.ch/-dee/en/-home.html Lausanne is a scenic medium-sized city situated on the edge of Lake Geneva. Life here is good. Its central location within Europe makes traveling by train and plane convenient. For outdoor enthusiasts, Lausanne sits at the base of Alps and Jura Mountains which offer year-round escape and fun.

Job information: Expected start date in position: 01.07.2021, negotiable Contract length: 1 year, renewable up to a maximum of 4 years, depending on funding availability Activity rate: 100% Workplace: University of Lausanne, Lausanne Switzerland

Key responsibilities: The details of the research project will be defined between the postdoc and group leader. Most of her/his time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. The job description stipulates:

~80% Personal research ~15% Participation to teaching/mentoring activities ~5% Various lab/institutional tasks.

Key experience and competencies: The candidate should be imaginative, dynamic and collegial. Computational experience is a necessity, as is a demonstrated ability to perform high-quality quantitative research, and capacity to formulate hypotheses, test them, and follow the work through to completion/publication.

Essential: - PhD degree in the biological sciences with strong computational expertise (i.e. evolutionary biology, neurobiology, developmental biology, systems biology) - Excellent computer programming (i.e. Python, R) and quantitative skills - Experience in genomics - Track record of writing papers as evidenced by publications, pre- prints or submitted manuscripts in referred journals - Evidence of data presentation at scientific meetings - Ability to work independently and within a group - Strong motivation and enthusiasm for science

Desirable: - Experience in evolutionary genomics - Experience with single-cell analysis and/or transcriptomics/epigenomics and/or systems biology - Experience working with large-scale datasets

For more information about the lab and projects, or for further questions, please visit: arguellolab.org or email Roman at: roman.arguello@unil.ch. Formal applications have to be made through HR and must include a cover letter detailing your research interests and background, a CV, and the names of references (2-3). Applications should both be uploaded through the University of Lausanne platform (via the link below), and sent as a single pdf to roman.arguello@unil.ch.

Application link: https://bit.ly/3mIF8NM Deadline :

15.05.2021

Roman Arguello Ecology & Evolution University of Lausanne Swiss Inst. of Bioinformatics arguellolab.org @EvoNeuroLab

roman.arguello@unil.ch

LinkopingU EvolutionaryGenetics

Postdoctoral position in evolutionary biology/genetics

A postdoctoral position is available to work on an ERC-funded project in the laboratory of Professor Dominic Wright, in the Department of Biology at Link?ping University, Sweden

For this position we are looking for a candidate with a strong background in evolutionary genetics, quantitative genetics and/or bioinformatics. The successful candidate will be part of an interdisciplinary team of researchers investigating the genomic basis of feralisation.

The project explores the molecular mechanisms underlying evolutionary transitions from domestication to re-wilding (feralisation) using a series of feral chickens derived from Hawaii and Bermuda. Using a powerful combination of genomics, transcriptomics, field assays and laboratory experimental evolution the project aims to reveal the genes and causal polymorphisms responsible for re-adaptation to a wild environment, and how these progresses. The project will involve a large amount of sequence data analysis, coming from single cell sequencing data (including both sc RNAseq and sc ATACseq data), as well as conventional whole genome re-sequencing and RNA-seq data.

The candidate will work on various projects, but one of the main ones will involve a combination of expression and ATAC seq QTL analysis using the data generated by single cell sequence data. In addition, selective sweep mapping and other forms of population genetic analysis will be performed. The candidate should therefore be proficient in some or all of these techniques or have specialisation in at least one.

The project will perform Genome Wide Association Mapping using a series of different populations of feralised chickens (domestic birds that have escaped and are now living wild throughout the Hawaiian Island chain), in combination with a wild x domestic chicken intercross to map the genes and polymorphisms underlying their rapid responses to newly imposed selective forces. In this instance the combination of integrating both single cell expression QTL and single cell ATAC-seq QTL will enable the identification of the genetic basis of transcriptomic regulation occurring between wild and domestic chickens down to the specific cell type, whilst the simultaneous mapping of epigenomic and transcriptomic data from the same nucleus should also enable the identification of both the causal elements and causal genes for the regulatory machine in the chicken hypothalamus. Similarly, sweep mapping and other population genetic parameters will be assayed in these feral populations to identify which regions are most important in the response to selection in these populations.

Representative papers for the populations to be used can be found in the following articles: H?glund et al. 2020 Nature Ecology and Evolution (https://doi.org/10.1038/s41559-020-01310-1), Johnsson et al. 2016 Genetics 202, 327-340 (https://doi.org/10.1534/genetics.115.179010) Johnsson et al. 2016 Nature Communications 7, 1-11. (https://www.nature.com/articles/ncomms12950.pdf)

This is an exciting opportunity to combine a wide variety of genomic and transcriptomic tools along with the opportunity for fieldwork and labwork as part of a vibrant and friendly team.

Please apply using the link below

https://liu.se/en/work-at-liu/vacancies?rmpage=job&rmjob=15974&rmlang=UK Rie Henrâ, Assistant professor

IFM Biology

Linköping University

58183 Linköping

SWEDEN

email: rie.henriksen@liu.se

Phone: +46 (0) 70 089 50 84

https://www.researchgate.net/profile/Rie_Henriksen https://liu.se/en/research/henriksen-group Rie Henriksen <rie.henriksen@liu.se>

LundU Paleogenomics

LundU.Paleogenomics A 2-years postdoc position is available at my Lab at Lund University, Sweden.

We aim to develop Machine Learning methods that date and biolocalize ancient genomes with application to Viking genomes and answer questions about their mysterious origins and whereabouts.

This is a multi-disciplinary project involving programming and modeling. In addition, the project will involve collaborations with researchers in other disciplines, including biomathematics, biostatistics, and molecular biology. The candidate is expected to have a strong grounding in programming in R and math/statistics. To read more and apply, click here: https://lu.varbi.com/what:job/jobID:390453/?lang=en Eran Elhaik <eran.elhaik@biol.lu.se>

LundU PlantGenomics

LundU.PlantGenomics A 2-years postdoc position is available at my Lab at Lund University, Sweden.

We are interested in developing an optimized system of using DNA and RNA NGS and mapping data to identify genes associated with how a crop plant responds to biotic treatment for biocontrol and biostimulation.

This is a multi-disciplinary project involving programming and modeling. In addition, the project will involve collaborations with researchers in other disciplines, including biomathematics, biostatistics, and molecular biology.

To read more and apply, click here: https://lu.varbi.com/what:job/jobID:390452/?lang=en Eran Elhaik <eran.elhaik@biol.lu.se>

MonashU Evolution mtDNA heteroplasmy

Research in Damian Dowling's laboratory is focused on the role the mitochondrial genome plays in evolutionary adaptation.

We seek a talented and highly-motivated postdoctoral researcher to join our laboratory group, to study the evolutionary implications of heteroplasmy V the scenario in which multiple mitochondrial DNA haplotypes exist within one individual. Recent studies indicate heteroplasmy is widespread, and can be caused by paternal transmission of mtDNA. But the effects of heteroplasmy on evolutionary processes remain unclear, and many important questions unanswered.

This project will integrate experimental techniques in molecular biology and evolutionary biology, leveraging the model species *Drosophila melanogaster*, to study the effects of heteroplasmy in shaping evolutionary responses to natural selection.

As the successful candidate, you will have a PhD degree, a record of publication in international journals, strong skills in molecular biology including genotyping and qPCR, prior experience of using *Drosophila* for genetics research, and an understanding of evolutionary concepts. Experience in microinjection, or mitochondrial-related research, is a plus.

You will have opportunities to co-supervise undergraduate and Master's level research projects within the Dowling group, and to collaborate with international leaders in the field of mitochondrial biology.

This role is a full-time position for a tenure of 24 months; however, flexible working arrangements may be negotiated.

Monash University is located in Melbourne Australia, and consistently ranks within the World's top 100 universities.

For full details of opportunity and associated position description: https://careers.pageuppeople.com/513/cw/en/job/617438/research-fellow Please send all enquiries to Professor Damian Dowling, Head, Experimental Evolutionary Biology Lab at Monash University's School of Biological Sciences: damian.dowling@monash.edu Closing Date Monday 10 May 2021, 11:55 pm AEST

Damian Dowling <damian.dowling@monash.edu>

MonashU MitochondrialEvolution

Research in Damian Dowling's laboratory is focused on the role the mitochondrial genome plays in evolutionary adaptation and in the evolution of sex differences. Maternal inheritance of the mitochondrial genome renders the mitochondrial DNA vulnerable to the accumulation of mutations that are harmful to males, but neutral or beneficial to females.

We seek a talented and highly-motivated postdoctoral researcher to join our laboratory group, to study the mechanisms that enable mitochondrial mutations to exert differences in their effects on each of the sexes.

The project will integrate experimental techniques in molecular biology, evolutionary genomics, and mitochondrial physiology.

As the successful candidate, you will have a PhD degree, a record of publication in international journals,strong skills in molecular biology, evolutionary genomics or mitochondrial physiology.

You will have opportunities to co-supervise undergraduate and Master's level research projects within the Dowling group.

This role is a full-time position for a tenure of 24 months; however, flexible working arrangements may be negotiated.

Monash University is located in Melbourne Australia, and consistently ranks within the World's top 100 universities.

For full details of opportunity and associated position description: https://careers.pageuppeople.com/513/cw/-en/job/616606/research-fellow Please send all enquiries to Professor Damian Dowling, Head, ExperimentalEvolutionary Biology Lab at Monash University's School of Biological Sciences: damian.dowling@monash.edu Closing Date Monday 17 May 2021, 11:55 pm AEST

Damian Dowling <damian.dowling@monash.edu>

Montpellier SpeciationGenomics

2-year postdoctoral position in population genomics and speciation in Montpellier, France

We seek a postdoctoral researcher with experience in population genomics to work on an ANR (French research agency)-funded project (ANR MECADAPT) addressing the mechanisms of adaptation and speciation in a phytophagous species, the pea aphid (Acyrthosiphon pisum). This pest species is a model system in ecological specialisation and speciation studies due to its complex of plant-specialised biotypes that form a continuum of divergence from closely related host races to incipient species. The postdoc will be in charge of population genomics approaches to explore the evolutionary history of biotype formation and diversification in the pea aphid complex. She/he will perform demographic inferences to reconstruct the evolutionary and demographic history of biotype diversification and genomic differentiation analyses to characterise loci involved in reproductive isolation and the dynamics of genomic differentiation as speciation unfolds. Datasets made of >200 pooled and individual resequenced genomes from worldwide samples will be available at the start of the project and will be expanded during the project. The project allows for much flexibility in the direction taken depending on the postdoc's interests and ideas.

The position will be based at CBGP (Centre of biology for the management of populations), Montferriez-sur-Lez, near Montpellier, France, in strong interaction with ISEM (Institute of Evolutionary Science of Montpellier). The postdoc will closely work with Carole Smadja (ISEM/CBGP), Emmanuelle Jousselin (CBGP), Mathieu Gautier (CBGP) and Renaud Vitalis (CBGP) and will benefit from the available expertise in population genomics, speciation/adaptation genomics and aphid evolution and biology at the host institution. The postdoc will also collaborate with the other partners of the ANR project based in Rennes (Jean-Christophe Simon, Julie Jaquiéry, Fabrice Legeai at IGEPP - INRAE), in Poitiers (Jean Peccoud at EBI - University of Poitiers), and Sheffield (Roger Butlin, Animal and Plant Sciences Department - University of Sheffield, UK). The postdoc will therefore benefit from a rich collaborative network, as well as a stimulating working environment in Montpellier, a centre of excellence in biodiversity research and known for its quality of life in the Mediterranean

region.

Applicants should have a PhD in a relevant area (evolutionary biology, population genomics). We are seeking someone with a vivid interest in evolutionary biology and speciation/adaptation research and with a strong background in population genomics and statistical genetics. Experience in handling genomic data and population genomics methods, as well as skills in bioinformatics and programming, are required. A plus would be a candidate with existing experience with methods for demographic inference. The candidate should have excellent skills in written and spoken English to be able to communicate the results of her/his work. Candidates will not need to speak French since the working language can be English.

The appointment is for 2 years minimum (up to 32 months, depending on the level of experience at which the postdoc will be hired), with a possible starting date between July and September 2021. Net monthly salary will be between 1950 and 2480 euros, depending on experience. Inquiries can be addressed to Carole Smadja (carole.smadja@umontpellier.fr) and Emmanuelle Jousselin (emmanuelle.jousselin@inrae.fr) for further information. Applications should be sent by email to Carole Smadja and Emmanuelle Jousselin, accompanied by a cover letter, a detailed CV, a list of publications, and two recommendation letters.

Deadline for application: 15/05/2021; Reviewing of applications will begin soon after the deadline but the position will remain open until a suitable candidate is identified.

Dr. Carole Smadja Directrice de recherche CNRS - CNRS Senior researcher Directrice adjointe de l'ISEM - ISEM Deputy director mailto:carole.smadja@umontpellier.fr phone : +33 (0)4 67 14 92 70

Institut des Sciences de l'Evolution de Montpellier - Institute of Evolutionary Science of Montpellier (ISEM) [https://isem-evolution.fr/ | https://isem-evolution.fr/en/] ISEM UMR 5554 cc065 Campus Triolet - University of Montpellier - 34095 Montpellier Cedex 05 - France

Carole Smadja <carole.smadja@umontpellier.fr>

NHM Oslo FungalSystematics

I have a 4-year postdoc position in fungal systematics announced at NHM, Oslo.

https://www.jobbnorge.no/en/-available-jobs/job/203962/postdoctoral-fellow-in-fungal-systematics?fbclid=-IwAR3DhAUwybL2uHo5OR0zGvshtA8wRzHAxc4vl7fTA7fuWAlSVve0

Mika Bendiksby Associate professor of Systematic Mycology and Curator of Fungarium (O) Natural History Museum, University of Oslo Postboks 1172, Blindern 0319 Oslo Norway

Mika Bendiksby <mika.bendiksby@ntnu.no>

NordUNorway AdaptationGenomics

2-year researcher/postdoc position on temperature adaptation in Littorina snails

We invite applications for a two-year researcher position in evolutionary biology at the Faculty of Biosciences and Aquaculture, Nord University (Bodø, Norway). The position is available from 1 June 2021. Applications must be submitted electronically (link below) by 2 May 2021.

The successful candidate will study the genomic basis of temperature adaptation in the marine snail Littorina saxatilis. Understanding how organisms adapt to their environment at the genomic level is a major goal in evolutionary biology; research on adaptation to local climatic conditions obtains great urgency in times of anthropogenic climate change. L. saxatilis is an emerging model system in evolutionary genomics and very suitable for studying temperature adaptation as it inhabits a large range of climatic environments, which often vary on small spatial scales.

The position will be part of an international project funded by the Research Council of Norway focusing on how temperature adaptation changes across space, e.g. whether the same traits and loci contribute to adaptation to warm temperatures in different geographical locations. Towards this goal, snail sampling across Europe will be combined with experimental and genomic approaches.

The successful candidate will have documented enthusiasm for evolutionary research questions, a strong academic record, and the ability to work independently while being part of a larger research team. Experience in the analysis of large-scale genomic data sets is essential. Ideally the candidate will have experience in one or more of the following areas: Quantitative genetics, analysis of gene expression (RNAseq) data, biological field work, experimental work. We are looking for a

researcher with the motivation and experience to supervise other members of the team. In addition, the researcher is expected to organise part of the fieldwork and experimental work independently.

The postdoc will be part of an international team of scientists across Europe (https://-littorina.group.shef.ac.uk), connected by a common interest in evolutionary processes and enthusiasm for discussion, creativity and diversity in research. The project will include work at the Tjärnö Marine Lab in Sweden and possibilities to visit European collaborators.

Further details about the position and how to apply can be found here: https://www.jobbnorge.no/en/-available-jobs/job/202881/researcher-position-2-years-in-evolutionary-biology-adaptation-genomics Anja Westram anja.westram@ist.ac.at

"anja.westram@ist.ac.at" <anja.westram@ist.ac.at>

NorthCarolinaStateU PlantMicrobeQuantGenetics

Our team is searching for a postdoctoral researcher to investigate mechanisms of microbe-dependent heterosis in maize. The background on this project can be found here: https://www.biorxiv.org/content/10.1101/-2020.05.05.078766v2 One of the objectives involves mapping the genetic architecture of responses to microbes at homozygous & heterozygous loci. The successful applicant will have a strong background in quantitative genetics, statistics, and/or breeding. At least some interest or background in plant-microbe interactions would be helpful but not required - this is an opportunity to develop experience in that field.

The position is for 3 years and based in Peter Balint-Kurti's lab at NCSU. It will also involve close collaboration with Maggie Wagner's lab at U. Kansas as well as Manuel Kleiner's at NCSU. NCSU is located in Raleigh, part of the Research Triangle region of North Carolina, USA.

Link to job ad: jobs.ncsu.edu/postings/142605

Applications will be reviewed starting May 3rd, 2021.

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

NorthCarolinaStateU PopulationGeneticsModeling

Postdoc: Modeling Gene Drive and Evolution of Insecticide Resistance in Mosquitoes

OVERVIEW: We have funding from NIH for a project titled "Combining Aedes aegypti genomics and modeling to improve gene drive strategies and our understanding of insecticide resistance evolution". Aedes aegypti is the primary vector of dengue, Zika, chikungunya, and urban yellow-fever. We are searching for a postdoc to work on the modeling aspects of the project.

PROJECT DESCRIPTION: The idea of using selfish genetic elements to drive specific transgenes into a mosquito population either to reduce its size or to render it unable to transmit a particular pathogen was proposed over 40 years ago. It is only recently, however, with the advent of CRISPR-based gene editing technology, that this approach has gained broad attention from researchers and the news media. The need for this new technology is in part due to evolution of mosquito resistance to insecticides.

The most straightforward approaches for building gene drives using CRISPR/Cas9 technologies are theoretically expected to result in spread of the gene drive to individuals in all populations that are connected by even minimal gene flow. These approaches are appropriate in some cases, but detailed mathematical models are needed to understand the dynamics of spread and the potential for resistance evolving to the gene drive mechanisms. Our group and others have proposed more complex approaches for developing gene drives that are spatially and/or temporally limited. Novel molecular approaches accompanied by modeling are needed for development of these limited gene drives.

We currently have a detailed spatial model that simulates the population dynamics and population genetics of Ae. aegypti in a city, Iquitos, in the Amazonian region of Peru. There are rich data sets on both mosquito dynamics and dengue epidemiology that have been collected in this city. One important characteristic of this mosquito is limited among house movement and strong population structure. A main goal of our NIH grant is to modify this model to explore how and to what extent population structure will impact insecticide resistance evolution and the performance of novel gene drive

strategies.

Dhole S, Lloyd AL, Gould F. 2020. Gene drive dynamics in natural populations: the importance of density-dependence, space and sex. Annu. Rev. Ecol. Evol. Syst. 51:505'V31

JOB DESCRIPTION: The postdoc in this position will lead efforts on modifying the detailed model and utilizing it to test hypotheses. The postdoc will have the option of also conceptualizing and developing general models to evaluate novel approaches for building spatially/temporally limited gene drives. Our project is strengthened by collaborations with a number of labs in the US and in Peru, and activity in the Genetic Engineering and Society Center at NC State that examines societal aspects of novel genetic technologies. The postdoc will interact with members of these other research groups. If desired, there will be an opportunity for some work in Peru and for mentoring undergraduate and graduate students. The appointment is for two-years with the potential to write new grants for extension beyond that period.

QUALIFICATIONS: We are looking for a postdoc with a solid background in population biology and population genetics who has experience with modeling and who wants to do applied research. Experience with C++ or related languages is desirable. Ability to work independently and to communicate effectively as a member of a team is essential.

To apply: email a cover letter and CV to Fred_Gould@ncsu.edu AND Alun Lloyd@ncsu.edu

Fred Gould <fgould@ncsu.edu>

Norway NordU PopulationGenomics

MSCA Postdoctoral Fellowships at Nord University: Molecular Ecology, Population genomics, Landscape Genomics, Ecological epigenetics, Genome evolution and more.

"Expressions of interest" by 1st May 2021

The Faculty of Biosciences and Aquaculture at Nord University in northern Norway (https://www.nord.no/-en/about/faculties-and-centres/faculty-of-biosciences-and-aquaculture/research/Pages/default.aspx) calls for expressions of interest from early career researchers to apply for an EU-funded Marie SkÃ¹odowska Curie Action Postdoctoral Fellowship (MSCA-PF-2021). We

will then work with selected applicants to write their full proposal for the 15th September 2021 deadline. Details at https://www.nord.no/no/forskning/Finansiering/-msca . Researchers at Nord University are especially interested to host and train post-doctoral fellows in the following subject areas:

Genomics - Molecular ecology, population genomics and landscape genomics of non- model organisms - Ecological epigenetics in macroalgae and/or seagrass - Microalgae genetics - basic and applied - Genome biology and vertebrate genome evolution - Developmental transcriptomics in fish

Aquaculture - Sustainable aquaculture - Effects of climate change on aquaculture production - Environmental impact and sustainable development of kelp farming

Ecology - Parasite biology and ecology - Terrestrial habitat management and conservation

Marine biology - Prioritising locations for Marine Protected Areas in Europe - Deep sea ecology - Marine biogeography and biodiversity - Kelp development and life cycle

Climate change - Climate change adaptation - Climate change impact on marine species, including macroalgae

Eligibility

- MSCA PF are open to excellent researchers of any nationality. - Researchers must be in possession of a doctoral degree. - At the call deadline, researchers must have a maximum of 8 years full- time equivalent experience in research, measured from the date that the researcher was in a possession of a doctoral degree. - Mobility rule: the researchers must not have resided or carried out their main activity (work, studies, etc.) in Norway for more than 12 months in the 36 months immediately before the call deadline.

Assessment and selection of candidates

Please send a one page covering letter outlining your relevant background, the kind of research project that would interest you and Curriculum Vitae by 1st May 2021 to mark.j.costello@nord.no.

Administrative information on MSCA from Vilija Duleviciute: vilija.duleviciute@nord.no.

In the first step of the process we will choose the candidates for developing competitive MSCA Postdoctoral grant applications. These qualified candidates will be invited to submit a proposal to the EU funded MSCA-PF programme. Applicants will be shortlisted by an internal panel and informed if they have been selected for the next stage within two weeks, by 15th May 2021.

There will be a training workshop for applicants at the

end of May 2021. The selected applicants will develop their MSCA-PF proposal in cooperation with their future supervisors at the Faculty of Biosciences and Aquaculture. In addition, they will be offered individual consultations and review of their MSCA-PF proposal.

Kind regards,

Joost Raeymaekers

– Joost Raeymaekers Faculty of Biosciences and Aquaculture Nord University N-8026 BodÂ Norway Email: joost.raeymaekers@nord.no Web: https://blogg.nord.no/landscapegenomics/ ResearchGate: www.researchgate.net/-profile/Joost_Raeymaekers Google Scholar: scholar.google.be/citations?user=EZdjfbYAAAAJ&hl=nl&oi=sra

"joost.raeymaekers@nord.no" <joost.raeymaekers@nord.no>

PennsylvaniaStateU EcolEvolGenomicsCorrected

The earlier post I sent had a broken link.

I am hiring a postdoctoral researcher to work on evolutionary & ecological genomics projects.

We are working on studies of local adaptation, gene expression plasticity, climate adaptation, and plant-microbe interactions.

Position here: https://psu.wd1.myworkdayjobs.com/-PSU_Academic/job/University-Park-Campus/-Postdoctoral-Scholar—Lasky-Lab_REQ_0000005303-1 Jesse Lasky

Department of Biology Pennsylvania State University

laskylab.org < http://www.laskylab.org >

jrl35@psu.edu

PennsylvaniaStateU EcologicalEvolutionaryGenomics

I am hiring a postdoctoral researcher to work on evolutionary & ecological genomics projects.

We are working on studies of local adaptation, gene

expression plasticity, climate adaptation, and plant-microbe interactions.

Position here: https://psu.wd1.myworkdayjobs.com/-PSU_Academic/job/University-Park-Campus/-Postdoctoral-Scholar_REQ_0000000871-1 Jesse Lasky

Department of Biology Pennsylvania State University

laskylab.org < http://www.laskylab.org >

"Jesse R. Lasky" <jrl35@psu.edu>

StockholmU EvolutionaryGenomics

Researcher position at Stockholm University We have an open position for a researcher in the ERC funded project SuperGenE.

The aim of this project is to investigate the genomic architecture underlying the balanced floral polymorphism termed distyly in wild Linum species. Specifically, the project aims to investigate the evolution of the genomic region (supergene) that governs distyly and the genetic causes and population genomic consequences of loss of distyly. Within the project we are generating and analyzing several new high-quality de novo genome assemblies for wild Linum species, as well as large population genomics, comparative genomics, and expression data sets.

The researcher will use genomic analyses to address questions on supergene and mating system evolution. The focus of this position is on bioinformatic and evolutionary analyses of large-scale genomic and transcriptomic data sets.

Researchers are appointed primarily for purposes of research and must hold a doctoral degree. In the appointment process, special attention will be given to research skills, in particular pertaining to genomic analyses. A strong interest in and training in bioinformatics, evolutionary genetics and/or population genomics is a merit.

The researcher will be based in the research group of Dr. Tanja Slotte (http://tanjaslottelab.se) at the Dept. of Ecology, Environment and Plant Sciences, Stockholm University. The position is initially for one year, with the possibility of extension, and the deadline to apply is May 10, 2021.

The complete ad with information on qualification re-

quirements and instructions on how to apply is available at the Stockholm University website at: https://bit.ly/-2QorROs (reference SU FV-1371-21)

For more information, please contact tanja.slotte@su.se directly.

Tanja Slotte PhD, Associate Professor Department of Ecology, Environment and Plant Sciences (DEEP) Stockholm University 106 91 Stockholm Sweden

"Tanja.Slotte@su.se" <Tanja.Slotte@su.se>

StockholmU YeastGenomicsEvolution

Postdoctoral position in Yeast Genomics and Evolution at Stockholm University, Sweden Start date: August 2021 (negotiable) Application date: 30 April 2021

We are looking for a postdoc to join our Yeast Evolution and Genomics lab at Stockholm University in Sweden. Applicants will have a strong interest in evolutionary processes, especially in adaptation mechanisms, speciation, and conservation genetics, and be familiar with the principles of quantitative and population genetics. Ideally, the candidate has experience in experimental evolution, molecular genetics/genomics, and bioinformatics. Prior training in experimentation with Saccharomyces yeast and strong quantitative skills are desirable. Applicants should be well-organized, self-motivated, good communicators, and happy to work in an international team. Applicants must hold a PhD in evolutionary biology or a similar subject.

Members of our lab are currently working on a range of topics including the effects of hybridization on rates and mechanisms of adaptation, the genetic basis of hybrid fitness, adaptation to environmental stress, epistasis, fitness landscapes, speciation mechanisms, transposable element evolution, and phylogenomics. We use both experimental and theoretical approaches. While the project the applicant will work on is flexible and depends on personal preferences and ideas, the applicant is encouraged to develop a project that harnesses the power of experimental evolution, genomics, and the model yeast system Saccharomyces, to address fundamental questions in evolutionary biology.

Candidates will benefit from training in a vibrant intellectual department with many opportunities for professional development. You will be part of a large collaborative lab, involving 10 researchers from 7 different countries. The position (100% research) is for 1 year with the possibility for extension.

The campus is located four metro stops from the centre of Stockholm, one of the most beautiful and dynamic European cities, surrounded by beautiful nature. The campus is home to a vibrant scientific community, including the Science for Life Laboratory (a leading genomics core facility that we routinely use) and the Swedish Museum of Natural History. Sweden is a free and open society, and strives to be one of the world's most innovative and research-positive nations. People here enjoy a respected system of democracy and individual rights, freedom of speech, a free press, and the right to scrutinize those in power. Most Swedes speak English well. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Further information about the position can be obtained from Dr. Rike Stelkens, Associate Professor, rike.stelkens@zoologi.su.se. Check out the lab website for recent news and publications (stelkens lab.com).

Rike Stelkens Associate Professor / Wallenberg Fellow Population Genetics, Department of Zoology Stockholm University, Sweden

email: rike.stelkens@zoologi.su.se tel: +46 (0) 816 4223 lab website: stelkenslab.com

Rike Stelkens <rike.stelkens@zoologi.su.se>

UAlabama BeeColdAdaptation

The lab of Dr. Janna Fierst at the University of Alabama is searching for multiple postdoctoral researchers to contribute to two exciting projects funded by the US National Science Foundation (NSF). The first project is funded through the NSF Understanding the Rules of Life: Epigenetics program and will use a combination of genomics, metabolomics, bioinformatic analyses and computational modeling to study the genetic networks underlying cold tolerance in bumblebees. There are also opportunities for fieldwork and physiology studies in collaboration with labs at the University of Wyoming and The Ohio State University. The second project is funded through the NSF CAREER program and will use genomics, bioinformatic analyses, computational modeling and phylogenetic comparative methods to study genome evolution in nematode worms.

Both projects involve empirical lab work, bioinformatic analyses of large datasets and computational modeling

and there is ample opportunity for researchers with diverse backgrounds (i.e., purely empirical or purely computational) to join our lab and learn new skills, develop new research directions and make unique contributions to a vibrant, diverse community of young scientists.

Both postdoctoral positions will involve bioinformatic analyses and computational modeling and prior background, or a willingness to learn, is preferred. The postdoctoral appointments will initially be for one year with the possibility of reappointment. For more information please visit our website at http://jfierst.people.ua.edu/ and contact Dr. Fierst at jlfierst@ua.edu. Please include your current vitae and a brief description of your research background and future interests with your email. If you are ready to apply the site is here:

https://staffjobs.ua.edu/en-us/job/512891/-postdocvisiting-scientist-biological-sciences-512891
More information about UA and life in Tuscaloosa is below:

About the University of Alabama: The University of Alabama is the flagship campus of the University System of Alabama, with an enrollment of over 35,000 students. The University is committed to achieving excellence as one of the country's primary centers of research and education. It is located in the vibrant college town of Tuscaloosa, AL, which boasts many cultural and athletic activities. The campus also benefits from its close proximity to the Birmingham metropolitan community. The University of Alabama is an Equal Employment/Equal Educational Opportunity Institution. All qualified applicants will receive consideration for employment without regard to race, color, religion, national origin, sex, sexual orientation, gender identity, gender expression, age, genetic information, disability, or protected veteran status, and will not be discriminated against because of their protected status.

Janna Fierst Assistant Professor Department of Biological Sciences

The University of Alabama

Tuscaloosa, AL 35487-0344

Office: SEC 2328

Phone: 205-348-9810

Janna Fierst <janna.l.fierst@ua.edu>

UArizona TheoryMutationLoad

Postdoc position: population genetics theory with high mutation rate

A postdoc position is available with PI Joanna Masel (http://www.eebweb.arizona.edu/faculty/masel/-people/joanna/) at the University of Arizona in Tucson. Being computational, the position is amenable to remote work, and efforts will be made to accommodate all situations. That said, collaboration with two in-Tucson Ph.D. students is expected, and Tucson is located in the biodiverse Sonoran desert, surrounded on all four sides by mountainous national and state parks, with an attractive climate for most of the year. Stipend is at NIH rates, and the cost of living in Tucson is relatively low.

The question we want to answer is, as Kondrashov put it, "why have we not died 100 times over?" given the estimated high $(U>1)$ prevalence of deleterious mutations https://doi.org/10.1006/jtbi.1995.0167. In current simulations of realistically high genome-wide deleterious mutation rates, relative fitness must constantly be renormalized so as not to be overwhelmed by a Muller's ratchet of fixations of small effect size deleterious mutations, even in large sexual populations.

We have devised a powerful new computational approach that can capture realistic linkage as well as realistically high population sizes and mutation rates for species such as humans. This postdoc's first task will be to finish adapting our relative fitness code to instead be grounded in absolute fitness. This will open up a variety of questions about population viability / mutational meltdown, reproductive compensation, and the best approach to modeling epistasis, depending on interests.

Excellent computer programming skills are required, ideally including both C and Python. Prior knowledge of theoretical population genetics is preferred, although exceptionally strong computational scientists from highly quantitative backgrounds outside evolutionary biology will also be considered, as will non-theoreticians who can demonstrate deep understanding of theoretical issues. Start date is negotiable, and funding is secured through December 2023.

Contact Joanna Masel at masel@email.arizona.edu for more information and to apply.

"Masel, Joanna - (masel)" <masel@arizona.edu>

UAutonoma Madrid PaleontologyNetworks

We have extended our search for a highly motivated and dynamic researcher for a 2-year postdoc position, commencing end of May, 2021.

The candidate will work on understanding and modelling species interactions from the fossil record of the Las Hoyas site, a Lower Cretaceous (Barremian, 129-125 Mya) paleowetland from Spain, focusing on interspecific ecological interactions, and in applying and developing new algorithms to such end.

The position will be based at the Unit of Paleontology, Dept. of Biology at the Universidad Autónoma de Madrid (UAM). Information on the department can be found at: https://www.uam.es/Ciencias/DBIO . Our group and research The successful candidate will be part of the Paleobiology Group at the UAM and CIPb- (Center for the integration of Paleobiology (https: //www.uam.es/UAM/CIPB?language=es). We are a small group, offering a creative and stimulating working conditions in a dynamic research and teaching environment, addressing fundamental questions on vertebrate, invertebrate and plant macroevolution, on the one hand, and the multidisciplinary study of the Las Hoyas fossil site, connecting diversity, palaeoecology and taphonomy, in particular.

Project description and your job This project aims to describe and understand the community structure of the paleowetland, by taking a multi-species complex network modelling approach. The project's team and collaborators are compiling data on the biotic interactions of the fossil species to integrate these into multi-species networks. The models should be implemented by programming algorithms in languages such as Python, R or Julia. The postdoc is expected to focus specifically on the multi-species network analysis and programming, but other collaborative projects are open within the lines of research of the team (both in their areas of expertise and research on the site) and would also be expected to assist in teaching and supervise undergrad thesis projects in the Biology Undergraduate program. The project is funded by the Ministry of Science and Technology of Spain.

Principal Investigators are: J. Marugán Lobón (jesus.marugan@uam.es) and A.D. Buscalioni (an-gela.delgado@uam.es).

Profile We are looking for a highly motivated and enthusiastic scientist with the following competencies and experience: Essential experience and skills: - A PhD in sciences (Biology and Ecology preferred, but Physics, Math and/or fields that tackle math extensively are accepted), at the time of expected start in the position.

- A reasonable publication record in international peer-reviewed literature.

- Experience with scientific data analysis and modelling.

- Experience with a computer language such as Julia, Python or R.

- Demonstrated communication skills and ability to work in teams.

- Excellent English skills, written and spoken.

Desirable experience and skills: - Experience in Paleobiology, macroevolutionary and large scope approaches.

- Experience in working with inter-specific interactions and their evolutionary and ecological consequences.

- An interest in combining paleontological field work data with modelling.

- Experience in teaching and supervising undergraduate and MSc students.

- A curious and open mind-set

Place of employment The place of employment is at the Department of Biology, UAM, with direct collaboration with members of CIPb.

The Universidad Autónoma's campus is situated in a beautiful suburban area less than 20' from the city and it's one of the best ranked universities in Spain. The city of Madrid is consistently rated among the most livable, culturally appealing and accessible cities in the world.

Terms of employment The employment as postdoc is a full time and fixed-term position for 2 years, starting in April-May 2021.

Questions For further information please contact Profs. JesÃos Marugán Lobón or Angela Delgado Buscalioni.

Application procedure Your online application must be submitted in English to the e-mail: re-dek2123@gmail.com, including the following documents/attachments - all in PDF format: 1. Motivated letter of application (max. one page).

2. Short CV incl. education, work/research experience, programming and language skills, plus other skills relevant for the position.

3. A certified/signed copy of PhD certificate.

4. List of publications.

Application deadline 20 April 2021, 23.59pm CET We reserve the right not to consider material received after the deadline, and not to consider applications that do not live up to the abovementioned requirements.

The further process After the expiry of the deadline for applications, the authorized

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UBern AfricanCichlidFishEvolution

Postdoc positions are available in the Aquatic Ecology & Evolution group of Ole Seehausen at the University of Bern and Eawag, Switzerland, to work on the Ecology and Evolution of African Cichlid Fish.

The radiations of cichlid fish in the Great Lakes of Africa created some of the largest known concentrations of endemic species in record time. Hundreds of endemic species evolved in less than 20'000 years in Lake Victoria, possibly unparalleled among contemporary animals elsewhere. The African cichlid fish are a great system also for studying interactions between adaptive radiation and ecosystems because complex new consumer food webs have evolved, unparalleled by any other recent species radiation. Unfortunately, African lake cichlids also experienced the fastest large scale extinction event ever observed by humans: about 200 endemic species have disappeared in the past 40 years in Lake Victoria. We study these fish in nature, breed them in our aquarium systems and study their genomic diversity and differentiation. We have sequenced the complete genomes of more than 250 species from Lake Victoria and most other lakes in the region. Our long term goals are to understand how this large radiation could emerge so incredibly fast, how its evolution and its loss affect the ecosystem, and what is required to safeguard diversity amidst environmental change. It is a perfect study system for anyone who wants to uncover the workings of evolution, its interactions with ecology and its relevance for nature conservation.

Because some of my recent Postdocs moved on to permanent positions, I am hiring new Postdocs. Fields of interest include evolutionary community ecology, island biogeography, integrative taxonomy, functional morphology, GWAS and QTL mapping, evolutionary genomics of speciation, hybridization and adaptive radiation and comparative phylogenomics.

Qualifications: PhD in evolutionary biology or a similar field. Strong conceptual background in speciation, excellent coding, data analysis and writing skills. Experience with fieldwork in tropical ecosystems and social skills for interactions with fisher folks and government authorities and some knowledge of Kiswahili are assets.

Funding is for two years, but continuation for additional years is strongly expected.

The Postdocs will also work closely with graduate students in my group and with our Lake Victoria paleoecology and aDNA team. The goal of the larger team is to achieve a holistic understanding of evolutionary diversification in an ecosystem context and to apply the knowledge to conservation.

The team of Ole Seehausen is based at the Institute of Ecology & Evolution of the University of Bern (https://www.iee.unibe.ch/) and at the Eawag Centre for Ecology, Evolution & Biogeochemistry (CEEB; https://www.eawag.ch/en/department/fishec/) in Kastanienbaum (Lucerne) and we have labs and fish rooms in both places. The Postdocs will become part of a large team of ecologists, evolutionary biologists and conservation biologists. The larger group works on the ecology, evolution and conservation of freshwater fish with a strong focus on the fish of the African Great Lakes region, the Alpine region of Europe and Greenland. The working language in the group, in the Institute of Ecology and Evolution and at the Eawag CEEB is English. Fluency in speaking and writing is required. Salary will be according to University of Bern salary scheme and commensurate with experience.

Because we work on African lakes, I wish to transfer system knowledge to young scientists that want to commit their career to the study and conservation of these systems. I therefore encourage applications from African countries. Because of persistent gender, ethnic and cultural biases in ecology, evolution and conservation, I especially encourage applications from women and scientists identifying as belonging to ethnic and cultural groups that are underrepresented in ecology, evolution and conservation.

Supervisor: Prof. Ole Seehausen, Institute of Ecology and Evolution The positions are available from May 15, 2021. Review of applications starts on April 30, 2021 and continues until all positions are filled. Please direct inquiries to Prof. Ole Seehausen,

ole.seehausen@iee.unibe.ch.

Applications: One pdf file only, with CV, short letter of motivation, publication list and contact details of three referees should be sent by email to ole.seehausen@iee.unibe.ch

ole seehausen

ole.seehausen@iee.unibe.ch

UBern FishEvolConservation

Three Postdoc positions in fish ecology, niche modelling and conservation are available (each 2-3 years) in the Aquatic Ecology & Evolution group of Ole Seehausen at the University of Bern, Switzerland

With the Wyss Academy for Nature, we are starting an ambitious freshwater conservation biology project with a focus on fish. Working initially at the scale of the largest Swiss catchment, the Aare, home to more than 60 different species of fish, we want to go all the way from field ecology, niche modelling and projections of range shifts under climate change to identifying priority areas for biodiversity conservation, and designing measures to mitigate predicted and recover past losses. As implementation partner, the Swiss Fisheries Competence Center will develop applications of such measures initially in a test region. The project is supported by the Wyss Academy for Nature at the University of Bern in partnership with the Canton of Bern and the Swiss Federal Office for the Environment (FOEN/Bafu). If successful, the project may continue for up to eight years, with the goals of upscaling projections to other catchments of Switzerland and a fully fledged mitigation program.

The Aare catchment contains several of the large perialpine lakes, each of which has endemic species of coldwater fish, several of which have already gone extinct. It also has many mountain rivers with environmental gradients stretching from the arctic-alpine to the temperate climate zone, including one of the most pristine braided rivers left on the North face of the Alps. We have an extensive data set on distribution records for most species of fish in Switzerland and many environmental variables. Our goal is to complement this data with additional dense sampling of fish and environmental variables across the entire Aare catchment. Our recent work has uncovered old cryptic species as well as postglacial ecological species within the broad

category of taxonomic "species" currently in use in management. Whenever possible we will do niche modelling and change projections at the level of these evolutionary significant units (ESUs). We will work with and add to our large collection of voucher specimens and tissue samples covering many populations of most Swiss fish species. We will develop data rich niche models for all species/ESUs of fish and also for some key aquatic invertebrates. We will combine the niche models with locally resolved climate and land-use change projections to predict habitat gains and losses and identify hotspots of expected biodiversity loss. We will use the results to develop mitigation strategies, components of which will be explored initially in a test region, in close collaboration with the Swiss Fisheries Competence Centre, the Wyss Academy for Nature, the Canton Bern office for the environment (LANAT) and the Federal Office for the Environment (FOEN).

We are hiring 3 Postdocs with 3 different profiles: 1. Fish ecologist, evolutionary or conservation biologist to co-lead the field work with emphasis on sampling, identification, integrative taxonomy, and ecology of fish. Employment at Postdoc/senior Postdoc level depending on experience. Qualifications: PhD in ecology/taxonomy/systematics with excellent knowledge of fish, fieldwork, population genetics, phylogenetics, good understanding of integrative taxonomy and excellent analytical skills. Social skills are required for interactions with stakeholders. Some knowledge of German/Swiss-German is an asset but not absolutely necessary. 2. Aquatic ecologist, evolutionary or conservation biologist to co-lead the field work with emphasis on ecological and environmental data collection and invertebrates. Employment at Postdoc/senior Postdoc level depending on experience. Qualifications: PhD in aquatic ecology/taxonomy/systematics with excellent knowledge of aquatic systems beyond fish and excellent analytical skills. Social skills are required for interactions with stakeholders. Some knowledge of German/Swiss-German is an asset but not absolutely necessary. 3. Ecologist or evolutionary biologist with strong modelling skills to lead the niche modelling and projection of population dynamics and range shifts under climate and land-use change. Employment at Postdoc/senior Postdoc level depending on experience. Qualifications: PhD in ecology, conservation or evolutionary biology with strong background in ecological niche modelling and/or projections of biodiversity under climate change scenarios.

Your responsibilities include field work and data collection (position 1 and 2), data analysis, writing papers and publishing in leading journals in the field (all 3 positions). Provided appropriate skills, one senior

Postdoc is expected to take on the responsibilities of overall project management. The project is part of the Hub Bern of the Wyss Academy for Nature (https://www.wyssacademy.org/). It will be implemented in close

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Equity and diversity are essential to academic excellence. An open and diverse community fosters the inclusion of voices that have been underrepresented or discouraged. We encourage applications from members of groups that have been marginalized on any grounds enumerated under the B.C. Human Rights Code, including sex, sexual orientation, gender identity or expression, racialization, disability, political belief, religion, marital or family status, age, and/or status as a First Nation, Metis, Inuit, or Indigenous person.

bleander@mail.ubc.ca

UBritishColumbia EvolMeiofauna

Research Associate Position: Evolution of Soft Bodied Meiofauna

A twelve-month, full-time Research Associate position is available in the Botany Department at The University of British Columbia. This position will provide group support for projects that examine the diversity and evolutionary history of soft bodied meiofauna, especially rhabdocoels, using high-resolution microscopy and genetic/genomic techniques.

The successful applicant must have a PhD in a relevant field and at least 5 years of postdoctoral research experience at the highest international standards relating to comparative anatomy, evolutionary biology, systematics, molecular phylogenetics and high-resolution microscopy of marine soft bodied meiofauna. The applicant must have extensive knowledge of the natural history of coastal environments in the Pacific Northwest and demonstrated skills in the extraction of soft bodied meiofauna from field samples, DNA barcoding, bioinformatics, molecular phylogenetics, scientific illustration and building manuscripts for publication in top-level scientific journals in the field.

Research will be conducted within the framework of the Tula Foundation's Hakai Institute. Additional responsibilities include the presentation of research findings at conferences, continued publication of research, and assistance with the day-to-day training of other research personnel.

To apply, please send a concise statement of research interests, CV and the names/emails of three references as a single PDF to Brian Leander (bleander@mail.ubc.ca). Closing date for applications is May 20, 2021 in anticipation of filling the position on September 1, 2021.

UBuffalo EvolutionaryAnthropology

The Department of Biological Sciences in the College of Arts and Sciences at the University at Buffalo is seeking an Evolutionary and Anthropological Genomics Postdoctoral Associate.

The Buffalo Evolutionary and Anthropological Genomics Laboratory (https://gokcumenlab.org) currently focuses on studying fundamental questions about human nature and diversity using high-throughput biological approaches and computational tools. We are particularly interested in the functional and evolutionary effects of genomic structural variants (SVs) (e.g., differences in copy number) of large segments of—DNA—between individuals. We believe that SVs represent a huge and unexplored area of evolutionary genomics. Within this framework, we are currently working on three broad areas:

(i) Investigating salivary proteome evolution in mammals as a framework to elucidate the mechanisms of functional change involving genomic structural variation

(2) Leveraging archaic hominin genomes to determine the origins and evolutionary impact of ancient genomic structural variants in the human lineage

(3) Experimental investigation of the functional effect of evolutionarily relevant structural variants using mouse models

Our laboratory has both wet and dry lab components. We routinely generate and integrate multiple high-throughput biological data, including long- and short-read sequencing of—DNA—and—RNA, proteomics, and digital—PCR—validations. We also have targeted experimental projects, using genetically modified mice and other models of evolution.

In this role: . You will conduct evolutionary genomics analyses - including genome assembly and population genetics research.

. The research involves wet lab experiments, sample management, and bioinfromatic analysis under the supervision of Dr. Gokcumen.

. You will be expected to work collaboratively, especially with Dr. Ruhl's laboratory in Oral Biology.

The successful candidates will have a chance to work with large genomic datasets involving multiple primates/mammalian species, as well as utilize state-of-the-art—DNA/RNAquantification technologies, such as digital—PCR. We have ongoing collaborations with researchers from anthropology, population genetics, evolutionary and molecular biology, cancer genetics, and immunology. Our research team is diverse and multidisciplinary. We are interested in recruiting from different backgrounds to continue this tradition.

The candidate should have a Ph.D. (or MD) preferably in population genetics, evolutionary biology, computational biology, bioinformatics, or anthropological genomics. Experience in handling large datasets (e.g., experience genome-wide sequencing data), programming and scripting (e.g., Python, R), and familiarity with—UNIX/LINUX—operating environments is preferred.

If you are interested, please submit your CV, names of three references, and a brief (no more than 1-page) cover letter outlining research interests and career goals. Applications will be accepted until the position is filled.

As an Equal Opportunity / Affirmative Action employer, the Research Foundation will not discriminate in its employment practices due to an applicant's race, color, religion, sex, sexual orientation, gender identity, national origin and veteran or disability status.

Omer Gokcumen <gokcumen@gmail.com>

UCalifornia Berkeley ConservationPopulationGenomics

Postdoctoral position in conservation and population genomics Nachman lab, UC Berkeley Details: https://-aprecruit.berkeley.edu/JPF02935 There is an opening for a Postdoctoral position to study conservation and population genomics of mammals as part of the California Conservation Genomics Project (CCGP) in the lab of Professor Michael Nachman in the Museum of Vertebrate Zoology at UC Berkeley. The California Conservation Genomics Project (CCGP) is a state-funded initiative with the goal of producing the most comprehensive, multispecies, genomic dataset ever assembled to help manage regional biodiversity. More information about this statewide effort can be found here: https://-www.ccgproject.org/. This position will involve bioinformatic analysis of whole-genome sequences from 750 individual mammal specimens representing 15 species. The primary goal of this project is to generate a map of genetic diversity for these 15 species across California. We are also interested in inferring historical demographic changes, assessing the extent to which selection has shaped patterns of genomic variation, and linking genotype to phenotype for traits of interest. The ideal candidate will have a strong background in population, conservation, or landscape genomics and significant experience in the analysis of large genomic datasets.

Research in the Nachman lab (https://-www.nachmanlab.org/) focuses on population, evolutionary, and ecological genetics and genomics. We are broadly interested in the genetic basis of evolutionary change, including the genetics of adaptation and the genetic basis of speciation. For example, we are interested in uncovering signatures of selection in patterns of DNA sequence variation and in linking specific genetic changes to specific adaptive phenotypes. Much of the current work centers on the genetic basis of adaptation to different environments. Our research utilizes a wide range of methods and approaches including field studies, genetic crosses in the laboratory, tools of molecular biology, genomics, and bioinformatics analyses of large datasets.

Michael Nachman Director, Museum of Vertebrate Zoology Professor, Department of Integrative Biology 3101 Valley Life Sciences Building University of California, Berkeley Berkeley, CA 94720-3160

(510) 642-1792 mnachman@berkeley.edu

"Prof. Michael Nachman" <mnachman@berkeley.edu>

UCalifornia SantaCruz ComparativePopulationGenomics

The Department of Biomolecular Engineering at the University of California, Santa Cruz seeks applications for a Postdoctoral Scholar position in the Corbett-Detig Lab, in the area of bioinformatics and population genomics, at 100% time to start as soon as possible.

Responsibilities: The postdoctoral scholar will be responsible for developing high throughput reproducible workflows for the California Conservation Genomics Project (https://www.ccgproject.org/). This project has a goal of using population genomic analyses across diverse taxa from across California to understand genetic structure and the impact of geographic subdivisions on California resident and endemic species. The postdoc will work in a diverse team and lead the assembly population genomic datasets and work closely with the landscape genomic analysis team led by Ian Wang at UC Berkeley and with the entire CCGP community. The postdoc will lead and collaborate on publications resulting from this large interdisciplinary project.

Basic Qualifications: PhD or equivalent international degree in population genetics, bioinformatics or related field. The candidate should have no more than four years of post-degree research experience by start date.

Preferred Qualifications: Candidates should have demonstrated experience with the analysis of population genomic data, including whole genome sequencing; data management and bioinformatics; statistical analysis; computer programming with Python and snakemake; and writing, publishing, and presenting original scientific work.

Appointment: This is a position in Prof. Russ Corbett-Detig's lab. The initial appointment will be at 100% time for one year with the possibility of extension.

Salary and Benefits: This position provides full benefits. Salary will be commensurate with qualifications and experience.

To Apply: Please send your CV and cover letter to Russ Corbett-Detig at rucorbet@ucsc.edu. I also welcome informal inquiries at any time. Application review will begin April 15th and continue until the position is filled.

Russ Corbett <russcd@gmail.com>

UCBerkeley EvolutionaryGenomics

The Department of Environmental Science, Policy, and Management at the University of California, Berkeley seeks applications for a Postdoctoral Scholar position in the Ian Wang Lab, in the area of ecological and evolutionary genomics, at 100% time with an expected start date of August 2021.

Responsibilities: The postdoctoral scholar will be responsible for conducting research on the ecological and evolutionary genomics of amphibians and reptiles. Research activities will include landscape genetics, analysis of genes underlying ecological divergence and local adaptation, bioinformatics, statistical and computational modeling, and applications to species conservation. The postdoc will be expected to collect genomic data from field collected specimens, including DNA extraction, library preparation, and next-generation sequencing. The postdoc will also be expected to manage and analyze the data, employing bioinformatics, population genetic analysis, and methods for integrating spatial genetic and ecological data, and to compose the results into publishable manuscripts. Training and providing oversight to undergraduates and beginning graduate students may also be required periodically. Opportunities to extend the postdoc's line of independent research may also be supported.

Basic Qualifications (At the time of application): PhD, or equivalent international degree, or enrolled in a PhD degree program, or equivalent international degree

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

Preferred Qualifications (By start date): Candidates should have demonstrated experience with the collection and analysis of population genomic data, including whole genome sequencing; data management and bioinformatics; statistical analysis; computer programming with R and/or Python; field work with amphibians and reptiles; and writing, publishing, and presenting original scientific work.

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

Salary and Benefits: This position provides full benefits. Salary will be commensurate with qualifications and experience and based on the UC Berkeley Postdoctoral Scholar salary scale (Table 23) available at https://www.ucop.edu/academic-personnel-programs/_files/1920/2020-postdoc-scales/t23.pdf To Apply: Visit: https://aprecruit.berkeley.edu/apply/-JPF02915 Specific questions regarding the recruitment can be directed to the PI, Professor Ian Wang at ianwang@berkeley.edu

Ian J. Wang Associate Professor Environmental Science, Policy, and Management University of California, Berkeley Office: 311 Hilgard Hall Phone: 510-664-4684 Mail: 130 Mulford Hall #3114 Berkeley, CA 94720

ianwang@berkeley.edu

UCBerkeley LandscapeGenetics

The Department of Environmental Science, Policy, and Management at the University of California, Berkeley seeks applications for a Postdoctoral Scholar position in the Ian Wang Lab, in the area of conservation and landscape genomics, at 100% time with an expected start date of July 2021.

Responsibilities: The postdoctoral scholar will be responsible for developing a landscape genomic analysis pipeline that will be used to examine critical components of genetic variation for a broad range of taxa as part of the California Conservation Genomics Project (https://www.ccgproject.org/). The postdoc will work closely with a bioinformatics workflow team led by Russ Corbett-Detig at UC Santa Cruz and with the CCGP community. Research activities will include analyzing whole genome sequence data to infer population structure and gene flow, quantifying the geographic and environmental factors contributing to the spatial distribution of genetic variation, identifying genes under selection, performing genotype-environment association analyses, conducting statistical and computational modeling, data visualization, and applications to species conservation. The postdoc will also be expected to manage and analyze large datasets and to contribute to the publication of manuscripts.

Basic Qualifications (At the time of application): PhD, or equivalent international degree, or enrolled in a PhD degree program, or equivalent international degree

Additional Qualifications (By start date): PhD or equiv-

alent international degree. The candidate should have no more than four years of post-degree research experience by start date.

Preferred Qualifications (By start date): Candidates should have demonstrated experience with the analysis of population genomic data, including whole genome sequences; landscape genetics; statistical analysis; spatial modeling; computer programming with R and/or Python; and writing, publishing, and presenting original scientific work.

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

Salary and Benefits: This position provides full benefits. Salary will be commensurate with qualifications and experience and based on the UC Berkeley Postdoctoral Scholar salary scale (Table 23) available at https://www.ucop.edu/academic- personnel-programs/_files/1920/2020-postdoc-scales/t23.pdf

To Apply: Please send a CV and cover letter to the PI, Ian Wang, at ianwang@berkeley.edu. Review of applications will begin on 4/22.

Ian J. Wang Associate Professor Environmental Science, Policy, and Management University of California, Berkeley Office: 311 Hilgard Hall Phone: 510-664-4684 Mail: 130 Mulford Hall #3114 Berkeley, CA 94720

"ianwang@berkeley.edu" <ianwang@berkeley.edu>

UCologne EvolutionGeneRegulation

The University of Cologne invites applications for a Postdoc position in the research group of Prof. Juliette de Meaux in the faculty of Natural Sciences.

Evolution of gene regulation and polygenic adaptation in Plants Research in the de Meaux lab investigates the role played by variation in gene expression regulation in processes of polygenic adaptation. Our lab has recently collected a transcriptomic time series to identify the cis- and trans- regulatory changes associated with the shift from perennial to annual growth in plants. The postdoctoral scientist will use this data to disentangle the effect of temperature and development on genetic differences in regulation between these species. The goal of the project is to identify the molecular components, whose regulation has been reshaped after the

shift in life-history. Using data previously generated by our lab on positive and negative evolutionary forces in these same populations, and ad-hoc datasets for the well known regulation of flowering time in these species, the scientist will investigate footprints of polygenic selection on the regulation of plant development.

The applicant must hold a PhD in Evolutionary Biology (Population genetics, Comparative Genomics, Evolutionary Genetics) and possess advanced skills in the bioinformatics of next generation sequencing data. Language in the lab is English. Applications or questions regarding the position should be sent by mail to jdemeaux@uni-koeln.de, with the following subject line - Postdoc application Evolution Gene Expression - de Meaux lab. A letter of motivation, a CV and the contact of 2-3 referees should be provided, all in a single pdf file.— Revision of applications will begin on April 25th and continue until the position is filled. Funding is for 24 Months starting as soon as possible.

Candidates planning to set up their own group as e.g. with application to Emmy Noether Early Career Grants are especially welcome to apply and will receive strong support. For more information on our lab and research visit our website https://ag-demeaux.botanik.uni-koeln.de/ The University of Cologne is an equal opportunity employer in compliance with German laws and our lab is committed to nurture diversity in its rows. People with disabilities are strongly encouraged to apply.

Cologne is Germany's vibrant Metropolis on the Rhine. The city is well known for its wild carnival (will resume after covid!), its famous Kölsch beer, its Cathedral and its vivid contemporary art and musical scene. Cologne is the fourth biggest city in Germany with over a million inhabitants from all over the world and an interesting mix of restored historic buildings and modern post-war architecture. Most importantly, Cologne University is one of the oldest and largest Universities in the Country. Our research group is hosted at the Biological Center of the University of Cologne and associated to the Excellence Research Cluster CEPLAS (http://ceplas.eu/de/), which fosters active interactions between plant scientists of the Universities of Cologne, Düsseldorf and the Max Planck Institute of Plant Breeding Research. In this context, our lab members are assured to unfold their scientific career in a world-class scientific environment.

Prof. Dr. Juliette de Meaux University of Cologne Plant Molecular Ecology Institute of Botany Biozentrum Zülpicher str. 47b D-50674 Cologne Germany

Tel: +49 221 470 8213 jdemeaux@uni-koeln.de

http://www.botanik.uni-koeln.de/1146.html   Juliette de Meaux <jdemeaux@uni-koeln.de>

UCologne ExptEvolutionAMR

Postdoc position in experimental evolution of antibiotic resistance

We seek a postdoc for a collaborative project between the groups of Prof. Joachim Krug, Prof. Tobias Bollenbach (both at the Institute for Biological Physics, University of Cologne) and Prof. Arjan de Visser (Laboratory of Genetics, Wageningen University) on predicting evolutionary pathways to beta-lactam resistance. The project combines theory and experiments and is part of the Collaborative Research Center 1310 "Predictability in Evolution" funded by Deutsche Forschungsgemeinschaft (DFG) and coordinated at the University of Cologne. The aim of the project is to identify key predictors of the evolution of beta-lactam resistance across time scales and levels of organization. The postdoc will perform evolution experiments with E. coli and TEM-1 beta-lactamase to develop and test predictions about the effect of genetic and ecological constraints on the choice and repeatability of evolutionary trajectories. The experimental work will be done in close collaboration with a theoretical postdoc appointed within the same project. The position is available immediately and will initially be until 30 June 2022, with possibilities for extension.

Profile: We seek a highly motivated person with a PhD in molecular evolutionary biology, microbial genetics or enzyme engineering. Solid experience with microbiological and molecular genetics and genome analyses are absolute requirements; experience with evolutionary theory and quantitative models are an asset. Experimental work will be carried out at the University of Cologne (lab of Tobias Bollenbach) and Wageningen University (lab of Arjan de Visser). Travel between Cologne and Wageningen takes a bit more than two hours by train. Salary will be paid according to level E13 of the German public service salary scale (TV-L). The project can start as soon as we have found a suitable candidate.

Applications: Submit enquiries and applications (including CV, letter of motivation and names and contact information of two references) before 14 May 2021 to Arjan de Visser or Joachim Krug. The University of Cologne is one of the leading German institutions in molecular and evolutionary genetics. Wageningen University is a leading university in the field of the life sciences. The University of Cologne is an equal opportunity employer in compliance with the German disability

laws. Women and handicapped persons are therefore strongly encouraged to apply.

Prof. Arjan de Visser Laboratory of Genetics Wageningen University, Radix building Droevendaalsesteeg 1 6708 PB Wageningen The Netherlands P: (+)31 317 483144 M: arjan.devisser@wur.nl W: https://arjandevisserlab.wordpress.com Prof. Joachim Krug Institute for Biological Physics Zülpicher Strasse 77 50937 Köln Germany P: (+)49 221 470 2818 M: jkrug@uni-koeln.de W: www.thp.uni-koeln.de/krug/ "arjan.devisser@wur.nl" <arjan.devisser@wur.nl>

UColorado Denver TranscriptionalPlasticity

University of Colorado, Denver: Postdoctoral position in Evolutionary Physiology

The Ragland lab in the Department of Integrative Biology at the University of Colorado, Denver is seeking a postdoctoral fellow to contribute to a new NSF-funded project on the thermal sensitivity of transcriptional dynamics, with the goal of better understanding the evolutionary interplay between plasticity and evolution. In addition, the postdoc will have opportunities to develop new lines of inquiry and to work with collaborators at multiple institutions.

Broader impacts are integral to this project, and the successful candidate will also work with Greg Ragland and Laurel Hartley (also in Integrative Biology) on the development and deployment of a Course Based Undergraduate Research Experience (CURE) aimed at improving participation and representation in STEM research. This would be an excellent opportunity for those interested in broadening both their research repertoire and their teaching experience to prepare for a future faculty position. The Office of Inclusive Excellence in STEM offers supporting resources, including opportunities for specific training in inclusive pedagogy.

The position is fully funded for three years at the NIH pay scale and can start as early as June 2021. Ideally, applicants will have a solid background in either evolutionary biology, genetics, or comparative/ecological physiology, and in one or both of two areas: 1) bioinformatic and statistical analysis of 'Â¥omics data sets, or 2) wet lab molecular biology, particular as it relates to NGS library preparation. Strong scientific curiosity and a collaborative mindset are a must.

The Ragland lab is broadly interested in comparative and evolutionary physiology, the genomic architecture of rapid adaptation, and adaptation in variable environments (see https://raglandlab.wordpress.com). We are a friendly and diverse group who ask questions that cross biological disciplines and collaborate broadly to tackle these questions from multiple angles. We encourage a welcoming and inclusive environment and like to mix in some play with work, taking advantage of the world class outdoor opportunities on the Front Range and the fantastic city amenities in Denver (the former more than the latter these days). There will also be opportunities to interact with students, postdocs, and faculty at the CU Denver medical campus and other nearby universities in the Rocky Mountain region.

Application review will begin 3 May and continue until the position is filled. Please submit a pdf file including 1) A brief cover letter outlining your experience, goals, and fit for the position, 2) CV, and 3) 1 'V 2 representative publications or pre-prints to Greg Ragland at gregory.ragland@ucdenver.edu. Informal inquiries welcome.

GREGORY.RAGLAND@ucdenver.edu

UDenver EvolutionaryGenomics

The Larson Lab at the University of Denver is accepting applications for a Postdoctoral Research Associate in evolutionary genomics. This position requires a PhD in evolutionary biology or related field, a demonstrated ability to conduct independent research and commitment to fostering an inclusive work environment. Salary and benefits are competitive.

This position will work on an NSF-funded project to study speciation in field crickets. The project focuses on the evolution and maintenance of variable reproductive barriers by connecting spatial variation in ecology, behavior and genomic architecture to patterns of gene flow across replicate hybrid zones. This project is a collaboration with the Tinghitella Lab (University of Denver) and the Maroja Lab (Williams College). More information on the project goals can be found at https://www.larsonlab.space/rol. There will also be opportunities to develop synergistic projects and participate in citizen science programs or develop Course-based Undergraduate Research Experiences. More information about the Larson Lab is at https://www.larsonlab.space/ . The ability and desire to work both independently and

collaboratively with other members of the lab is critical to the success of this position. Duties will include generating and analyzing genomic datasets, conducting field collection trips, project coordination, training and supervising other personnel and disseminating results through publications and conference presentations. The preferred candidate will have expertise in any of the following areas: speciation, population genetics, genome evolution, or sexual selection. Additional consideration will be given to applicants with experience and willingness to do field collections and/or experience in animal care. Applicants with minimal experience analyzing genomic data, but an enthusiasm to learn and a strong background in evolutionary biology, should still apply.

The initial hire is for 1 year with renewal for up to 3 additional years (4 years total), pending satisfactory progress. The start date is flexible. Applications should be submitted directly to

https://jobs.du.edu/cw/en-us/job/493679/-postdoctoral-research-associate-evolutionary-genomics .Applications should include a cover letter (2 pages) describing the applicant's interests and expertise, a CV, and the names of three references. Questions about the position should be sent to Dr. Erica Larson (erica.larson@du.edu). Review of the applications will begin May 14th and will continue until the position is filled.

This project is a collaboration with the Tinghitella Lab (University of Denver) and the Maroja Lab (Williams College). The Larson and Tinghitella labs share a lab space with a highly interactive research group. In addition, the University of Denver has a growing group of faculty, students, and postdocs studying Ecology and Evolution (see https://dueeb.weebly.com). The University of Denver is situated in an awesome western city of ~700,000 people with a vibrant art community, music and nightlife, and access to amazing recreation in the Rocky Mountains. We also have 300 days of sunshine a year!

Erica Larson <Erica.Larson@du.edu>

UFribourg AncientDNA

Postdoc position in Ancient DNA Bioinformatics

Statistical and Computational Biology Group (Daniel Wegmann) University of Fribourg, Switzerland

Who we are We are a young, international, interdisciplinary and enthusiastic research group at the University of Fribourg, Switzerland, aiming at understanding the evolutionary and ecological processes shaping the realm of biological diversity we see today. To achieve this, we design and develop new statistical and computational approaches, and apply them to big data from many biological fields. A current focus of the lab is on dedicated tools for ancient DNA (aDNA) bioinformatics and their use to study past human societies.

Your tasks We develop ATLAS (https://-bitbucket.org/wegmannlab/atlas), a dedicated tool to conduct bioinformatic analyses from raw-sequence data to population genomics. We seek a highly motivated Postdoc to extend the machine learning models of ATLAS that are used for genotyping, in particular regarding post-mortem damage and recalibration, and to support the analysis of ancient DNA data within larger consortia.

The position is fully funded with a competitive salary for two years, with the possibility to extend by another two years. The successful candidate should ideally start in Summer 2021. The project does not involve lab work.

What we offer We offer a stimulating research environment, well embedded in the strong bioinformatic and conservation communities in western Switzerland. We are part of the Swiss Institute of Bioinformatics (SIB) and boost excellent research facilities, including state-of-the-art high-performance computational infrastructures. Fribourg is a lively university town with pleasant surroundings (such as the Alps) and an excellent quality of life. It is located only 20 minutes from the capital of Switzerland, Bern, and just a little over an hour from Geneva and Zürich. While some knowledge of German or French is beneficial for living in Switzerland, it is not essential. The working language in our lab and institute is English.

What you bring You should have a PhD degree in bioinformatics, population genomics, computational biology, computer science, statistics or a related field, and a strong interest in applying these skills to ancient DNA. Good programming skills are expected, ideally in C++. Also, we expect some knowledge in statistical inference and machine learning, for which we are happy to provide further training. Good knowledge of written and spoken English is expected.

How to apply To receive full consideration, apply before May 15 at https://forms.gle/-vGbkHULcHWz9dD7j9 with a single PDF file including - a cover letter with a brief summary of your previous research and motivation for the position, - a Curriculum Vitae, - names, addresses and emails of two professional references.

Further information on our lab http://-www.wegmannlab.com https://www.sib.swiss/-daniel-wegmann-group ****Recent papers on the topic**** https://doi.org/10.1101/105346 https://-/doi.org/10.1534/genetics.116.189985 https://-doi.org/10.1016/j.cub.2020.08.033 https://doi.org/-10.1126/science.aaf7943 https://doi.org/10.1073/-pnas.1523951113 – Prof. Dr. Daniel Wegmann Department of Biology University of Fribourg Chemin du Musée 10 1700 Fribourg Switzerland

wegmannlab.com

+41 (0)26 300 89 49 daniel.wegmann@unifr.ch

Daniel Wegmann <daniel.wegmann@unifr.ch>

UGeorgia ReproductiveEvolution

Available immediately: Postdoctoral researcher to help develop CRISPR in the insect systems studied in the laboratories of Patricia Moore and Allen Moore, targeting evolutionary reproductive biology. We are evolutionary biologists with an interest in reproductive systems, behavior, and evolution. Athens is a vibrant college town with a strong evolutionary biology community and our laboratories are inclusive and interactive. Contact either pjmoore@uga.edu or ajmoore@uga.edu for informal discussions before applying. Salary will be on the NIH pay scale. Visit our lab websites at https://site.caes.uga.edu/trishjmoorelab/ or https://-site.caes.uga.edu/ajmoorelab Allen J. Moore Distinguished Research Professor Associate Dean for Research College of Agricultural and Environmental Sciences University of Georgia 109 Conner Hall 147 Cedar Street Athens, GA 30602-7503 USA P: 706.542.2151

Assistant: Kelly Eisele (agresch@uga.edu) https://-site.caes.uga.edu/ajmoorelab 11811-00-00001111

ajmoore@uga.edu

UGuam MarineInvertPopulationGenomics

The Lemer Invertebrate Genomics Lab (https://-wwww.tinyurl.com/lemerlab) at the University of Guam

Marine Laboratory seeks to recruit a motivated, independent, and creative postdoctoral researcher as part of an NSF funded, multi-disciplinary research project. The postdoctoral researcher's immediate supervisor will be Dr. Sarah Lemer, who will be leading several individual studies within a large seascape genomics research project. The Postdoc's project will combine population genomics of reef-associated invertebrates with oceanographic data to quantify and characterize connectivity among Micronesian reefs and identify local adaptations within the context of climate change. Studied taxa include (but are not limited to) molluscs, crustaceans and echinoderms. Funding is available for 2 years.

The postdoc's primary duties will be to conduct field work, generate genomic data such as RADSeq or shallow genome resequencing, and apply new methods and analytical tools to investigate population genomic patterns of the studied taxa across oceanic islands. They are expected to write publications and assist with other projects in the lab depending on skills and interests. The postdoc will also be involved in mentoring graduate and undergraduate students and will benefit from a range of mentorship opportunities within the context of the "GECCO" project.

The project is funded by the U.S. National Science Foundation's Established Program to Stimulate Competitive Research (NSF EPSCoR) and is integrated in The Guam Ecosystems Collaboratorium for Corals and Oceans (GECCO). GECCO is a multi-disciplinary research project staffed by researchers from the University of Guam and collaborators from other institutions. The successful candidate for this position will join a vibrant laboratory and will have the opportunity to contribute to a variety of projects in the fields of population genetics and evolutionary genomics within the scope of the GECCO project (see Guam EPSCoR's GECCO Strategic Plan - https://gepscor-cdn.uog.edu/wpcontent/uploads/-2021/03/12021134/GECCO-strategic-plan-2020.pdf).

Minimum Qualifications - PhD in biology or related field - Experience in genetics, genomics and marine biology - Experience in analyzing large genetic/genomic datasets - Proficient in R, command-line tools and scripting - Excellent writing and generally good communication skills - Scientific field work experience - Experience working with invertebrate taxa

Minimum Knowledge, Abilities, and skills - Team oriented and interested in helping and mentoring. - Highly motivated and pro-active - Excellent time management skills and the ability to prioritize work. - Attention to details, strong problem-solving, training, and mentoring

abilities. - Ability to work independently with minimal supervision, establish work priorities, and take initiative in pursuing activities that further project goals.

Preferred Qualifications - Experience with population genomic datasets and analysis - Experience with Python or Pearl - Scientific dive certification (AAUS), ideally with experience working on tropical reefs - Island experience - Basic knowledge of marine invertebrate biology and taxonomy - Working in an island setting.

Character of Duties The Post-Doctoral Researcher will be responsible for: - Leading the implementation of a seascape genomics research project. - Conducting field work activities to collect samples. - Generating genomic data such as RADSeq or shallow genome resequencing. - Applying analytical tools to investigate population genomic patterns of the studied taxa across oceanic islands. - Writing publications. - Assisting with other projects in the laboratory, depending upon skills and research interests. - Participating in mentoring of graduate and undergraduate students

Application Process: see https://www.tinyurl.com/-seascapepostdoc for details. 1. Applicants must complete the RCUOG online job application at https://-www.uog.edu/rcuog/employment-application and attach 1) Cover letter outlining the applicant's interest in the position, past academic accomplishments, and applicant's contribution to the GECCO Project 2) Curriculum Vitae 3) A list of three references with contact information. Application deadline: position open until filled. The initial review of applications will occur on April 30, 2021 (Chamorro Standard Time/UTC+10).

Start date: August 20, 2021 (flexible within reason) Salary: Grade N, Step 1, $45,014 per annum. Benefits:Social Security, Medical and Dental Insurance, 4 hours annual leave and 4 hours sick leave per pay period, holiday pay, up to 3% 403(b) match based upon employee contribution of 3%.

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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

UHouston DrosophilaEvolution

Dear EvolDir,

I am seeking a post-doctoral associate who is interested in using genetic and genomic approaches to understand the evolution, developmental impacts and regulation of transposable elements in Drosophila oogenesis. There are multiple potential projects in the lab that are ripe for development by a postdoctoral trainee, including mechanisms of germline tolerance to transposition, evolution of tolerance factors, and natural variation in response to DNA damage. Read more about our research here: http://nsmn1.uh.edu/eskelleh/ The starting appointment would for 1 year with potential extension for three additional years assuming a good fit with the lab (4 years total). Funding is provided by an R35 and pay-scale is NIH. Start date is flexible, now through December. My lab is a small but active and supportive group.

University of Houston has a strong evolutionary genetics and genomics group that includes Richard Meisel, Rebecca Zufall, Ricardo Azevedo and Dan Graur. Additionally, there are lots of opportunities for interactions with our local colleagues at Rice University and sister institutions at the Texas Medical Center (Baylor, MD Anderson, UT Health etc). TMC also offers numerous professional development opportunities that are accessible to our trainees.

Houston remains an affordable, diverse and culturally-rich city for people of all ages.

Please forward this along to any trainees you are aware of who might be interested. Applicants should contact me directly (eskelleher@uh.edu). Thank you!

best wishes,

Erin

Erin Kelleher Associate Professor Biology and Biochemistry University of Houston eskelleher@uh.edu

Office: Science and Research 2 Rm 421D Lab: Science and Research 2 Rm 428 Office Phone: (713) 743-3640 http://nsmn1.uh.edu/eskelleh/ "Kelleher, Erin S" <eskelleh@Central.UH.EDU>

ULeicester InsectGenomicImprinting

Advert closes midnight on: 05 May 2021

3 year post-doc on mechanisms of genomic imprinting in a social insect The Mallon Lab in the Department of Genetics and Genome Biology at the University of Leicester (http://www2.le.ac.uk/departments/genetics/-

people/mallon) is seeking highly qualified candidates for a Postdoctoral Research Associate in insect epigenetics. We are searching for a motivated individual to perform independent and team-oriented studies on epigenetics of the bumblebee, Bombus terrestris using whole genome/epigenome/transcriptome sequence data. A major focus of this work will be to identify the mechanisms of genomic imprinting in the bumblebee after the lab???s discovery of imprinted genes in this species (https://pubmed.ncbi.nlm.nih.gov/33312684/). In addition, there will be opportunities to develop independent research projects.

See link (https://jobs.le.ac.uk/vacancies/2939/research-associate.html) to apply

Please contact Eamonn (ebm3@le.ac.uk) for informal enquires

Dr. Eamonn Mallon Associate Dean of Research for the College of Life Sciences Associate Professor of Evolutionary Biology Adrian Building Room 220 Genetics and Genome Biology University of Leicester LE1 7RH

"Mallon, Eamonn B. (Dr.)" <ebm3@leicester.ac.uk>

UMaryland EvolutionaryTheory

Postdoc position in evolutionary and ecological modeling at University of Maryland. We are looking for a postdoc with a quantitative background to join our group at Maryland and work on an NIH-funded grant on the evolution and ecological consequences of correlated resistance to multiple pathogens. The goal of the project is to develop general theoretical models that examine the co-evolutionary processes that give rise to host resistance correlations (both positive and negative) between endemic and foreign pathogens. The project is in collaboration with Michael Hood's lab at Amherst college and Janis Antonovics at University of Virginia. The theoretical models developed as part of the project at Maryland will complement empirical research into resistance correlations in a model plant-disease system: anther-smut disease on *Silene vulgaris. *The postdoc would have the opportunity to travel between labs to collaborate with a growing network of anther-smut biologists as well as to participate in field work in the western Italian Alps*.*

Candidates with a background in quantitative biology and experience in evolutionary biology, population genetics, or disease ecology are encourage to apply!. This is a two-year, funded appointment, with preference for a summer 2021 (or earlier) start date. To apply please email Emme Bruns ebruns@umd.edu and attach a cover letter, CV, and contact for 3 references. Position will remain open until filled.

– Emily (Emme) Bruns Assistant Professor of Biology University of Maryland College Park, MD 20741 (301) 405-7684 ebruns@umd.edu http://biology.umd.edu/emily-bruns.html "ebruns@umd.edu" <ebruns@umd.edu>

UMinnesota EvoEcotoxicology

The new Minneapolis-St. Paul (MSP) Urban Long Term Ecological Research (LTER) project, funded by the National Science Foundation, is seeking a postdoctoral scientist to join our research team. The MSP-LTER team is building a long-term program of research related to urban nature. This post doc will lead a project investigating why species vary in their tolerance to urban toxins. We are considering suites of toxins elevated in human dominated environments, including heavy metals, salts, nutrient pollution, and microplastics. We are taking a comparative approach, contrasting species of butterflies, bees, and other animals, testing how their evolutionary history with toxins, and certain ecological and behavioral traits, shape toxin tolerance. The position will present opportunities for collaborations within the MSP LTER, as well for engaging with community partners and the LTER network. Start time of the position is somewhat flexible, as early as July 2021 and as late as May 2022. For more information on the MSP LTER see https://mspurbanlter.umn.edu/ New applications will be reviewed until the position is filled, but application before May 15, 2021 is encouraged to ensure full consideration. To apply, submit a CV, statement of research interests, and contact information for three references to https://hr.myu.umn.edu/jobs/ext/340156 .For more information, please contact Emilie Snell-Rood (emilies@umn.edu)

Required Qualifications:

-

PhD in Ecology, Evolutionary Biology, or related fields
-

Experience with analysis of comparative datasets -

Ability to work independently, and effectively work with a large team -

Commitment to broad engagement with the LTER, external partners and the public

Preferred Qualifications include one or more of the following:

-

Experience with insect pollinators (butterflies, bees) or other invertebrates -

Experience in urban ecology or anthropogenic change -

Experience with ecotoxicology, heavy metals, or anthropogenic chemical stressors -

Some proficiency with GIS

Duties:

40% Designing and conducting field and experimental work studying urban insect pollinators

40% Synthesis and analysis of comparative data across species of insect pollinators

10% Manuscript writing

10% Coordinate and participate in LTER meetings, and working groups

< http://twitter.com/SnellRoodLab >

"emilies@umn.edu" <emilies@umn.edu>

UPennsylvania HumanPopulationGenetics

The Mathieson Lab at the University of Pennsylvania (https://www.med.upenn.edu/mathieson-lab/) is searching for two postdoctoral researchers to work on projects in the areas of population genetics, human evolution and disease genetics. More information here: https://www.med.upenn.edu/apps/my/index.php?_app_id=606bc0c082a9a . To apply, please email your CV with contact details of 2-3 references, and a brief description of your research interests to Iain Mathieson (mathi@pennmedicine.upenn.edu). Please also contact me for informal enquires.

mathi@pennmedicine.upenn.edu

UQueensland MathematicalBiologist

Research Fellow Job No: 513604 Area: Faculty of Science Salary (FTE): Academic Research Level B1 ($99,542.80 - $118,206.73) Work type: Full Time - Fixed Term 5 years Location: St Lucia Contact: Professor Diane Donovan: dmd@maths.uq.edu.au

Welcome to UQ! https://youtu.be/yvQzh30_HDo The School of Mathematics and Physics

The School of Mathematics and Physics is internationally recognised for its teaching and research excellence. Many staff members in the school have won university and national awards for their teaching innovation and excellence. Details of the teaching and research interests of academic staff may be accessed on the School'Âs web site at http://www.smp.uq.edu.au/ The School of Mathematics and Physics has 110 full-time academic staff members and 21 professional staff who provide professional, technical, and administrative support. The School teaches a comprehensive undergraduate program in science, mathematics, statistics, and physics and performing service teaching for students of engineering and the life sciences. There is also an extensive postgraduate research program with more than 100 Research Higher Degree students enrolled.

About This Opportunity

The ARC Centre of Excellence for Plant Success in Nature and Agriculture has been funded for 7 years, ending December 2027. This position will work with the School of Mathematics and Physics with Professor Diane Donovan and other Centre of Excellence research group members.

This position's primary purpose is to apply mathematical techniques to study the properties of genetic networks for plants. The aim is to explore relationships within the network, mapping genotypes to phenotypes. The focus will be on illuminating and interpreting physical relationships in terms of theoretical constructs within complex graphical networks.

This position is located at our picturesque St Lucia campus, renowned as one of Australia'Âs most attractive university campuses, and located just 7km from Brisbane'Âs city centre. Bounded by the Brisbane River on three sides and with outstanding public transport connections, our 114-hectare site provides a perfect work environment 'V you can enjoy the best of both worlds:

a vibrant campus with the tradition of an established university.

Our Ideal Candidate

Our ideal candidate will have a PhD in discrete mathematics or a related field and demonstrated ability to carry out research in discrete mathematics, design theory, and graph theory, with strong knowledge of relevant computational methods.

Visa sponsorship may be available for this appointment.

We value diversity and inclusion and actively encourage applications from those who bring diversity to the University. Our Diversity and Inclusion webpage contains further information if you require additional support. Accessibility requirements and/or adjustments can be directed to recruitment@uq.edu.au.

What We Can Offer

This is a full-time, fixed-term position at Research Academic level B.

The full-time equivalent base salary will be in the range $99,542.80 - $118,206.73, plus super of up to 17%.

You will be able to take advantage of UQ Sports Facilities, recreation leave loading, salary sacrificing options, on-campus childcare, discounted private health insurance, cheap parking, development programs and many other benefits.

For further information, please review The University of Queensland's Enterprise Bargaining Agreement 2018-2021.

Position Description

Download File SMP-CoE-position-description-academic Level B_4E8E (1).pdf

Our Selection Process

Please note that Interviews have been scheduled for the week commencing 17 May 2021 at The University of Queensland's St Lucia campus.

The University of Queensland is committed to ensuring all candidates are provided with the opportunity to attend the panel interviews, however, for those candidates who are unable to attend in person, video interview options will be available.

Questions?

To discuss this role, please contact Diane Donovan: dmd@maths.uq.edu.au.

For application queries, please contact recruitment@uq.edu.au stating the job number in the subject line.

Want to Apply?

To submit an application for this role, use the apply button. All applicants must supply the following documents:

Cover letter Resume Responses to the Selection Criteria

To satisfy pre-requisite questions and ensure your application can be considered in full, all candidates must apply via the UQ Careers portal by the job closing deadline. Applications received via other channels, including direct email, will not be accepted.

– Daniel Ortiz-Barrientos ARC Future Fellow The University of Queensland School of Biological Sciences St Lucia, QLD 4072 Australia Email: d.ortizbarrientos@uq.edu.au

Daniel Ortiz-Barrientos <d.ortizbarrientos@uq.edu.au>

UTexas Austin EvolutionComplexTraits

Open positions in the Harpak Lab at the University of Texas at Austin

The Harpak lab is a new research group at the University of Texas at Austin studying evolutionary, statistical and population genomics.The lab is part of both the Department of Integrative Biology and the medical school, and enjoys collaborative ties with both medical and basic science groups at UT Austin and beyond. More information about the lab can be found at our website:http://www.harpaklab.com . We are looking to hire postdoctoral colleagues (for graduate student positions, please see our website) to work with us on method development and data analysis. A current focus in the lab is on questions falling broadly within the scope of complex trait genetics, including the evolution of complex traits, complex genetic architecture, gene-by-environment interactions, trait prediction (with polygenic scores) and their portability across groups. Nonetheless, we always foster self-driven research and are happy to branch out into new questions in evolutionary, statistical and population genetics beyond our current focus.

Prospective postdocsmust have a strong quantitative background, programming skills and/orextensive experience with genomic data analysis, as well as a sincere interest in tackling biological questions.We welcome applications from underrepresented and diverse backgrounds.

Austin is a fantastic place to live. Postdoctoral posi-

tionsin the lab offera competitive salary and benefits. Applications will be considered on a rolling basis and the start date is flexible. Informal inquiries as well as full applications should be sent toarbelharpak@utexas.edu. Full applications include'Xmost importantly'X a brief description of your research experience, interests and goals , as well as your CV and lettersfrom 2-3professional references (sent separately).

Arbel Harpak <arbelharpak@utexas.edu>

UWisconsin Madison EvolutionaryComparativeGenomics

Postdoctoral Position in Evolutionary Population and Comparative Genomics

A postdoctoral position is available to work on an NSF-funded project in the laboratory of Professor Carol Lee, in the Department of Integrative Biology at the University of Wisconsin, Madison.

This project focuses on Rapid Evolutionary Responses to Global Change using the copepod Eurytemora affinis species complex as a model system. With changes in global climate, coastal high latitude waters are experiencing rapid declines in salinity, due to increases in ice melt and precipitation. We have found evolutionary shifts in ion transport function, genome-wide gene expression, and population genomic signatures of selection associated with changes in salinity (see pubs in the links below). This postdoc project will entail conducting comparative genomic and population genomic analyses associated with temperature and salinity change in wild and laboratory populations.

The E. affinis complex presents an exemplary model, with its short generation time (20d), ease of culturing large numbers (thousands per population), and ability to generate inbred lines. The Lee Lab is generating multiple full reference genomes (PacBio and Oxford Nanopore) from the E. affinis species complex to the chromosome level. Additionally, the multiple independent environmental clines have enabled us to observe exceptional cases of parallel polygenetic adaptation (to the level of SNPs).

The ideal candidate should hold a Ph.D. and have publications in peer-reviewed journals. A background in evolutionary genetics is required, especially in population genetics/genomics or comparative genomics. Relevant areas of expertise include molecular evolutionary genetics, computational and programming skills, and statistics.

Review of applications will begin immediately and will continue until the position is filled. The appointment could persist for up to three years. Interested candidates should email their application to Prof. Carol Lee (carollee@wisc.edu), including: (1) a CV, (2) a list of references (recommenders), and (3) samples of first authored publications. Enquiries regarding this position are most welcome.

The University of Wisconsin-Madison offers a large and intellectually vibrant community of evolutionary/population biologists, providing ample opportunities for interaction with excellent scientists (see https://evolution.wisc.edu/people/faculty/) and first rate departments of Statistics and Biostatistics, computational facilities, and a Biotech Center. Madison is a culturally-rich community, in relative close proximity to Chicago.

Representative publications: https://carollee.labs.wisc.edu/pdfs/Stern&Lee_NatureE&E_2020suppfiles.pdf https://carollee.labs.wisc.edu/pdfs/PosaviEtal_2020.pdf https://carollee.labs.wisc.edu/pdfs/Eyun_etal2017.pdf https://carollee.labs.wisc.edu/pdfs/Posavi_etal2014.pdf The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi LEE Professor Department of Integrative Biology University of Wisconsin, Madison Madison, WI 53706 carollee@wisc.edu

Carol Eunmi LEE <carollee@wisc.edu>

UWisconsin Madison EvolutionaryComparativeGenomics2

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Representative publications: https://carollee.labs.wisc.edu/pdfs/Stern&Lee_NatureE&E_2020suppfiles.pdf https://carollee.labs.wisc.edu/pdfs/PosaviEtal_2020.pdf https://carollee.labs.wisc.edu/pdfs/Eyun_etal2017.pdf https://carollee.labs.wisc.edu/pdfs/Posavi_etal2014.pdf The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi LEE Professor Department of Integrative Biology University of Wisconsin, Madison Madison, WI 53706 carollee@wisc.edu

Carol Eunmi LEE <carollee@wisc.edu>

UZurich PlantEvolution

Postdoc Position in the Group of Prof. Dr. Beat Keller, University of ZÂÂ[1]rich:

Molecular Identification of Plant Immunity Genes Involved in Non-Host Resistance of Triticale to the Wheat Powdery Mildew Pathogen

The successful applicant will use genetic, molecular and bioinformatic approaches to identify the host genes involved in host determination of the mildew pathogen that has recently adapted to the Triticale host. The work builds on earlier findings of hybridization as the cause of adaptation of mildew to triticale (https://www.nature.com/articles/ng.3485 , https://nph.onlinelibrary.wiley.com/doi/abs/10.1111/nph.15529) and the genetic analysis of host determinants in the mildew pathogen (MÂÂ[1]ller et al., unpublished). Based on the pathogen analysis, corresponding genes involved in non-host resistance will be identified using mutagenesis and mutant chromosome sequencing (https://link.springer.com/article/10.1186/s13059-016-1082-1). Functional analysis will include studies in wheat and Triticale as well as in the heterologous N. benthamiana system. For recent publications in the group also see: scholar.google.com/ (Beat Keller).

Requirements and requested skills: - Proven experience (including publications in international well recognized journals) in evolutionary genetics or molecular biology, ideally in the field of host pathogen interactions. - Strong bioinformatic background to handle large genomic sequencing datasets. Programming skills (e.g. Python) are preferred. - Experience in phytopathology is desirable but not essential. - Ability to frame questions and to test them experimentally and bioinformatically. - Writing skills for scientific publications. - Very good English communication skills and ability to both work in a team and individually.

Starting date: Ideally, early Summer 2021 (position is open immediately), but given the current situation we are flexible. The position is available for 2-3 years. The successful candidate will be involved in some teaching activities (1 week/year).

Application procedure: - Send a single PDF titled Hostspecifity_familyname to

javier.sanchezmartin@botinst.uzh.ch with CV including publication list, a short (max. 2 pages) motivation letter explaining your interest in, and qualification for the position and contact details of 2-3 referees. - Applications will be reviewed until the position is filled.

The Department of Plant and Microbial Biology provides an excellent in-house infrastructure as well as access to the central genomics facilities (https://fgcz.ch/). We offer an international, English-speaking work environment. ZÂÂ¹rich is located centrally in Europe and offers easy access to outdoor activities particularly in the Swiss alps.

The position is funded by a grant from the University Research Priority Programme "Evolution in Action" https://www.evolution.uzh.ch/en.html. Questions on this position can be addressed to javier.sanchezmartin@botinst.uzh.ch, marion.mueller@botinst.uzh.ch or Prof. Dr. Beat Keller (bkeller@botinst.uzh.ch).

javier.sanchezmartin@botinst.uzh.ch

ViennaU PDF and PhD EvolutionaryGenomics

Title: ViennaUniversity 2 Evolutionary Genomics postdoc positions

Starting in August 2021, 2 positions (details below) for a postdoctoral researcher (3 years) and a data scientist/postdoc (2 years) will be opening in the group for Computational Admixture Genomics, with funding from the WWTF. We will study admixture landscapes in genomes of multiple species (primates, humans) using present-day, historical and ancient DNA.

Lab members will have access to all necessary resources and excellent computational infrastructure at the new biology center of the university. The group will be part of a multi-disciplinary Evolutionary Anthropology department which is currently expanding in evolutionary genetics and ancient DNA research. There will be opportunities for collaborations inside and outside the department. Vienna is a hotspot for evolutionary research and a city of high quality of living.

Salaries follow the collective agreements of the university. The University of Vienna, the Department of Anthropology, and I as group leader support equality and diversity.

1. Postdoctoral fellow (3 years)

The main project of the postdoctoral fellow will focus on developing strategies for analysing patterns of gene flow in large datasets of different species, mostly primates including humans, and possibly other species. These strategies will rely on computational methods, including demographic modeling, Bayesian methods, or machine learning, to identify introgressed material in different species. Applicants should have experience in such approaches, as evidenced by publications/PhD thesis. Prospective applicants should hold a PhD degree in Computational Biology, Evolutionary Genomics, Statistics, Bioinformatics, or related fields. The position is for a period of 3 years (with the possibility of extension).

2. Data Scientist/Postdoctoral fellow/Bioinformatician (2 years)

The data scientist/postdoc will process, curate and analyse large genomic datasets from ancient, historical and present-day genomes from humans and other species. A background in bioinformatics and/or data analysis is required for this position, either a PhD in the field, or experience as evidenced by publications (like public analysis pipelines or similar).

For all positions, to apply, please send a cover letter explaining your motivation, a curriculum vitae, and contact information of 3 references to martin.kuhlwilm@freenet.de or martin.kuhlwilm@upf.edu.

Group leader: https://martinkuhlwilm.wixsite.com/-maku Department: https://www.anthropology.at/ Faculty: https://lifesciences.univie.ac.at/ ——

Title: ViennaUniversity Evolutionary Genomics PhD student

Starting in August 2021, a position (details below) for a PhD student (4 years) will be opening in the group for Computational Admixture Genomics, with funding from the WWTF. We will study admixture landscapes in genomes of multiple species (primates, humans) using present-day, historical and ancient DNA.

Lab members will have access to all necessary resources and excellent computational infrastructure at the new biology center of the university. The group will be part of a multi-disciplinary Evolutionary Anthropology department which is currently expanding in evolutionary genetics and ancient DNA research. There will be opportunities for collaborations inside and outside the department. Vienna is a hotspot for evolutionary research and a city of high quality of living.

Salaries follow the collective agreements of the university. The University of Vienna, the Department of Anthropology, and I as group leader support equality

and diversity.

PhD student (4 years)

The main project of the PhD student (4 years) will be work on gene flow in large ancient/historical genome data from humans (and possibly other species). This could involve spatiotemporal approaches on introgression landscapes, the analysis of ancient DNA data from modern humans or historical primate samples.

This will integrate with the method development of other group members, as well as the ancient DNA lab of Prof. Pinhasi (https://www.pinhasilab.at/), a leading expert in ancient DNA research and key collaborator. Prospective students should hold a Master's degree in biology or a related field, and be willing to analyse large datasets using computational methods.

The PhD student will be part of the Doctoral School of Ecology and Evolution (https://vds-ecology-evolution.univie.ac.at/).

To apply, please send a cover letter explaining your motivation, a curriculum vitae, and contact information of 2 references to martin.kuhlwilm@freenet.de or martin.kuhlwilm@upf.edu.

Group leader: https://martinkuhlwilm.wixsite.com/-maku

— / —

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

WayneStateU EvolConsFishes

Please post this advertisement for a postdoctoral fellow in my lab. Thanks!

The Dowling lab in the Department of Biological Sciences at Wayne State University invites applications for a Postdoctoral Fellow. Research in the lab is focused on evolution and conservation of fish biodiversity, with focus on species from the southwestern United States.Specific research responsibilities for this position are focused on using genomic and bioinformatics methods for characterization and management of the endangered fish, the razorback sucker, and a close relative, the flannelmouth sucker. This is part of joint projects being conducted in collaboration with researchers from the University of New Mexico, University at Buffalo, and Marsh & Associates (Tempe, AZ).

Applicants are expected to have a PhD degree in biology or a related field, with bioinformatic and laboratory experience required. Strong organizational and communication skills are also required. Principal duties will be the collection and analysis of genomic data and writing reports and manuscripts. Applicants should have experience with basic molecular procedures (DNA/RNA extraction, PCR, electrophoresis, sequencing) and be proficient with command line data analysis (e.g., R or Python). Preferred qualifications include experience with Linux shell scripting and preparation of NextGen sequencing libraries for generation of SNP data. Salary will be commensurate with training and experience. Additional information on the position and instructions for application are provided at the following web address:

https://jobs.wayne.edu/applicants/Central?quickFind 8780

Posting is job number 045502 as a Post-Doctoral Fellow.

Southeastern Michigan provides many opportunities for recreation and exploration in all seasons, including a rejuvenated city of Detroit (https://www.michigan.org/-regions/southeast#?c=44.4299:-85.1166:6&tid=-10&page=0&pagesize=20&pagetitle=Southeast), as does the rest of the state (https://www.michigan.org/).

If you have any questions, please email Tom Dowling (thomas.dowling@wayne.edu).

Thomas Dowling Department of Biological Sciences 5047 Gullen Mall Wayne State University Detroit MI 48202 313-577-3020

Thomas Dowling <thomas.dowling@wayne.edu>

WorkshopsCourses

Florida AdaptiveEvolution Aug16-17

NSF-sponsored Workshop: Detecting adaptive evolutionary events in genomes of polar species at the Whitney Laboratory for Marine Bioscience, St. Augustine, Florida August 16'V17, 2021 A two-day workshop will be held at the Whitney Laboratory for Marine Bioscience (University of Florida) during August 16-17, 2021. Participants should plan to arrive on the afternoon of August 15th and depart in the afternoon on August 18th. The workshop organizers, Dr. Scott Santagata and Dr. Joseph Ryan, will lead participants through a series of computational exercises having the following goals

'P Construct orthologous gene assignments (OrthoFinder), prune paralogous genes (PhyloPYPruner), align orthologous gene (MAFFT), and multi-gene phylogenetic relationships (RAxML).

'P Establish collaborative research groups to test for genes under positive selection from diverse organisms and habitats (e.g., polar, terrestrial, marine, tropical) using genomic and transcriptomic datasets.

'P Evaluate current analytical methods for determining positive selection (e.g., PAML, HyPHy) and their statistical significance.

Participants are encouraged to work with their own NGS-based datasets, but sample datasets will also be provided and analyzed using a bioinformatics platform. Applicants with transcriptomic datasets that span ecological boundaries (e.g. high vs. low latitudinal habitats, marine vs. freshwater habitats, deep vs. shallow water habitats, etc.) will be given priority. However, anyone who is interested in learning these techniques is encouraged to apply.

Lodging will be provided in the Research Village Cabins at the Whitney Laboratory (https://www.whitney.ufl.edu/about/housing/) at no cost to participants. Funds will also be provided to offset the costs of round trip travel based on the number of participants and demonstrated need. Workshop facilities and housing are in accordance with ADA guidelines, and we will work with any students needing accommodations. Researchers from underrepresented groups and/or with disabilities are particularly encouraged to apply. Workshop will include a code of conduct to help ensure a safe and inclusive space. The workshop will incorporate structured participation to ensure balance in participation and encourage inclusion. It will include activities that facilitate interaction within small groups. Mentorship opportunities will be facilitated through encouraging post-workshop interaction and mentoring. To apply please visit http://ryanlab.whitney.ufl.edu/polar_workshop/ .The application (due date: June 1st, 2021) requires: A) Current CV, B) 400-word description detailing your research experiences and how this workshop fits into your overall career goals, and C) Estimated funds needed for round trip travel[JR1]. D) Sars-CoV-2 Vaccination Status[JR2]. Applications may be accepted after the due date depending on the number of applicants and amount of available funds.

Scott Santagata, Associate Professor Department of Biology Life Sciences Building, Room 261 Long Island University-Post 720 Northern Blvd. Greenvale, NY 11548-1300 Phone:516-299-3029 Website: https://sites.google.com/site/scottsantagata/Labpage Researchgate: https://-

www.researchgate.net/profile/Scott_Santagata   Scott
Santagata <Scott.Santagata@liu.edu>

Online ConservationGenomics Sep27-30

Dear all,

registrations are now open for our 4-day course on "Conservation Genomics", which will occurr online in September (27th-30th): (https://www.physalia-courses.org/-courses-workshops/course62/)

This course will introduce biologists to how the tools of population genomics can be used to inform conservation. The instructors will guide students through study design, genomic data collection methods, handling of raw genomic data, and SNP filtering to produce a dataset. Then, we will work through a suite of analyses looking at population structure, local adaptation, effective population size, inbreeding and relatedness. We will provide background on the theory and application of these analyses, and then run hands-on exercises running analyses and interpreting results. Through hands-on exercises, the course will teach basic bioinformatics skills and how to manipulate, visualize and interpret genomic data and patterns in a conservation related context.

Learning outcomes

Study design and genomic data collection methods 2. Handling genomic data from raw reads to a filtered dataset of SNP genotypes 3. Assessing population structure using multiple methods 4. Searching for signals of adaptation 5. Estimating effective population size 6. Calculating inbreeding 7. Estimating relatedness

Program: (https://www.physalia-courses.org/courses-workshops/course62/curriculum62/)

The full list of our online courses can be found here: ((https://www.physalia-courses.org/courses-workshops/))

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

"info@physalia-courses.org"   <info@physalia-courses.org>

Online EvolQuantGenet Jul12-16

The Evolutionary Quantitative Genetics Workshop for 2021, sponsored by Friday Harbor Laboratories of the University of Washington, will occur online this year, from July 12-16. The Workshop is led by Stevan Arnold and Joe Felsenstein, with 6 other lecturers. It will involve lectures, discussion, and computer lab exercises. It is described further at its website: https://fhl.uw.edu/courses/course-descriptions/course/-evolutionary-quantitative-genetics-workshop-2021 which can also be reached at https://tinyurl.com/EQG2021 A link to the application form will be found there. The workshop will review the basics of evolutionary genetics of quantitative characters and its connection to evolution observed at various time scales. An aim of the workshop is to build a bridge between the traditionally separate disciplines of quantitative genetics and comparative methods. It is intended for graduate students, postdocs, and junior faculty. There is a cost of $105+tax, payable by those who are accepted.

Cheers

Joe

Joe   Felsenstein   felsenst@gmail.com, joe@gs.washington.edu   Department   of   Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USAGolding@McMaster.CA

Joe Felsenstein <joe@gs.washington.edu>

Online GeneDrives Jun21-24

Dear colleagues,

We are organizing an online workshop on synthetic gene drives on June 21-24, 2021. The worshkop is interdisciplinary and will feature various sessions: molecular biology, evolutionary ecology, theoretical models, risk assessment, ethical issues, governance and social issues.

Program, list of invited speakers, registration link, and further details can be found on the workshop'Âs

webpage: https://flodebarre.github.io/genedrive2021/-index.html . Registration is free. A few slots are available for contributed talks.

Deadlines:

-17 May 2021 for contributed talks,

-13 June 2021 for other attendees.

Best wishes,

Flo Débarre & Nicolas Rode

Contact: genedrive2021@groupes.renater.fr

– Nicolas O. Rode INRAE Researcher UMR CBGP 755 avenue du Campus Agropolis CS 30016 34988 Montferrier-sur-Lez cedex France tel: +33 430 630 443 web: http://bit.ly/norode Nicolas Rode <nicolas.rode@inrae.fr>

Online GWAS Jun21-25

Dear all,

registrations are now open for the 3rd edition of the Physalia course "Introduction to genome-wide association studies (GWAS)" which will be delivered remotely in June (21st-25th)

Limited number of seats available

(https://www.physalia-courses.org/courses-workshops/-gwas-2/)

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.

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 mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

"info@physalia-courses.org"   <info@physalia-courses.org>

Online IntroToBiodiversityGeographicAnalyses May24-28

Dear colleagues,

Transmitting Science is offering a new course: Introduction to Geographic Analyses of Biodiversity.

Dates and schedule: May 24th-28th, 2021. Online live sessions from Monday to Friday from 15:00 to 17:00 and from 19:00 to 21:00 (GMT+2, Madrid time zone).

Instructors: Miriam Zelditch (University of Michigan, USA), Donald Swidersky (University of Michigan, USA) and Pascal Title (Stony Brook University, USA)

Course overview:

In this course instructors will introduce different conceptual biological reasons why it might be interesting to examine biodiversity data in a geographic context, focusing on the relationships between species richness, trait similarity and phylogeny, as well as patterns of turnover in those relationships. In this overview, they will discuss what these can reveal about patterns of community assembly, ₋in situ₋ diversification vs immigration, as well as the potential connections between these patterns and environmental/climatic/elevational gradients.

In this workshop, instructors will cover how to obtain the various types of data (geographic, environmental/climatic and elevation; morphological and phylogenetic), how to work with them in R, the metrics of diversity, and how to map them for purposes of visualization and how to conduct the statistical analyses, taking geography into account.

This workshop is primarily intended for (but is not exclusive to) graduate students and postdocs with a degree in biological sciences.

The instructors will supply datasets but participants are encouraged to bring (or download) geographic information, phylogeny and morphological data.

More information and registration:

https://www.transmittingscience.com/courses/-evolution/introduction-geographic-analyses-biodiversity/

Best wishes

Sole

– Soledad De Esteban-Trivigno, PhD. Scientific Director www.transmittingscience.com [1]

Twitter: @soledeesteban Instagram: @soledaddeesteban Researchgate: https://www.researchgate.net/-profile/Soledad_De_Esteban-Trivigno ORCID: https://-orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Links:

[1]   http://www.transmittingscience.com
        Soledad   De   Esteban   Trivigno
<soledad.esteban@transmittingscience.com>

Online LandscapeGeneticsUsingR May24-28 Finalcall

FINAL CALL!

ONLINE COURSE 'V Landscape genetic data analysis using R (LNDG04) This course will be delivered live

https://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg04/   24th - 28th May

This is a 'Â¥LIVE COURSE'Â 'V the instructor will be delivering lectures and coaching attendees through the accompanying computer practical'Âs via video link, a good internet connection is essential.

TIME ZONE 'V Eastern Standard Time 'V however

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

Course Overview: The term 'Â¥landscape genetics'Â has been applied studies that integrate ecological context and intervening landscape into population genetic analyses of contemporary processes such as gene flow and migration. This course will cover the basics of both quantitative landscape ecology and population genetics, focusing on how we develop and evaluate spatial/genetic analyses using the R platform.

Email oliverhooker@prstatistics.com with any questions

Upcoming courses

Stable Isotope Mixing Models using SIBER, SIAR, MixSIAR (SIMM07) 19 April - 22 April 2021 https://www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm07/ Data wrangling using R and Rstudio (DWRS02) 21 April - 22 April 2021 https://www.prstatistics.com/course/data-wrangling-using-r-and-rstudio-dwrs02/ Introduction to Python and Programming in Python (PYIN02) 28 April 2021 - 29 April 2021 https://www.prstatistics.com/course/-introduction-to-python-and-programming-in-python-pyin02/ Introduction to Scientific, Numerical, and Data Analysis Programming in Python (PYSC02) 5 May 2021 - 6 May 2021 https://www.prstatistics.com/course/-introduction-to-scientific-numerical-and-data-analysis-programming-in-python-pysc02/ Machine Learning and Deep Learning using Python (PYML02) 12 May 2021 - 13 May 2021 https://www.prstatistics.com/-course/machine-learning-and-deep-learning-using-python-pyml02/ Species distribution modelling with Bayesian statistics in R (SDMB02) 17 May - 21 May 2021 https://www.prstatistics.com/course/-species-distribution-modelling-with-bayesian-statistics-in-r-sdmb02/ Introduction to spatial analysis of ecological data using R (ISPE04) 18 May - 28 May 2021 https://www.prstatistics.com/course/introduction-to-spatial-analysis-of-ecological-data-using-r-ispe04/ Introduction/Fundamentals of Bayesian Data Analysis statistics using R (FBDA01) 19 May 2021 - 20 May 2021 https://www.prstatistics.com/course/fundamentals-of-bayesian-data-analysis-statistics-using-r-fbda01/ Landscape genetic data analysis using R (LNDG04) 24 May - 28 May 2021 https://www.prstatistics.com/-course/landscape-genetic-data-analysis-using-r-lndg04/ Bayesian Approaches to Regression and Mixed Effects Models using R and brms (BARM01) 26 May 2021 - 27 May 2021 https://www.prstatistics.com/course/-bayesian-approaches-to-regression-and-mixed-effects-models-using-r-and-brms-barm01/ Introduction to Bayesian modelling with INLA (BMIN02) 31 May 2021 - 4 June 2021 https://www.prstatistics.com/course/-introduction-to-bayesian-modelling-with-inla-bmin02/ Introduction to Stan for Bayesian Data Analysis (ISBD01) 2 June 2021 - 3 June 2021

— / —

Online MachineLearningForBiologists Sep20-24

Dear all,

registrations are now open for the Physalia course on "INTRODUCTION TO DEEP LEARNING FOR BIOLOGISTS", which will be held online from the 20th to the 24th of September

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

The course is aimed at advanced students, researchers and professionals interested in learning what deep learning is and how to develop a deep learning model for applications in biology. It will include information useful for both absolute beginners and more advanced users willing to delve into some aspects of the implementation of deep learning. We will start by introducing general concepts of deep learning presenting a functioning model and then we will progressively describe the main building blocks of a deep learning model and how the internal machinery works. Attendees are expected to have a background in biology and the research problems involving prediction, inference, pattern discovery; previous exposure to predictive experiments would be beneficial. There will be a mix of lectures and hands-on practical exercises using mainly Python, Jupyter Notebooks and the Linux command line. Some basic understanding of Python programming and the Linux environment will be advantageous, but is not required.

Learning outcomes

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

- the basic theoretical background of deep learning, both in terms of basic building blocks and of commonly used, state-of-the-art architectures

- differences between classification, regression, segmentation, and how to frame a real-world problem in terms of these classes

- the main steps involved in building a deep learning model for prediction problems in biology, comprising how to evaluate prediction accuracy and how to compare and choose different models

- how to use real-world data for statistical learning, comprising data preparation and data augmentation

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

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

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

"info@physalia-courses.org"   <info@physalia-courses.org>

Online MicrobialMetabarcoding Oct4-8

Dear all,

registrations are now open for the Physalia course "16 S/ITS Metabarcoding of microbial communities" - ONLINE - 4th-8th October

Course website: (https://www.physalia-courses.org/-courses-workshops/course30/)

Instructors: Dr. Daniel Pass (University of Cardiff, UK); Dr. Xavier Harrison (University of Exeter, UK); Dr. Bruno Fosso (CNR, Italy); Dr. Anna Sandionigi (University of Milan Bicocca, Italy)

This course will provide a thorough introduction to the application of metabarcoding techniques in microbial ecology. The topics covered by the course range from bioinformatic processing of next-generation sequencing data to the most important approaches in multivariate statistics.

After completing the course, the participants should be able to understand the potential and limitations of metabarcoding techniques as well as to process their own datasets to answer the questions under investigation.

Here you can find the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

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

All the best,

Carlo

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Online RNAseq denovoTranscriptome Apr12-15

The University of Connecticut's Computational Biology Core is offering a workshop on non-model RNA-seq focused on identifying differentially expressed genes using a de novo transcriptome and annotation.

The workshop will cover de novo transcriptome assembly, annotation, including the identification of contaminants, quantification of expression level, exploratory analysis, differential expression analysis and functional enrichment analysis.

The workshop will take place over 4 days for three hours each day.

Dates: April 12 - 15 (4 days)

Time: April 12: 8:30am-12:00pm. Other days: 9.00am - 12.00pm

Location: Online

Cost: $475 (discount available for UConn affiliates).

Workshop schedule

Day 1: Introduction to Linux, High performance computing

Day 2: Basic data QC, Transcriptome assembly and annotation.

Day 3-4 : Expression quantification, exploratory analy-

sis/QC, statistical analysis, functional enrichment.

Registration

To register, please follow this link: https://forms.gle/-5k4NfzGK5EVRUGvS9 Workshop FAQ

Who should attend?

Anyone who wants to learn the fundamentals of RNA-seq analysis with an ad hoc researcher-generated transcriptome. Prior course participants have included faculty, post docs, grad students, advanced undergraduates, staff, and industry researchers.

What are the prerequisites?

Prior bioinformatic experience is not required. We have dedicated the first day of workshop to the basics of Linux and high performance computing.

What do I need?

You will need your own laptop to use, have a recent version of R, RStudio installed, and some other applications. We will send you details of software and installation instructions with your registration acknowledgement email.

Can I bring my own data?

We will provide experimental datasets for use during the workshop, as this helps to keep the workshop moving. There will be time, however, to discuss your own datasets and how you might work with them outside of the workshop.

How much does it cost?

The registration fee is $475.

How do I pay?

The fee is due at the time of registration. UConn affiliates can use KFS accounts. The only other means of payment we currently accept is credit card. Due to some complications we cannot accept international wire transfers at this time.

Where is the workshop?

It will be held on Blackboard-Collaborate platform, and will run from 9:00am to 12:00pm on the dates indicated.

How do I apply?

All registration is "first-come, first-served." There is no application process. Sign up as soon as possible to ensure your place in the workshop.

Questions?

If you have any questions, please don't hesitate to contact us at cbcsupport@uconn.edu

"Reid, Noah" <noah.reid@uconn.edu>

Online Tidyverse Jul19-22

Dear all,

registrations are now open for the Physalia course "DATA ANALYSIS WITH THE TIDYVERSE"

When: Online, 19-22 July 2021

Course website: (https://www.physalia-courses.org/-courses-workshops/tidyverse/)

In this course, participants will learn:

- to import into R data frames from various sources (CSV files, Excel, the web)

- Clean, wrangle and reshape complex data frames.

- Create appealing data visualizations.

Program

Day 1 (2-8 pm Berlin time)

- Data loading with {readr}, {readxl}. - Very fast data loading with {vroom}. - Introduction to web scraping with {rvest}.

Day 2 (2-8 pm Berlin time)

- Using the {magrittr} pipe operator. - Data cleaning and wrangling with {dplyr}. - Data reshaping with {tidyr}.

Day 3 (2-8 pm Berlin time)

- Data visualization with {ggplot2}.

Day 4 (2-8 pm Berlin time)

- Introduction to Functional Programming with {purrr}. - String manipulation with {stringr}. - Handling date data with {lubridate}.

The full list of our online courses can be found here: ((https://www.physalia-courses.org/courses-workshops/))

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

"info@physalia-courses.org"   <info@physalia-courses.org>

Online VirtualDnaSkills May3-Jul25

PDNA-7001-SA Virtual DNA Skills Training Course:

The Virtual DNA Skills Training Course is designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation. This non-credit course is offered as an online virtual course.

The cost of the online virtual training course is $600.00 CDN.

The next scheduled time for the Virtual DNA Skills Training Course is: May 3 to July 25, 2021.

For more information please contact us at 807-343-8877 or email paleodna@lakeheadu.ca or visit our website at www.ancientdna.com and click on 'Training Courses'.

Thank you.

Karen.

Karen Maa Administrative Assistant Lakehead University Centre for Analytical Services (LUCAS) 955 Oliver Road Thunder Bay, ON P7B 5E1

Karen Maa <kmaa@lakeheadu.ca>

Online WholeGenomeSequencing Oct11-14

Dear all,

registrations are now open for the 2nd edition of the Physalia-course "Population genomic inference from low-coverage whole-genome sequencing data", which will be delivered remotely in October (11th-14th).

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

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

In this course, we will explore workflows and the underlying rationale behind producing, processing, and analyzing low-coverage sequencing data for population genomic

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

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

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

Here you can find the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

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

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

"info@physalia-courses.org"   <info@physalia-courses.org>

Virtual EvolutionaryMedicineSummerInstitute May24-28

Applications are open for the Evolutionary Medicine Summer Institute (EMSI)!

The Triangle Center for Evolutionary Medicine (TriCEM) is now accepting applications for the 2021 EMSI, to be held virtually May 24th through 28th.

EMSI provides computational training in evolutionary biology to students, postdocs, and faculty from diverse fields, plus clinicians and other medical, veterinary, and public health practitioners. The goals of EMSI are to:

* Introduce core evolutionary principles * Apply evolu-

tionary perspectives to a wide range of topics (including infectious disease, microbial resistance, cancer, the microbiome, and more) * Provide training in computational methods used in evolutionary and ecological research * Foster new collaborations across the evolutionary sciences, human and veterinary medicine, and public health

Through lectures, hands-on computational exercises, and team-based learning projects, participants will gain the background and the tools to apply evolutionary biol-

ogy to questions of medical and veterinary importance.

For more information and to apply, please visit the EMSI website: https://sites.duke.edu/emsi/. Applications are due April 30, 2021.

Please feel free to contact Meredith Spence Beaulieu (meredith.spence.beaulieu@duke.edu) with any questions.

"meredith.spence.beaulieu@duke.edu"   "meredith.spence.beaulieu@duke.edu"

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly 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.