
E v o l D i r

May 1, 2022

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

Foreword

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

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

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



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Conferences

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Asilomar California ASN symposiaProposals

AsilomarCalifornia.ASN.Symposium.Call.2023

The American Society of Naturalists

Proposals for Symposia at the ASN stand-alone meeting in Asilomar 2023

Due July 01, 2022

The American Society of Naturalists will be going back to Asilomar in Pacific Grove, California, to hold our stand-alone conference - Asilomar 2023 - on 6-10 January 2023!

Have an idea for a special symposium? We want to hear it!

The ASN Symposium Committee invites you to submit proposals for a special symposium. Proposed symposium topics should support the Society's goal to advance the conceptual unification of the biological sciences and to further knowledge in evolution, ecology, behavior, and organismal biology. Topics could center around important emerging issues in evolution, ecology, or behavior or focus on a pivotal historical paper, tracing

its impact and exploring current cutting-edge research inspired by this work. A budget of up to \$8,000 is available to defray travel, registration, and lodging costs for speakers.

Proposals should include (1) a title; (2) a description of the symposium topic (up to one page); (3) a list of six speakers, including institutional affiliations, who have agreed to participate in the symposium; (4) a justification for the symposium, explaining why the topic and speakers are appropriate for an ASN symposium (up to one page).

Please submit proposals by email (rachel.spigler[at]temple.edu) no later than midnight Eastern Time on July 01, 2022. Send your proposal as a single pdf attachment, under subject heading "ASN Asilomar 2023 Symposium Proposal". A confirmation email will be sent within 1-2d of receipt.

In line with theASN'scommitment to diversity, we encourage including speakers from groups who have been historically excluded from STEM. Therefore, proposals that include a diverse list of speakers from a range of backgrounds, institutions, career stages, geography, gender, race etc. are especially encouraged. The Society's selection committee will evaluate proposals based on their potential to attracting substantial audience and stimulate discussion, the significance and timeliness of the topic, and on the topic's differing substantively from

recent symposia hosted by the Society. Applicants will be notified of the decision before the end of July 2022.

Rachel Spigler ASN Symposium Committee Chair Department of Biology Temple University rachel.spigler[at]temple.edu

Rachel Spigler <rachel.spigler@temple.edu>

CIGENE HumanGut Apr6

Hi all!

The next seminar is in just one week and we are thrilled to present our internal speaker; Dr. Sabina Leanti La Rosa, researcher at NMBU, who will present:

Decrypting the mechanism for xanthan gum processing by human gut bacteria through multi-omics and enzymology

Abstract: Microbial communities and their enzymes process many of the “typical” dietary nutrients accessible in the human gastrointestinal tract and play an essential role in host health and nutrition. Eating habits of industrialized countries and gluten-free diets reflect an increasing consumption of processed foods, hence concomitant increased intakes of “atypical” nutrients such as food additives. While often believed to be inert, little is known about the interactions of food additives with the human gut microbiota and their fate in the gut. In this talk, I will present results showing that the human gut microbiota can process xanthan gum, a common food additive used in bakery products, beverages and in gluten-free foods. Metagenomic and metatranscriptomic analyses revealed the presence of a common uncultured Ruminococcaceae genus (R. UCG13) equipped with a gene cluster responsive to xanthan gum. Detailed biochemical studies supported a model whereby extracellular hydrolysis of xanthan gum generates oligosaccharides that are subsequently depolymerized to monosaccharides by a cocktail of intracellular enzymes. In some cases, oligosaccharides produced by the primary degrader R. UCG13 also cross-feed other bacterial populations equipped with their own specific catabolic pathway. A survey of 2441 public human gut metagenomes revealed the broad, diet-specific, distribution of these xanthan utilization loci across the world. Overall, we show that this food additive is not inert and has driven the evolution of interlinked trophic relationships between at least two populations within the human gut microbiota, an adaptation that reflects the

incorporation of xanthan gum into human diets in the past 50 years.

Time: Wednesday, April 6th, 12-13 CET Place: This will be an online seminar: Click here for access to the Zoom seminar. < <https://nmbu.zoom.us/j/67064421833> >

For more information, check out the seminar website: <https://cigene.no/cigene-seminar-series/> 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 Saito <marie.saitou@nmbu.no>

Cleveland Evolution Jun24-28

REMINDER: The early registration discount for EVOLUTION 2022, the joint annual meeting of the ASN, SSB, and SSE, is available until May 1.

Evolution 2022 is hybrid; join us in-person and/or online: June 21 & 22: virtual conference June 24-28: in-person in Cleveland, OH

For everyone’s safety, we have strict vaccine and mask requirements. Event staff will also be masked.

Information: <http://www.evolutionmeetings.org> Registration: <https://www.xcdsystem.com/evolution/-attende/index.cfm?ID=4LdX6xZ> Highlights * Many events and programs in support of diversity, equity and inclusion * Talk & poster submission are available once you complete main registration. * Talk sign-up is first-come, first-served, with all submissions accepted until capacity is reached or until May 15, WHICHEVER IS EARLIER. * All posters are accepted until June 1. * Hotel and dorm accommodations are available * Conference-ending Super Social is a private event at the incredible Rock & Roll Hall of Fame! * Hoping to compete for the SSB Mayr or SSE Hamilton awards? Pay careful attention to instructions: <https://www.evolutionmeetings.org/student-awards.html> * Free on-site childcare * Cleveland has a vibrant and attractive downtown with ample options for food and drinks near the convention center

Howard Rundle <hrundle@uottawa.ca>

ESEBCongress AbstractSubmissionExtended

ESEB Congress 2022 - ABSTRACT SUBMISSION EXTENDED UNTIL 22 April 2022!

The European Society for Evolutionary Biology invites you to submit your abstract for the next ESEB congress from 14-19 August 2022 in Prague, Czech Republic.

The list of symposia is available at <https://www.eseb2022.cz/en/symposia>. Details about submitting an abstract are available at <https://www.eseb2022.cz/en/call-for-abstracts-page>. Please note the following dates:

22 April 2022 - Abstract submission closes
10 May 2022 - Communication of selection of contributed talks/posters
15 June 2022 - Early bird registration closes

Further details are available at <https://www.eseb2022.cz>
Dr. Ute Friedrich | Email: office@eseb.org European Society for Evolutionary Biology | www.eseb.org ESEB Office <office@eseb.org>

ESEBSymposium TandemRepeats 2022

Dear evoldir community,

We would be very happy to welcome you at our ESEB 2022 symposium “Tandem repeats: their role in molecular evolution and methods” (S27), which is open for submissions until April 15th (see <https://www.eseb2022.cz> for further details).

Keynote speakers:

Melissa Gymrek, UCSD, California

Miguel Andrade, Johannes Gutenberg University, Mainz

Abstracts can be submitted on:

<https://www.eseb2022.cz/en/call-for-abstracts-page>.
Deadline is April 15 2022.

Tandem repeats (TRs) are adjacent repetitive stretches of genomic DNA, found in abundance across all kingdoms of life. TRs provide a rich source of variation

in populations, hence a perfect playground for natural selection forces. Especially, shorter TRs are known for their orders of magnitude high mutation rates compared to SNPs and indels. TR-suitable methods and resources are emerging one after the other allowing accurate TR annotation and genotyping integrated into existing genomic pipeline workflows. Analysis of TR variation in populations and over longer evolutionary time suggest STRs as a major contributor to complex traits heritability with a major impact on protein function and expression.

This symposium will focus on the typing approaches, evolution, and functional analysis of these highly polymorphic elements. We aim to bring together both researchers who develop and apply methods for accurate STR genotyping, and identification of STRs relevant for phenotypic evolution, and recent adaptations. This way, the symposium will facilitate interactions between researchers from different backgrounds and promote the interdisciplinary study of the STRs, an emerging major source of phenotypic variation. Therefore, we expect this symposium to be of interest to a broad range of researchers in the fields of bioinformatics, population genomics, and evolutionary biology.

Organisers:

Tugce Bilgin, Columbia University, New York

Maria Anisimova, ZHAW, Zurich

ESEB also proposes a grant in order to ensure equal opportunities. For further details:

<https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/> For more information email tb2879@columbia.edu

Dr. Tugce Bilgin Sonay Lecturer in Discipline Department of Ecology, Evolution, and Environmental Biology Columbia University Yoga Instructor Head of Evolutionary Genomics Winterschool

tugebilgin.net

Tugce Bilgin Sonay <tb2879@columbia.edu>

Groningen BehavBiol Jul20-23

Dear colleagues,

We have extended the deadlines for abstract submission and registration for the European Conference on Behavioural Biology, which will be held in Groningen this

summer (July 20-23): <https://ecbb22.wordpress.com/> .
Deadline for abstract submission: May 9
Deadline for early bird registration: May 25

After a long period of restricted interactions, the theme of the conference is “All of Life is social!”. We explore the many facets of social life, from proximate to ultimate mechanisms in a wide variety of species. You can submit your contributions (talks and posters) to one of the parallel symposia with themes ranging from social foraging to animal welfare and from cultural evolution to epidemiology - or to one of the open symposia. For symposium information, see <https://ecbb22.wordpress.com/program-2/> . Keynote speakers: David J. Anderson (California Institute of Technology), Nicola Clayton (University of Cambridge), Audrey Dussutour (University Paul Sabatier), Rose Thorogood (University of Helsinki), Peter Kappeler (University of Göttingen), Joel Levine (University of Toronto, Missis-sauga), Franjo Weissing (University of Groningen).

For more information see <https://ecbb22.wordpress.com/> We hope to see you in Groningen this summer!

The organizing committee Jean-Christophe Billeter, Pleunie Kraak, Martine Maan & Simon Verhulst

Groningen Institute for Evolutionary Life Sciences (GELIFES) <https://www.rug.nl/research/gelifes/>
m.e.maan@rug.nl

Lisbon SocietyEvolMedicine Jul5-8

The Annual Meeting of the International Society for Evolution, Medicine, and Public Health will be in-person in Lisbon, Portugal, July 5-8. All are welcome to join this gathering of researchers, teachers, students, and clinicians who share an interest in how evolutionary biology can help improve the understanding and treatment of disease. Full information at <https://ISEMPH.org> Submit your abstract now! The deadline is April 15. All topics related to evolution, disease and health are welcome.

Discounted meeting registration is open now; refunds are available if your plans change.

VENUE <https://isemph.org/ISEMPH2022-Travel-and-Lodging> The conference will be held at the Fundação Calouste Gulbenkian (FCG, in the Portuguese acronym) in Lisbon. FCG is a pleasant, iconic, and easily accessible place in the center of Lisbon, with ample indoor

and outdoor spaces. Around the FCG, there are many options for accommodation and food, covering a wide range of prices and styles, suitable for all.

KEYNOTE SPEAKERS <https://isemph.org/ISEMPH-2022-Program> Sebastian Bonhoeffer, ETH, Switzerland, Combination therapy and the evolution of drug resistance

Mhairi Gibson, University of Bristol, UK, The social and evolutionary dynamics of female genital mutilation/cutting (FGM/C) abandonment

Isabel Gordo, Instituto Gulbenkian de Ciência, Portugal, Eco-evolutionary dynamics of *Escherichia coli* when it colonizes the intestinal tract

Joseph L. Graves, North Carolina A&T State University, USA, Racial health inequality is a solved problem: Now what do we do about it?

Gunther Janssen, Pharma PHC Centre of Excellence, Hoffman-La Roche / Genentech, Switzerland, Afternoon Discussion and Q&A on Pharma in and Evolutionary World C.

Jessica Metcalf, Princeton University, USA, What we can and can't predict about the evolutionary trajectory of SARS-CoV-2

Luca Ermini, Winner of the George. C. Williams Prize for work on Evolutionary selection of alleles in the melanophilin gene that impacts on prostate organ function and cancer risk

Winner of the \$5,000 Omenn Prize, TBA. NOMINATE your article or another article this week: The deadline is April 8. <https://isemph.org/Omenn-Prize> Questions welcome. Manager@isemph.org or HostingCommittee@ISEMPH.org or ProgramCommittee@ISEMPH.org or nesse@umich.edu

Lisbon SocietyEvolMedicine Jul5-8 AbstractDeadline

ABSTRACT DEADLINE THIS WEEK! The deadline is April 15. All topics related to evolution, disease and health are welcome.

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Napoli EuroEvoDevo May31-Jun3 Registration

Dear Evo-Devo scientists, join us at

EURO EVO DEVO 2022 Napoli 31 May - 3 June

REGISTRATION AND POSTER SUBMISSION STILL OPEN!

For more information visit: <https://www.evodevonapoli.eu/> - More than 400 participants - More than 200 talks - 28 symposia - In beautiful Naples - Chance to visit one of the cradles of EvoDevo: Stazione Zoologica Anton Dohrn

Plenary speakers:

- Paola Oliveri - Robert Cerny - Stephanie Hoehn - Chelsea Specht

For the time table see: <https://www.evodevonapoli.eu/-timetable/> Covid regulations: We take covid-19 very seriously and strictly follow the prescribed rules:

<https://www.evodevonapoli.eu/covid-19-measures/>

The local organizing committee The executive committee of the European Society for Evolutionary Developmental Biology

EED Society <eed.soc@gmail.com>

Netherlands NLSB Jun27-28

Registration for the NLSEB (Netherlands Society for Evolutionary Biology) 2022 meetings is now open

NLSEB 2022 main meeting

Date: 28 June 2022

Place: Akoesticum, Ede, the Netherlands

The meeting brings together scientists from all disciplines working on evolutionary questions. This yearly meeting aims to build a broad community of evolutionary biologists based in the Netherlands, and connect with researchers abroad. We have exciting plenary talks by Eric Snijder (LUMC), Jaap Kaandorp (UvA) and Katja Peijnenburg (Naturalis), and by the winner of the

2021 Netherlands Evolutionary Biology Prize. We are looking forward to see you in Ede!

NLSEB 2022 PhD/Postdoc Meeting

Date: 27 June 2022

Place: Akoesticum, Ede, the Netherlands

Our aim is to bring together early-career researchers for networking, skill building opportunities and social interactions. To achieve this goal, we offer an afternoon program in which participants can pitch their research interests to facilitate networking conversations, join diverse workshops for improving both transferable and specialised skills, and listen to an exciting plenary talk by Nico van Straalen.

Information about program and registration for both meetings: <http://nlseb.nl/nlseb-2022-meetings/>. Deadline for abstract submission for the main meeting is 2 May 2022 and deadline for registration for both meetings is 10 June 2022.

We look forward to meeting you in person in June!

“Visser, Arjan de” <arjan.devisser@wur.nl>

Online ConGen Sep6-17

CONGEN 2022: September 6-17, 2022 Conservation Genetics, Population Genomics, and Molecular Ecology Workshop

The goal of ConGen 2022 is to provide training in conceptual and practical aspects of population genomic data analyses to improve understanding of the evolutionary and ecological genomics of natural and managed populations. We will have more than 15 expert instructors from multiple countries to help teach a breadth of concepts and applications.

ConGen teaches fundamental statistical and computational approaches that will help prepare students and professionals to use population genomic data in their work. Emphasis will be on next-generation sequence (NGS) data analysis (RADs, DNA capture, and genome sequencing/resequencing) and interpretation of output from fundamental and novel statistical approaches and software programs (including R and Linux command line). The course promotes interactions among early-career researchers (e.g., grad students & postdocs), mid-career faculty and agency researchers, and leaders in population genomics to help develop our “next gen-

eration” of conservation and evolutionary geneticists. We will identify and discuss developments needed to improve data analysis approaches to advance the field. This course often feels like a workshop because multiple instructors ask questions and provide helpful comments during another instructor’s lecture to help advance learning of basic and advanced concepts and approaches.

This course will cover concepts and methods including the coalescent, Bayesian, and likelihood-based approaches. Special lecture sessions and hands-on exercises will be conducted on assessing population structure, testing for HW proportions, detecting selection, genetic monitoring ($of_i \frac{1}{2} Ne, i_i \frac{1}{2} FST, i_i \frac{1}{2} Nm, i_i \frac{1}{2}$ etc.), landscape genomics, inbreeding detection (RoH), GWAS, population assignment, gene flow estimation, whole-genome sequencing & assembly, and more. It will include daily sessions with hands-on data analysis activities, including genotyping and data analyses using NGS data.

This course is sponsored by the American Genetic Association, the Journal of Heredity, NASA (the National Aeronautics and Space Administration), NSF (the Dimensions in Biodiversity program), along with DoveTail Genomics, and support from publications such as Environmental DNA, Evolutionary Applications, Molecular Ecology Resources, and Conservation Genetics. Some sponsors give talks on new and future technologies (e.g., Dovetail, PacBio). Many of the expert instructors will lead hands-on data analysis sessions using your data and dummy data sets provided by instructors. This course/workshop has led to publications describing the main topics, course outcomes, and recent advances in the field that facilitate data analysis for population geneticists worldwide. For example, see 4 pubs below: * Schweizer et al. 2021: <https://doi.org/10.1093/jhered/esab019> * Stahlke et al. 2020: <https://academic.oup.com/jhered/article/111/2/227/5731771> * Hendricks et al. 2018: <https://onlinelibrary.wiley.com/doi/full/10.1111/eva.12659> * Benestan et al. 2016: <http://onlinelibrary.wiley.com/doi/10.1111/mec.13647/-full> * Andrews and Luikart 2014: <http://onlinelibrary.wiley.com/doi/10.1111/mec.12686/-abstract> COST TO ATTEND ONLINE The cost to participate in ConGen 2022 is \$840 US if you pay before July 1st or \$890 US if you pay after July 1st. This cost includes lectures (live and recorded) by at least 15 expert instructors, online question and answer sessions during and after hands-on exercises with worksheets and dummy datasets, copies of lecture PowerPoint slides, along with ConGen-2022 Swag (T-shirt, mug). Course materials are also available after the end of the course to all students in a box repository including all recorded lectures and class materials and slides for

many months after ConGen.

The online course supports a virtual server implementation for a majority of the software and tools for the course. This allows students to jump into data analysis with less downtime needed to install bio-informatics tools. Linux line commands will be used for several analyses during the course. A 1-2 hours tutorial on Linux will be given a week before the course for those needing to learn Linux line commands for population genomics data analysis, before the course.

The 2022 course will be online using Zoom along with a blog/forum (via

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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>

Online EvolutionInformedProteomics Apr12

ISCBacademy EvolCompGen/SMBE Webinar

COMBINING EVOLUTION AND PROTEOMICS TO DISCOVER PROTEIN COMPLEXES CONSERVED ACROSS PLANTS

Claire McWhite, PhD

April 12th, 10:30 EDT

Participation is free for members of ISCB or SMBE, but registration is required. https://www.iscb.org/cms_addon/registration_conference/cosi28 Plants are foundational for global ecological and economic systems, but most plant proteins and many protein complexes remain uncharacterized. In plants, highly duplicated protein families pose challenges for protein identification, which is heavily reliant on unique peptides. To address this problem, we developed an evolution-informed proteomics strategy that combines orthology analysis with mass spectrometry. We applied this strategy to 13 plant species of scientific and agricultural importance, greatly expanding the known repertoire of stable protein complexes in plants. We recovered known complexes, confirmed complexes predicted to occur in plants, and identified previously unknown interactions conserved over 1.1 billion years of green plant evolution. The resulting map offers a cross-species view of

conserved, stable protein assemblies shared across plant cells and provides a mechanistic, biochemical framework for interpreting plant genetics and mutant phenotypes.

McWhite et al. A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. *Cell*. 2020;181(2):460-474.e14. <https://doi.org/10.1016/j.cell.2020.02.049> The joint EvolCompGen/SMBE webinar serves as an online journal club to promote discussion of recent results presented by early career researchers.

For further information, contact: Dannie Durand, Carnegie Mellon University, durand@cmu.edu

Online HumanPopGenetics Apr20

Hi all!

At the next seminar, Eaaswarkhanth Muthukrishnan, Research Scientist, New York University Abu Dhabi will present:

Insights into the fine-scale population structure and contributions of ancient genetic adaptations to metabolic traits in modern-day Kuwaiti Arabs.

Abstract: Being at the crossroads between Africa and Eurasia, the Arabian Peninsula has experienced several waves of human migrations despite the prevailing extreme and varying environmental conditions; therefore, the resident populations have a high genetic diversity. In this talk, I will present our recent works that explored the regional genetic heterogeneities and admixture history of populations inhabiting the Peninsula. In addition, I will highlight interesting ancient genetic adaptations once key to survival for Kuwaiti ancestors in the harsh desert environment that predispose their descendants to debilitating metabolic diseases.

Time: Wednesday, April 20th, 12-13 CET Place: This will be an online seminar: Click here for access to the Zoom seminar. < <https://nmbu.zoom.us/j/67064421833> >

For more information, check out the seminar website: <https://cigene.no/cigene-seminar-series/> *We have two postdoc positions* <https://www.jobbnorge.no/en/-available-jobs/job/224555/postdoctoral-fellows-within-genome-biology> 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 Saito <marie.saitou@nmbu.no>

Online LowMutationLoad Apr27

Hi all!

The next seminar is in just one week and we are pleased to present Professor Leif Andersson, Uppsala University. He will give a talk entitled:

Low mutation load in a supergene underpinning alternative male mating strategies in ruff.

Abstract: Ruffs are shorebirds with an elaborate lekking behavior involving three male morphs with different mating strategies: Independents, Satellites, and Faeders. The latter two are heterozygous for different versions of a supergene maintained by an inversion that were estimated to have occurred about 4 million years ago. Faeders carry an intact inversion while the Satellite allele is recombinant, both of which are expected to accumulate high mutational load because they are recessive lethals. Here we have constructed a highly contiguous genome assembly of the inversion region for both the Independent and Satellite haplotypes. The recombination event(s) between an inverted and non-inverted chromosome creating the Satellite allele must have occurred recently (within the last 100,000 years) based on the minute sequence divergence between the Satellite and Independent alleles in the recombinant regions. Contrary to expectations, we find no expansion of repeats and only a very modest mutation load on the Satellite allele in the nonrecombinant region despite high sequence divergence (1.46%). The essential centromere protein CENPN gene is disrupted by the inversion, and surprisingly is as well conserved on the inversion haplotypes as on the noninversion haplotype. The results suggest that the inversion may be much younger than previously thought.

Time: Wednesday, April 27th, 12-13 CET Place: This will be an online seminar

For more information, check out the seminar website: <https://cigene.no/cigene-seminar-series/> 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 Saito <marie.saitou@nmbu.no>

Online Phylogenetics Apr26

Dear Colleagues,

We would like to invite you to our ongoing virtual seminar series: "Horizontal evolutionary processes in phylogenetics" (<https://www.shh.mpg.de/2022486/tide-seminar-series>).

We are excited to announce our next speaker in the series: Elizabeth Hayman (University of Oxford).

The event will take place on Tuesday 26 April 2022 at 2pm (CET).

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Title: Recoverability of ancestral recombination graph topologies

Abstract:

Ancestral recombination graphs (ARGs) are the extension of phylogenetic trees to include recombination, a powerful evolutionary process that shapes the genetic diversity of many species. The topology of this graph gives us important information on the evolution of a species, but algorithms to reconstruct an ARG from species data are often reliant on sample sequences carrying informative patterns of mutations. In this talk I will present exact results concerning the probability of recovering the true topology of an ARG under the coalescent with recombination and gene conversion. These expressions give us an indication of the uncertainty in reconstructed ARGs, and we see that for parameter values realistic for biological species (in particular SARS-CoV-2), the probability of reconstructing genealogies that are close to the truth is low. This is joint work with Anastasia Ignatieva and Jotun Hein (<https://arxiv.org/abs/2110.04848>).

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To attend the seminar, please subscribe to our mailing list onto which a zoom link will be sent prior to the event. Use the form at the bottom of this page: <https://www.shh.mpg.de/2022486/tide-seminar-series> Feel free to circulate to anyone who might be interested.

Looking forward to seeing you there!

The tide research group <https://www.shh.mpg.de/tide> Max Planck Institute for the Science of Human History Tide Seminars <tide-seminars@shh.mpg.de>

Paris EvolutionOfSexChromosomes Jun9-10

Dear all, We are thrilled to announce a conference on the evolution of sex chromosomes and supergenes, in Paris, France, June 9-10th 2022, at the College de France. Attendance will be free and without registration (within room limits) and talks will be available online afterwards. More information soon here: <https://www.college-de-france.fr/site/tatiana-giraud/symposium-2022-06-09-09h00.htm> We will have talks by Doris Bachtrog, Laurent Keller, Tanja Slotte, Thomas Lenormand, Jessica Abbott, Tatiana Giraud, Stephen Wright, Alison Wright, Paul Jay, Daniel Jeffries, Emma Berdan, Tim Connallon, Deborah Charlesworth, Mathieu Joron, Aline Muyle, Simon Martin, Iulia Darolti, Yannick Wurm, Christelle Fraïsse, Ricardo Rodriguez de la Vega, Gabriel Marais, Nicolas Perrin, Diego Cortez, Michel Hood Organizing comitee: Tatiana Giraud, Paul Jay, Ricardo Rodriguez de la Vega Funding: College de France, Fondation Jean-François et Marie-Laure de Clermont Tonnerre

Tatiana Giraud

Directrice de recherches CNRS Professeur au Collège de France Membre de l'académie des sciences IDEEV, Bâtiment 680, 12 route RD128 91190 Gif-sur-Yvette Université Paris-Saclay 91400 Orsay France

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English: <https://www.ese.u-psud.fr/en/team-members/tatiana-giraud/> Français: <https://www.ese.u-psud.fr/personnel/tatiana-giraud/> @GenEcoEvo <http://www.ese.u-psud.fr/> Tatiana Giraud <tatiana.giraud@u-psud.fr>

Prague DomesticationWithAncientDNA Aug14-19

Dear colleagues,

We'd like to kindly remind you that the abstract submission

deadline for our symposium titled "Domestication: Fresh insights from ancient genomics" is approaching.

The symposium will be part of the ESEB meeting in Prague between August 14-19, 2022.

More information about the ESEB meeting can be found below and at the conference website: www.eseb2022.cz

S33: Domestication: Fresh insights from ancient genomics

Animal and plant domestication events have fundamentally changed human societies in multitude ways, while biologically shaping the domesticated species themselves. The tempo and mode of domestication processes, the subsequent dynamics of transport, breeding and introgression between domesticates and their wild relatives, the genetic bases of selected traits, as well as the social and biological impacts of animal husbandry and farming on humans have long been investigated, using either archaeological evidence or inferences from biological studies of extant species. The advent of ancient genomics, however, has been a game changer. The last few years have seen a wide range of spectacular work that rewrote domestication histories of different species, from dogs to chicken. This session aims to bring together the most recent and exciting work on animal and plant domestication, covering both the reconstruction of demographic history, analyses of selective sweeps, evidence for relaxation of constraints, as well as studies on ancient pathogens.

Invited speakers

Dr. Laurent Franz, Ludwig-Maximilians-Universität München, Germany

Dr. Catarina Ginja, Universidade do Porto, Portugal
Organisers

Mehmet Somel, Middle East Technical University, Turkey (somel.mehmet@gmail.com)

Anders Götherström, Stockholm University, Sweden (anders.gotherstrom@arklab.su.se)

Eva-Maria Geigl, Institut Jacques Monod, CNRS, France (Eva-maria.GEIGL@ijm.fr)

Dates

Registration opens: February 2022

The abstract submission deadline: April 15, 2022

Selected contributions to be announced by: May 10, 2022.

Early-bird registration closes: June 15, 2022

Useful links

Abstract submission page: <https://www.eseb2022.cz/>

[en/call-for-abstracts-page](https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/) Equal opportunities grant: <https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/> Looking forward to seeing you in Prague!

Eva-Maria, Anders, and Mehmet

Mehmet Somel METU Dept. Biology / ODTÜ $\frac{1}{2}$ Biyoloji BİL $\frac{1}{2}$ Lİ $\frac{1}{2}$ Mİ $\frac{1}{2}$ 06800 Ankara, Turkey Tel: +90-543-9799060; Office: +90-312-2106460 Email: msomel@metu.edu.tr Lab: compevo.bio.metu.edu.tr aDNA Lab: <http://adna.bio.metu.edu.tr/> Eco-Evo Society of Turkey: <https://ekoevo.org> Mehmet Somel <msomel@metu.edu.tr>

Prague ESEB InvasiveSpecies Aug14-19

Dear Eco-Evo Enthusiasts,

Take the opportunity to submit your contribution for an oral talk or poster at the symposium “Eco-evolutionary dynamics and feedbacks in invasive species” (S19), that will be held in Prague, The Czech Republic as part of the Congress of the European Society for Evolutionary Biology (14-19 August 2022, <https://www.eseb2022.cz>). The symposium aims to discuss the integration of eco-evo concepts in biological invasions. Abstract submission is open until 22 April: <https://www.eseb2022.cz/en/call-for-abstracts-page> Symposium description: Introduced alien species are remarkable in their unusual ability to experience rapid evolutionary and ecological changes on relatively short time scales following their introductions to novel ranges. As a result, biological invasions offer valuable insights into processes that contribute to our understanding of population responses to climate change, ecosystem function, extinction and diversification events, with implications for species management and conservation. While a rich literature exists on the ecology and evolution of invasive species, much less is known about how ecological properties and evolutionary changes influence one another, namely, the so-called “eco-evolutionary dynamics” and “eco-evolutionary feedbacks”. Thus, this symposium aims to discuss the innovative integration of concepts from these two fields into the study of invasion biology. In particular, we welcome studies that focus on topics such as interactions between genome architecture and environmental change, adaptive traits and their ecological consequences, post-introduction evolution, feedbacks between organisms and resource dynamics, effects of

evolution of dispersal on range expansions, and the interplay between theoretical population genetics and ecological demography. In addition, talks could focus on evolutionary diversification, niche displacement or extinction of resident species induced by invaders. We also encourage studies on ecological genomics that could be applied to non-model invasive populations.

Invited speakers: Carol Eunmi Lee (University of Wisconsin), <https://carollee.labs.wisc.edu/-CarolPersonal.html> Katrina Dlugosch (University of Arizona), <https://www.dlugosch-lab.net/people> Travel aid ESEB provides funding opportunities to attend the meeting for students and young researchers: (<https://eseb.org/prizes-funding/conference-travel-award/>) as well as for underrepresented groups including care giving women: <https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/> . Early-bird registration is open until 15 June 2022.

Symposium organizers: Ramona Irimia, Isolde van Riemsdijk (University of Tübingen, Germany) and Armand Cavé-Radet (University of Rennes 1, France and University of Tübingen).

For questions related to the symposium, please contact us at: ramona-elena.irimia@uni-tuebingen.de.

We look forward to receiving your abstracts and meeting you in Prague!

Ramona-elena Irimia <ramona-elena.irimia@uni-tuebingen.de>

Prague ESEB InvasiveSpecies Aug14-19

Dear Eco-Evo enthusiasts,

Take the opportunity to submit your contribution for a talk or poster at the symposium “Eco-evolutionary dynamics and feedbacks in invasive species” (S19), that will be held in Prague, The Czech Republic as part of the Congress of the European Society for Evolutionary Biology (14-19 August 2022, <https://www.eseb2022.cz>).

The symposium aims to discuss the integration of eco-evo concepts in biological invasions. Abstract submission deadline is open until 22 April: <https://www.eseb2022.cz/en/call-for-abstracts-page> Symposium description: Introduced alien species are remarkable in their unusual ability to experience rapid evolu-

tionary and ecological changes on relatively short time scales following their introductions to novel ranges. As a result, biological invasions offer valuable insights into processes that contribute to our understanding of population responses to climate change, ecosystem function, extinction and diversification events, with implications for species management and conservation. While a rich literature exists on the ecology and evolution of invasive species, much less is known about how ecological properties and evolutionary changes influence one another, namely, the so-called “eco-evolutionary dynamics” and “eco-evolutionary feedbacks”. Thus, this symposium aims to discuss the innovative integration of concepts from these two fields into the study of invasion biology. In particular, we welcome studies that focus on topics such as interactions between genome architecture and environmental change, adaptive traits and their ecological consequences, post-introduction evolution, feedbacks between organisms and resource dynamics, effects of evolution of dispersal on range expansions, and the interplay between theoretical population genetics and ecological demography. In addition, talks could focus on evolutionary diversification, niche displacement or extinction of resident species induced by invaders. We also encourage studies on ecological genomics that could be applied to non-model invasive populations.

Keynote speakers: Carol Eunmi Lee (University of Wisconsin), <https://carollee.labs.wisc.edu/-CarolPersonal.html> Katrina Dlugosch (University of Arizona), <https://www.dlugosch-lab.net/people> Travel aid ESEB provides funding opportunities to attend the meeting for students and young researchers: (<https://eseb.org/prizes-funding/conference-travel-award/>) as well as for underrepresented groups including care giving women:

<https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/> . Early-bird registration is open until the 15 June 2022.

Symposium organizers: Ramona Irimia, Isolde van Riemsdijk (University of Tübingen, Germany) and Armand Cavé-Radet (University of Rennes 1, France and University of Tübingen). For questions related to the symposium, please contact us at: ramona-elena.irimia@uni-tuebingen.de

We look forward to receiving your abstracts and meeting you in Prague!

danimontesinos@gmail.com

Prague ESEB RapidEvolutionOfColorPatterns Aug14-19

Dear colleagues,

The abstract submission deadline for the ESEB 2022 conference has been extended to the 22nd of April, so there is still time to submit your abstract to our symposium S15 “Rapid evolution of color patterns”.

The symposium will be held at the Congress of the European Society for Evolutionary Biology in Prague, 14-19 August 2022 (<https://www.eseb2022.cz/>). Symposium description

Animal and plant color patterns are labile characters that are involved in important biological functions such as reproduction, predator evasion, pollinator attraction, and thermoregulation. A fascinating feature of color variation is that it can evolve rapidly in new environments, as highlighted by dramatic examples in peppered moths, cichlid fishes, and *Heliconius* butterflies. Beyond these classic cases, technological advances in high-throughput sequencing, phenotyping, and gene editing, have opened new pathways to study rapid evolution using color patterns in a diversity of models. Among other examples, recent studies have highlighted the role of transposable elements in buffalo coat coloration, chromosome re-arrangement in butterfly wing patterns, and transgenerational plasticity in flower coloration in response to predation. This symposium will assemble researchers who use animal and plant color patterns as models to evaluate the diversity of factors driving and constraining rapid phenotypic evolution. We will foster transdisciplinary discussions addressing long-standing questions on the genetic substrate of recurrent adaptation and the mechanistic scale of convergence. Ultimately, we hope to gain a more comprehensive understanding of the mechanisms underlying rapid adaptation.

Invited speakers

Mar Sobral, Universidade de Santiago de Compostela, Spain

Patricia Beldade, Universidade de Lisboa, Portugal
Abstract submission deadline: 22 April 2022
Abstract submission page: <https://www.eseb2022.cz/en/call-for-abstracts-page> Conference attendance aid grant: <https://eseb.org/prizes-funding/equal-opportunities->

[initiative/congress-attendance-aid-grant/](#) For any questions, contact Sandra Goutte (sg5533@nyu.edu) or Yann Bourgeois (yann.bourgeois@port.ac.uk) We look forward to reading your abstracts! Sincerely, Sandra and Yann

– Sandra Goutte, Ph.D. Research Associate New York University Abu Dhabi Saadiyat Island campus P.O. Box 129188 Abu Dhabi, United Arab Emirates

+971 505 8383 96 Twitter: @sandra.goutte CalPhoto: http://calphotos.berkeley.edu/-cgi/img_query?where-genre=Animal&where-photographer=Sandra+Goutte > Flickr: <https://www.flickr.com/photos/133250906@N05/> < <https://www.flickr.com/gp/133250906@N05/g4196q> >

Sandra Goutte <sg5533@nyu.edu>

Prague ESEB Resurrection Ecology Aug14-19

Dear colleagues, Submission deadline for the ESEB 2022 conference has been extended to the 22nd of April.

We invite your submission to the Symposium 12 “Resurrection ecology as a tool for the study of rapid evolution” at the ESEB 2022 conference in Prague.

Link for submissions and other key information are below.

Invited speakers: Niek Scheepens, Goethe-Universität Frankfurt, Germany Luisa Orsini, University of Birmingham, UK

Abstract

It is now accepted that rapid evolution (within a dozen generations) can occur, contrary to the classical Darwinian view that assumes slow pace of evolution. Rapid evolution is particularly frequent in response to contemporary anthropogenic modification of the environment (e.g. climate change, pollution), although demonstrating its adaptive character remains challenging.

Resurrection ecology (RE) is an inventive approach to study evolution based on the ancestral populations reviving (decades old) from dormant forms (seeds, spores, cysts). Comparing ancestral and current genotypes is a powerful methodology for demonstrating adaptive rapid evolution, although often limited by the fortuitous availability of ancestral material in sediments or seed banks. Being at its beginnings, it is important that good RE

practices are established to set up the premises for future studies.

This symposium covers various challenges and innovations of RE: 1) practical issues such as constituting or recovering appropriate propagule banks, their conservation, and the limits of available model organisms in relation to their life history traits, 2) analytical methodology (population and quantitative genetics) disentangling selective from stochastic evolutionary processes, and 3) case studies in various organisms illustrating the power of RE to demonstrate rapid evolution. We thus aim at providing insights into RE possibilities, but also inspiring actions for future RE studies.

Abstract submission deadline: 15. April 2022

Registration opens: February 2022

Early-bird registration closes: 15. June 2022

Abstract submission page: <https://www.eseb2022.cz/en/call-for-abstracts-page> Equal opportunities grant: <https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/> For any further questions, contact bojana.stojanova@osu.cz or pierre-olivier.cheptou@cefe.cnrs.fr

Sincerely,

Bojana Stojanova, Ostrava University, Czech Republic Pierre-Olivier Cheptou, CEFE-CNRS, Montpellier, France AneÅka EliÅová, Ostrava University, Czech Republic

Bojana S <bojana.stojanova@gmail.com>

Prague Predator Cognition Aug14-19

Dear colleagues,

Abstract submission deadline for the ESEB 2022 Congress has been extended until 22 April, so if you are considering attending the symposium “Predator cognition and the evolution of prey defence strategies” (S.16), there is a little more time for submitting your abstracts.

The meeting will be held in Prague, Czech Republic on 14-19 August 2022; see <https://www.eseb2022.cz> for further details.

Symposium description: Animals employ numerous strategies to avoid predation, and the evolution of camouflage, aposematism, mimicry and other forms of antipredator defence is at the core of research interest of evolutionary biologists. As shown by recent studies

focused on interactions between prey defences and predator cognitive mechanisms, understanding the selective forces driving the evolution of prey defence strategies requires studying their coevolution with predator perception, cognition, and subsequent behavioural responses. Furthermore, these studies have also highlighted the importance of studying predator cognition in ecologically relevant settings and testing behavioural responses in addition to investigating sensory capabilities. This approach has made it possible to address new questions, such as what factors influence predator decisions to attack potentially dangerous prey, how prey defences and predator cognitive mechanisms interact through the predation sequence, how predators respond to multicomponent and multimodal defences, and how predators use individual and social information about prey. This symposium aims to bring together current experimental, comparative and theoretical approaches to study interactions between predator cognitive mechanisms and prey defence strategies, identify the factors shaping predator behavioural responses, establish critical gaps in our understanding of the evolution of antipredator defences, and outline directions for future research.

Our keynote speakers are Johanna Mappes (University of Helsinki) and Tom Sherratt (Carleton University).

Abstracts can be submitted on: <https://www.eseb2022.cz/en/call-for-abstracts-page>. The call is open until the 22nd of April 2022.

Early-bird registration is open until the 15th of June 2022.

ESEB also proposes a conference attendance aid grant. For further details, see: <https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/>

If you have any questions or for further information please contact us.

All the best, Bibiana & Alice

Alice Exnerova Department of Zoology, Charles University, Prague, Czech Republic exnerova@natur.cuni.cz

Bibiana Rojas Department of Interdisciplinary Life Sciences, Konrad Lorenz Institute of Ethology, University of Veterinary Medicine, Vienna, Austria bibiana.rojas@vetmeduni.ac.at

“doc. Mgr. Alice Exnerová¹/₂, Ph.D.”
<alice.exnerova@natur.cuni.cz>

Prague PredatorCognition Aug14-19 AbstCallReminder

CALL FOR ABSTRACTS CLOSING 22 APRIL

Dear colleagues,

The call for abstracts for the ESEB 2022 Congress closes on 22 April, so if you are planning to attend the symposium “Predator cognition and the evolution of prey defence strategies” (S.16), please submit your abstract at your earliest convenience.

You can access the abstract submission portal by visiting <https://www.eseb2022.cz/en/call-for-abstracts-page>. The meeting will be held in Prague, Czech Republic on 14-19 August 2022; see <https://www.eseb2022.cz> for further details.

Early-bird registration is open until the 15th of June 2022.

Symposium description: Animals employ numerous strategies to avoid predation, and the evolution of camouflage, aposematism, mimicry and other forms of antipredator defence is at the core of research interest of evolutionary biologists. As shown by recent studies focused on interactions between prey defences and predator cognitive mechanisms, understanding the selective forces driving the evolution of prey defence strategies requires studying their coevolution with predator perception, cognition, and subsequent behavioural responses. Furthermore, these studies have also highlighted the importance of studying predator cognition in ecologically relevant settings and testing behavioural responses in addition to investigating sensory capabilities. This approach has made it possible to address new questions, such as what factors influence predator decisions to attack potentially dangerous prey, how prey defences and predator cognitive mechanisms interact through the predation sequence, how predators respond to multicomponent and multimodal defences, and how predators use individual and social information about prey. This symposium aims to bring together current experimental, comparative and theoretical approaches to study interactions between predator cognitive mechanisms and prey defence strategies, identify the factors shaping predator behavioural responses, establish critical gaps in our understanding of the evolution of antipredator defences, and outline directions for future research.

Our keynote speakers are Johanna Mappes (University

of Helsinki) and Tom Sherratt (Carleton University).

If you have any questions, please contact us.

All the best, Bibiana & Alice

Alice Exnerova Department of Zoology, Charles University, Prague, Czech Republic exnerova@natur.cuni.cz

Bibiana Rojas Department of Interdisciplinary Life Sciences, Konrad Lorenz Institute of Ethology, University of Veterinary Medicine, Vienna, Austria bibiana.rojas@vetmeduni.ac.at

“doc. Mgr. Alice Exnerová¹/₂, Ph.D.”
<alice.exnerova@natur.cuni.cz>

Prague Predator Cognition Prey Defences Aug 14-19

Dear colleagues,

Our ESEB 2022 symposium “Predator cognition and the evolution of prey defence strategies” (S.16) is now open for abstract submissions (see <https://www.eseb2022.cz> for further details) and registration.

The meeting will be held in Prague, Czech Republic on 14-19 August 2022.

Symposium description: Animals employ numerous strategies to avoid predation, and the evolution of camouflage, aposematism, mimicry and other forms of antipredator defence is at the core of research interest of evolutionary biologists. As shown by recent studies focused on interactions between prey defences and predator cognitive mechanisms, understanding the selective forces driving the evolution of prey defence strategies requires studying their coevolution with predator perception, cognition, and subsequent behavioural responses. Furthermore, these studies have also highlighted the importance of studying predator cognition in ecologically relevant settings and testing behavioural responses in addition to investigating sensory capabilities. This approach has made it possible to address new questions, such as what factors influence predator decisions to attack potentially dangerous prey, how prey defences and predator cognitive mechanisms interact through the predation sequence, how predators respond to multicomponent and multimodal defences, and how predators use individual and social information about prey. This symposium aims to bring together current experimental, comparative and theoretical approaches to study interac-

tions between predator cognitive mechanisms and prey defence strategies, identify the factors shaping predator behavioural responses, establish critical gaps in our understanding of the evolution of antipredator defences, and outline directions for future research.

Our keynote speakers are Johanna Mappes (University of Helsinki) and Tom Sherratt (Carleton University).

Abstracts can be submitted on: <https://www.eseb2022.cz/en/call-for-abstracts-page>. The call is open until the 15th of April 2022.

Early-bird registration is open until the 15th of June 2022.

ESEB also proposes a conference attendance aid grant. For further details, see: <https://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/>

Should you have any questions or for further information please contact us.

All the best, Bibiana & Alice

Alice Exnerova Department of Zoology, Charles University, Prague, Czech Republic exnerova@natur.cuni.cz

Bibiana Rojas Department of Interdisciplinary Life Sciences, Konrad Lorenz Institute of Ethology, University of Veterinary Medicine, Vienna, Austria bibiana.rojas@vetmeduni.ac.at

“doc. Mgr. Alice Exnerová¹/₂, Ph.D.”
<alice.exnerova@natur.cuni.cz>

Prague Repeated Evolution Aug

Olá jovens amigos,

please consider submitting an abstract to the *ESEB 2022 symposium: S09. Parallel and repeated evolution in adaptive radiation*; organized by me, Rosemary Gillespie and Michael D. Martin.

Invited talks Jae Young Choi - “Ancestral polymorphisms shape the adaptive radiation of *Metrosideros* across the Hawaiian Islands” Joana I. Meier - “The genomics of parallel adaptive radiations in cichlid fishes and Neotropical butterflies” Gabriel Jamie - “The persistence of polymorphisms across species radiations”

Symposium description The interplay between abiotic and biotic factors in shaping evolution is best understood when species evolve repeatedly under similar se-

lective regimes, providing evolutionary 'replicates' to understand the processes of adaptation and diversification. Adaptive radiation, in particular, can often provide a link between lineage diversification, ecology and the phenotype. Recent advances in sequencing technologies have allowed the understanding of the genetic basis underlying some adaptive radiations (e.g. a beak diversification locus in Darwin Finches) and have confirmed the role of hybridization and reshuffling of alleles into novel and favourable combinations that facilitate the repeated exploration of ecological space (e.g. extended evolutionary synthesis). In parallel, progress in ecological analysis, such as the determination of niche-occupation (e.g. hypervolumes) has the potential to clarify the role of ecology in driving repeated evolution and the evolvability of phenotypes. These advances, currently underway, still lack integration. To fill this gap, we propose a symposium focusing on integrating genomics, ecology, and phenotype, and specifically benefiting from repeated evolution in adaptive radiations. We will welcome contributions from diverse study systems, as well as multidisciplinary approaches including various sources of data (genetics, morphology, ecology, physiology).

To those submitting We encourage submissions from early-career researchers and underrepresented groups in science.

Direct link <https://www.eseb2022.cz/en/call-for-abstracts-page> *Deadline April 15th, 2022*

My best to you, José –

[jcerca.github.io](https://github.com/jcerca)

Twitter (@IslandGenomics) < <https://twitter.com/IslandGenomics> >

Postdoctoral researcher in Evolutionary Genomics & Bioinformatics

Norwegian University of Science and Technology

José Cerca <jose.cerca@gmail.com>

Prague HostPathCoevolutionImmunity Aug14-19

As part of the 2022 conference of the European Society for Evolutionary Biology (ESEB), we are organizing Symposium S38, entitled:

Molecular evolution and trade-offs in host-pathogen interactions and host immunity

The ESEB conference will be held August 14-19 in Prague

Deadline for abstract submission is April 15

Registration: <https://www.eseb2022.cz/en/call-for-abstracts-page> Symposium abstract:

Host-pathogen interactions are considered one of the major drivers for evolutionary change and maintenance of genetic diversity. Host immune systems constantly adapt to the rapidly evolving pathogens, utilising receptor variability and diverse and redundant effector mechanisms to recognise and fight the wide range of infecting agents. Thus, understanding the genotype-phenotype interactions ensuring resistance is challenging. Furthermore, it is becoming increasingly apparent that the evolutionary trajectories of these immune systems are not only shaped by parasites, but also constrained by various immunological and metabolic trade-offs or the need to differentiate self from non-self in order to prevent autoimmunity. Different life-history strategies of the host and fluctuating environmental conditions, including changes in parasite communities, might require different degrees of immune plasticity and immune investment strategies. This symposium aims to bring together theoretical concepts and empirical examples highlighting these factors that shape the evolution of an optimal immune response, considering immunogenetic, cellular, metabolic, and ecological perspectives. We also welcome examples of host-parasite interactions and research in disease ecology influencing the evolutionary trajectory of host immunity. Our aim is to attract a wide range of presentations that will allow discussion of the main current challenges in the evolutionary research of host immunity.

Invited speakers:

1) Prof. Andrea Graham (Princeton University): “The evolution of powerful yet perilous immune systems”

2) Prof. Sophie Armitage (Freie Universität Berlin): “Selecting for tolerance: Examining the consequences for host and pathogen”

3) Prof. Dana M. Hawley (Virginia Tech): “Integrative studies of host and pathogen evolution in a songbird: what immune systems can tell us about tolerance and virulence”

4) Prof. Lars Riber (Lund University): “The causes of pathogen-mediated balancing selection”

Organizers:

Ana Teles, Helena Westerdahl, Michal Vinkler, Robert Peñalva, Tobias Lenz

We would be happy to see you in Prague!

Prof. Dr. Tobias Lenz, Heisenberg-Professor Research Unit for Evolutionary Immunogenomics University of Hamburg Department of Biology Institute of Cell and Systems Biology of Animals Martin-Luther-King-Platz 3 20146 Hamburg, Germany

Email: tobias.lenz@uni-hamburg.de

<http://www.biologie.uni-hamburg.de/evolutionaryimmunogenomics> Tobias Lenz
<tobias.lenz@uni-hamburg.de>

Prague Posttranscriptional Regulation In Evolution Aug14-19

Dear colleagues,

The conference of the European Society for Evolutionary Biology (ESEB) will be held in Prague, Czech Republic 14-19th of August. We invite abstracts to our symposium S28:

Beyond transcription: the role of post-transcriptional gene regulation in adaptation and evolution

The selected presenters will be invited to contribute to a Special Issue with the journal *Heredity*, edited by the symposium organizers.

Abstract submission is open until April 15th <https://www.eseb2022.cz/en/call-for-abstracts-page> Symposium description: Gene expression regulation plays a central role in adaptive divergence and evolution, yet our understanding of adaptive post-transcriptional divergence is in its infancy. Recent studies have demonstrated the potentially important role of variation in alternative

transcript splicing and other post-transcriptional processes in adaptation and evolution in several systems. For example, multiple studies have shown the important role of splicing differences in encoding for discrete adaptive phenotypes; many others have demonstrated independent evolution in splicing and transcript abundance, providing alternative paths for selection to act upon. However, compared to transcription levels, many questions remain e.g., regarding the role of variation in transcript splicing under different eco-evolutionary contexts, the rate of splicing versus expression evolution, or the mechanisms through which splicing alters phenotypes. We argue that now is the time for a symposium on the role of post-transcriptional processes in adaptation and evolution to set the path for future research. The aim of this symposium is to synthesise our current level of understanding on the role of post-transcriptional variation in different eco-evolutionary contexts and diverse taxa, and highlight the role of novel analytical and technological approaches, such as long-read sequencing, in driving our understanding of post-transcriptional processing across the tree of life.

Keynote speakers: Dr. Alison Wright, University of Sheffield, UK Dr. Manuel Irimia, Centre for Genomic Regulation, Spain

We are committed to equal and diverse representation of groups among the selected presentations/posters.

For any questions do not hesitate to contact us. We are looking forward to your contributions!

Symposium organizers, Jukka-Pekka Verta (University of Helsinki) & Arne Jacobs (University of Glasgow)

Jukka-Pekka Verta, Ph.D. Evolution, Conservation and Genomics research group University of Helsinki, Finland <https://researchportal.helsinki.fi/en/persons/jukka-pekka-verta> “Verta, Jukka-Pekka” <jukka-pekka.verta@helsinki.fi>

Yosemite Natl Park Symbiosis May13-15 Deadline Ext

EARLY BIRD REGISTRATION EXTENDED TO APRIL 15 (THIS FRIDAY!) No limits on number of individuals per lab

Dear Colleagues,

After a two-year absence, The TENTH annual Yosemite Symbiosis Workshop will take place on May 13th-15th,

2022 at the Sierra Nevada Research Institute, Yosemite National Park. We have really missed having this meeting over the last two years. In the previous nine years, this meeting became a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2022!

Keynote speaker 2022: Michelle Nishiguchi, UC Merced
COVID19 Safety:

Attendees will be required to attest to full vaccination status against SARS-CoV2 during the registration process.

Rapid antigen tests will be made upon arrival at the conference (provided by us) to provide an extra layer of safety for attendees

The meeting will occur indoors, and masks will be required during meeting sessions when the opportunity for social distancing will be limited.

Meals, and coffee/snack breaks will be provided outside weather permitting. Temperatures in mid-May are usually mild, but there is always some chance that it will be cold and or rainy during the meeting.

Information about our meeting:

Why attend?

Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our 10th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who will be there?

The meeting is small by design (~50 participants) and we seek to focus on scientists interested in cooperation, mutualism, and symbiosis. In the past we have covered a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems.

We have removed restrictions on the number of individuals per lab.

When is the meeting?

The talks and formal meeting will be held May 14th and 15th, 2022, though we make accommodation arrangements available for attendees to arrive on Friday the 13th to provide opportunities to enjoy the park. There will be a welcome party on the evening of arrival, Friday May 13th. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting. Abstract and early bird registration will be due on APRIL 15 2022.

Where is the meeting?

This is the best part! The meeting takes place at the Sierra Nevada Research Station, in Wawona California, within the border of Yosemite National Park!

What will it cost?

Advanced Registration (deadline April 15th, 2022) Students: \$230, Postdocs \$250, PIs \$300 Late registration (deadline April 19th, 2022) Students: \$260, Postdocs \$280, PIs \$330

Registration AND payment page is here: <https://snri.ucmerced.edu/form/symbiosis-workshop-2022>

Please make sure to REGISTER first then PAY

Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

Joel L. Sachs (he, him, his) *Professor, *Department of Evolution Ecology & Organismal Biology University of California, Riverside Zoom: <http://ucr.zoom.us/my/Sachsevolution> Office (951) 827-6357 / Fax (951) 827-4286 / <http://www.sachslab.com> *Post address*: Sachs Lab - UC Riverside 3401 Watkins Dr., 1229 Spieth Hall, Riverside, CA 92521

Joel Sachs <joels@ucr.edu>

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AarhusU EvolutionSpermatogenesis

PhD position: Evolution of spermatogenesis across primates and its consequences for fertility and speciation

A PhD position is open (application deadline May 1, 2022) in the group of Mikkel H. Schierup at the Bioinformatics Research Centre, Aarhus University, with a start date between August and December 2022. The project will employ large scale single cell transcriptomics from testis samples of more than ten different primate species to infer evolutionary processes and their consequences for sperm quality (fertility) and the creation of reproductive barriers between emergent species. The hypothesis of genetic conflicts between the sex chromosomes for transmission to the mature sperm cell will be investigated. According to the interest of the candidate, the PhD can be purely computational/method development or be a mixture of computational and experimental work. For a more detailed description and application, please visit

<https://phd.nat.au.dk/for-applicants/open-calls/february-2022-1/single-cell-analysis-of-spermatogenesis-in-primates-drivers-of-reduced-male-fertility-and-speciation> . Interested candidates are encouraged to contact Mikkel Heide Schierup (mheide@birc.au.dk) for further information.

Get your graduate degree at a top 100 university

The Graduate School of Natural Sciences at Aarhus University is looking for a number of bright, enthusiastic and ambitious candidates who are interested in pursuing a PhD education. The University is located in Aarhus, Denmark, which provides international students with a safe and stable environment, a high standard of living and a wealth of social opportunities. Besides having an excellent reputation that enables our PhD graduates to find outstanding employment prospects, Aarhus University offers attractive working conditions, research support and campus resources. Read more about all the benefits here. Applications are accepted from college students and graduates with an academic record corresponding to a Bachelor's or Master's degree.

Application deadline is 1 May 2022 at midnight (23:59 CEST), with a starting date of 1 August 2022 or later.

Mikkel Heide Schierup Novo Nordisk Distinguished Investigator Bioinformatics Research Centre, Aarhus University, CF Mollers Alle Building 1110, 8000 Aarhus C Denmark Ph: +4527782889 Email:mheide@birc.au.dk <http://www.birc.au.dk/~mheide> Mikkel Heide Schierup <mheide@birc.au.dk>

AarhusU HaploidSexSpecificSelection

Applications are invited for a PhD fellowship/scholarship at Graduate School of Natural Sciences, Aarhus University, Denmark, within the Computer Science programme. The position is available from August 2022 or later.

Title: Haploid and sex-specific selection: modelling and detection in deep mutational scanning of sperm samples and trios

Research area and project description: Background: Traditionally, population genetics models focus on selection in the diploid phase. However, there is also in principle ample potential for selection to occur during the haploid phase both in female and male gametes. In principle, haploid selection can be very effective relative to diploid where dominance often occurs and blurs the effect of positive or negative selection. A few documented cases in animal plants and fungi attest to the potential importance of haploid selection and theory demonstrates that haploid selection is a neglected mechanism that can potentially affect rates of adaptation, the magnitude and purging of inbreeding depression and the load of deleterious mutations detected in genomes or even provide a plausible explanation for sex differences in recombination rates (a ubiquitous find that remains poorly understood). However, empirically detecting haploid selection is challenging.

Project: This project is a unique opportunity to do that: we will generate deep mutational scanning datasets that can also be leveraged to examine in detail how haploid selection can affect both new variants but also pre-existing variants (SNPs where the father is heterozygous). The project is funded by the Novo Nordisk foundation as an interdisciplinary Data Science collaborative project between the Department of Growth and Reproduction at Copenhagen University Hospital (Kristian Almstrup), and Aarhus University with the department of Mathematics (Asger Hobolth), the department of Molecular Medicine (Søren Besenbacher & Lasse Marrety) and the Bioinformatics Research Centre (Mikkel Heide Schierup & Thomas Bataillon).

The candidate will work on developing new evolutionary methods to analyze data from testes and sperm samples as well as pre-existing trio data. The relative weight of

theoretical modeling, methods development and data analysis will depend on the interests of the candidate.

Candidates interested in further information should please contact Thomas Bataillon (tbata@birc.au.dk).

For technical reasons, you must upload a project description. When - as here - you apply for a specific project, please simply copy the project description above, and upload it as a PDF in the application. If you wish to, you can indicate an URL where further information can be found. Please note that we reserve the right to remove scientific papers, large reports, theses, and the like.

Qualifications and specific competences: Applicants must have at least one year of a Master's degree in molecular biology, mathematics, statistics, bioinformatics or similar and have an interest in addressing biological problems with large scale data analyses. An interest in evolutionary biology and/or population genetics will be an advantage. The PhD study can be three years (with an MSc) or four years (with one year of an MSc completed at the time of enrollment)

Place of employment and place of work: The place of employment is Aarhus University, and the place of work is Bioinformatics Research Center, Aarhus University, Universitetsbyen 81, DK-8000 Aarhus C., Denmark.

Contacts: Applicants seeking further information for this project are invited to contact: Associate Professor Thomas Bataillon, e-mail: tbata@birc.au.dk Professor Mikkel Schierup, e-mail: mheide@birc.au.dk

How to apply: For information about application requirements and mandatory attachments, please see the Application guide < <https://phd.nat.au.dk/for-applicants/application-guide/> >. Please read the Application guide thoroughly before applying and note the GSNS language skills requirement.

When ready to apply, go to <https://phd.nat.au.dk/for-applicants/apply-here/> (Note, the online application system opens 1 March 2022)

1. Choose May 2022 Call with deadline 1 May 2022 at 23:59 CEST. 2. You will be directed to the call and must choose the programme "Computer Science". 3. When filling in information about the project, please choose: "Haploid and sex-specific selection: modelling and detection in deep mutational scanning of sperm samples and trios (Hssmdd)" in the dropdown menu in the box named "Study".

Please note:

* The programme committee may request further information or invite the applicant to attend an interview. * The project will only be initiated if final funding (from

the graduate school/the faculty) is secured.

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27 840 andreas.altenburger@uit.no The Arctic University Museum of Norway UiT The Arctic University of Norway

Andreas Altenburger <andreas.altenburger@uit.no>

ArcticU Norway Marine sedaDNA

PhD Fellowship in Marine sedaDNA of Northern Ecosystems

A PhD position is available at the Arctic University Museum of Norway, UiT - the Arctic University of Norway. The appointed PhD Fellow will be part of the newly established Norwegian Centre for Arctic Ecosystem Genomics (ArcEcoGen) and will be part of the coastal working group.

The position will focus on increasing our understanding of long-term changes in marine northern ecosystems, especially within coastal environments. The aim is to reconstruct whole ecosystem dynamics through time by extracting sedimentary ancient DNA (sedaDNA) from Arctic marine sediment cores.

Goals of the positions are

- * Quantify the sensitivity of the sedaDNA method for marine sediments.
- * Reconstruct past eukaryotic communities from sediment cores.
- * Compare the past with modern eukaryotic communities.
- * Establish new reference sequences for hitherto undescribed/unsequenced species.

The modern-day data produced in this study will serve as a reference point for the assessment of human impact in coastal ecosystems in the future. Data will be explored to include trait analyses and other proxies, which will increase our understanding of different environmental drivers on ecosystem development and changes.

More information and application through jobbnorge: PhD Fellowship in Marine sedaDNA of Northern Ecosystems (222583) | UiT The Arctic University of Norway (jobbnorge.no) <<https://www.jobbnorge.no/en/available-jobs/job/222583/phd-fellowship-in-marine-sedadna-of-northern-ecosystems>>

Andreas Altenburger Associate Professor, curator of marine invertebrates P: +47 77 64 49 02| M: +47 461

AuburnU EvolutionPlantParasites

I'm looking for a PhD or MS student to join my lab at Auburn University and work on the evolution of plant pests and pathogens. Our goal is to increase the sustainability of agriculture by advancing our understanding of the evolution of two important traits: resistance to pesticides, and virulence (that is, just how harmful a parasite or pathogen is to its host). This is a cross-disciplinary project and students will have opportunities to participate in evolutionary modeling, data science, and experimental research with bacterial pathogens, their insect vectors, and some of their host plants.

The position starts in August 2022, that is, the start of the fall semester. It comes with a competitive twelve-month stipend, health insurance, and a tuition waiver. Candidates who would add to the ethnic, gender, and socioeconomic diversity of the academy are strongly urged to apply. If you're interested, please send me an email with your CV and any questions you might have about the position before the end of April.

Cheers! Nate B Hardy

Associate Professor Department of Entomology and Plant Pathology Auburn University Email: n8@auburn.edu Website: <http://hardylab.skullisland.info> Hardy Lab | Making sense of insect diversity <<http://hardylab.skullisland.info/>> Our best guess is that about one third of all multicellular species are insects that eat plants. It's only a guess because most species are undocumented. hardylab.skullisland.info

Nathaniel Hardy <nbh0006@auburn.edu>

Australian NatIU Conservation Genomics

This project will suit a student with an interest in conservation genetics, molecular biology and bioinformatics

The Lord Howe Island stick insect, thought to be extinct but recently rediscovered, has become emblematic of the dangers faced by island species in the face of anthropogenic change. A planned reintroduction effort aims to rescue this species, one of the rarest insects in the world, from the brink of extinction. Our aim is to explore the unique genome biology of this insect, and use it as a model for adaptation to captivity and to the post-release environment. Our project was just funded for three years, and will build on the recent development of numerous genomic resources, such as a high-quality genome assembly. The project will combine cutting-edge molecular techniques and innovative approaches to genotyping of unusual material (historical and non-destructively sampled in the field) with analysis of next-generation sequencing data. This project will blend fundamental science investigating genome evolution with research outcomes that will directly contribute to ongoing conservation efforts. Thus, skills obtained during this degree will be relevant to academia, as well as the conservation sector, including government and NGOs.

Suitable applicants need to be highly motivated with a strong academic and research background. Demonstrated ability to conduct independent research is required, with experience in the molecular lab, and some experience in programming or data analysis being desirable. Applicants should hold first class honours or equivalent experience. The successful student will need to apply to ANU for enrollment, for international applicants ideally by this year's April 15 deadline. The successful applicant will receive a stipend scholarship and research funds, including computer and travel funding.

Location: We will be based in the Division of Ecology and Evolution at the Research School of Biology at the Australian National University in Canberra, Australia. The project will also be supported by Zoos Victoria, who hold a large captive population of the LHI stick insects at Melbourne Zoo, and are closely involved with the recovery effort on Lord Howe Island. Field work to collect additional samples is likely to be involved.

Expression of interest: Expressions of interest should be submitted directly to Alexander.Mikheyev@anu.edu.au. International applicants should contact me by April 5, 2022, though the earlier the better so that we can coordinate the ANU application due on the 15th. Please include a brief statement on why you are interested in this project, a CV and contact details for references. Following assessment of applications one applicant will then be invited to formally apply to the ANU. The successful applicant will be able to start as soon as possible. You can also find out more information about the graduate program by clicking on the "Higher Degree by Research" tab at <http://biology.anu.edu.au/education/-degree-programs> alexander.mikheyev@anu.edu.au

Estonian U LifeSci eDNA Crayfish Pathogens

Estonian_Uni_Life_Sci.Crayfish_Pathogens.eDNA

PhD student position in freshwater crayfish pathogens

We are seeking a highly motivated student holding a Master's degree in Biosciences, Genetics, Environment, or a similar field for a four-year fully-funded PhD to study freshwater crayfish and their pathogens using environmental DNA (eDNA) and other molecular methods.

The research will be carried out at the Estonian University of Life Sciences (Institute of Veterinary Medicine and Animal Sciences, Chair of Aquaculture) on the topic of "Detection of crayfish pathogens and distribution of invasive alien crayfish species in Estonia using modern molecular methods". The successful applicant will join a collaborative project under the supervision of Dr Katrin Kaldre, Dr Lilian Pukk and Dr Jane Oja. The Chair of Aquaculture has a multinational team of postdocs, PhD and master students and technicians, and the applicant will have the opportunity to work extensively with other team members.

The PhD student will participate in the following research tasks: 1) Applying eDNA methodology for the detection of non-native invasive crayfish species (NICS) and the causative agent of crayfish plague *A. astaci* in Estonia; 2) Mapping the distribution of NICS and pathogen *A. astaci* in Estonian waterbodies using eDNA methodology; 3) Mapping the spread of burn spot disease and its causative agents from diverse species, both in Estonian natural waterbodies and in crayfish farms, using eDNA metabarcoding; 4) Developing and imple-

menting a procedure to detect DNA from pathogen(s) from tissue or water samples by using species-specific qPCR assay.

Requirements: - The PhD candidate should be highly motivated, intellectually curious and sociable; - Should have at least basic experience working in a molecular laboratory, as well as some basic bioinformatics skills; - Willing to participate in fieldwork; - Ability to work both independently and in a team; - Must be fluent in English (written and spoken).

Following are an advantage: - Experience with physiology experiments; - Experience with pathogens or crayfish; - Willingness to present project results at international conferences and be a co-author in research publications.

How to apply:

Applications should be sent to katrin.kaldre@emu.ee and include a motivation letter (less than 1 page with academic background, research experience, interests, and goals) and a CV and contact details of two references and a copy of your master's degree certificate.

Submission deadline is June 1, 2022.

Starting date: September 2022.

Salary/Scholarship: According to local agreement for PhD students (approximately 1400 EUR/month).

If you have questions, contact Katrin Kaldre (katrin.kaldre@emu.ee).

Katrin Kaldre <katrin.kaldre@emu.ee>

ETH Zurich Evolutionary Ecosystem Ecology

PhD position in evolutionary ecology of aquatic ecosystems

The open PhD position is based at Eawag, the Swiss Federal Institute of Aquatic Science and Technology, in the Department of Fish Ecology & Evolution, in Kastanienbaum.

The position is based in the group of Dr Blake Matthews and is part of a 4-year funded SNF project, entitled: "The eco-evolutionary effects of predators in aquatic ecosystems". The Matthews group focuses on the ecological dynamics of natural selection, and the reciprocal interactions among ecological, ecosystem, and evolutionary dynamics. The successful applicant will be a

doctoral student at ETH Zurich, and be co-supervised by Prof. Dr Jukka Jokela in the department of Environmental Systems Science. The funded project is in collaboration with the groups of Dr Philine Feulner (Eawag) and Dr Ryan Greenway (University of Konstanz).

The PhD project will involve extensive field work in Southern Greenland, in order to explore how stickleback affect the species composition and trait variation of macroinvertebrate communities and life history evolution of zooplankton, and how stickleback evolve in response to both predation and prey community dynamics.

Ideally, the candidate has a background in evolutionary ecology, some experience with field work in aquatic settings, and an interest in learning about aquatic invertebrate taxonomy (primarily benthic communities) and life-history evolution of zooplankton. The group's working language is English and fluency in writing and speaking is required. Knowledge of German or French is not required.

The position is situated in the Department of Fish Ecology & Evolution: The Department is part of Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB), which is located on the shore of Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science. The PhD student will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science. More information about the current research group and ongoing projects can be found at www.blakematthewslab.com. Eawag offers an excellent working environment where staff can contribute their strengths, experience and ways of thinking. We promote gender equality and are committed to staff diversity and inclusion. The compatibility of career and family is of central importance to us. For more information about Eawag and our work conditions please consult www.eawag.ch and www.eawag.ch/en/aboutus/working/employment. We strongly encourage applications from researchers identifying as a member of a historically marginalised group.

Applications should include a cover letter with a concise statement about your previous education and research experience, your vision for the future and in particular your motivation to work on this project (1 page maximum), a curriculum vitae including (if applicable) any publications or a copy of a MSc thesis, copies of your academic qualifications, and names and contact information of 2-3 academic references (please do not include letters with the application).

Any questions about the position can be directed to blake.matthews@eawag.ch

Screening of applicants will begin immediately, and the closing date is 30 April 2022.

We look forward to receiving your application. Please send it via this link: <https://apply.refine.ch/673277/-0929/pub/1/index.html> any other way of applying will not be considered. The link can also be found here: <https://www.blakematthewslab.com/news> Blake.Matthews@eawag.ch

INRAE BordeauxU OakPangenomicAdaptation

We are looking for a highly motivated student for a PhD position within the project “Pan-genome evolutionary dynamics and role of structural variants in local adaptation within the European white oak species complex”.

PhD STUDENT POSITION - Pangenomic and role of structural variants in oak adaptation - Based at UMR Biogeco INRAE - University of Bordeaux - Subject area: Population genetics and genomics - Application deadline: 20 May 2022.

PROJECT DESCRIPTION This PhD project will focus in understanding the evolutionary dynamics of genomes in perennial species and construct a pan-genome to investigate the role of structural variants (SVs) in key adaptive traits such as drought resistance and bud burst. The PhD candidate will be in charge of the bioinformatics, comparative and population genomics analyses of the data already available at UMR Biogeco for the white oak species (high quality genome assemblies, long and short read sequencing, pool-seq...). More information at <https://www.adum.fr/as/ed/propositionFD.pl?site=ed.se> (see below for more instructions).

PROFILE We expect candidate profiles with skills in evolutionary ecology/population genomics and strong will to deepen his/her bioinformatics skills or alternatively candidates with skills in bioinformatics/computing science and strong interest in evolutionary processes. The work involves mostly computer work and programming with opportunities for field work.

SUPERVISION The PhD student will be supervised by Dr. Ludovic Duvaux and Dr. Christophe Plomion (INRAE - Biogeco) and will be registered at the “Sciences et environnements” Doctoral School (<https://ed-environnements.u-bordeaux.fr/en>) of the University of

Bordeaux.

Contacts: - Ludovic Duvaux: ludovic.duvaux@inrae.fr - Christophe Plomion: christophe.plomion@inrae.fr

HOW TO APPLY Interested applicants should contact the supervisors to get more details (ludovic.duvaux@inrae.fr and christophe.plomion@inrae.fr) then apply by May 20, 2022.

- Go to <https://www.adum.fr/as/ed-propositionFD.pl?site=ed.se> - click the tab “Spécialité de biologie évolutive, fonctionnelle et des communautés” - click the link “Dynamique évolutive du pan-génome et rôle des variants structuraux dans l’adaptation locale au sein du complexe d’espèces des chênes blancs européens” - click the button “candidater” - choose the language on the top left “EN” or “FR” - then Create an account if needed

COLLABORATIONS AND NETWORKING The PhD student will be able to interact with our network of collaborators. Locally, strong interactions already exist with Veronique Decroq & Quynh-Trang Bui (BFP, INRAE Bordeaux). They work on the genomic bases of adaptation and domestication in apricot trees and share the same interest in SV and tree pan-genome dynamics. Thus, a long term collaboration is ongoing. The candidate will also collaborate with national experts in genome assemblies and annotations (Jean-Marc Aury from Genoscope, William Marande from CNRGV, INRAE URGI staff members), structural variation analyses (Olivier Panaud, from Perpignan University), comparative genomics and population genetics (within the BIOGECO and BFP).

FULL SUMMARY WITH OBJECTIVES: Structural variation (SV) - i.e. pieces of DNA being deleted, inserted, or rearranged among chromosomes - strongly influences gene content and genome structure within and between closely related species. SV may have strong impacts on phenotypes of ecological and agronomical interest but are poorly captured when genotypes are produced in comparison to one single reference genome. Consequently, the evolutionary dynamics of SV in natural populations (mutation rate, role of selection in shaping genetic variation) and their role in local adaptation remain poorly documented compared to that of single nucleotide polymorphisms (SNPs), especially in forest tree species. Hence, in order to capture variation of SV and its impact on phenotypic variation, comparative and evolutionary genomics areas are now turning to pan-genome based analyses of genetic variation. White Oaks are species of ecological, economic and cultural importance in Europe, accounting for a third of the metropolitan French forests (i.e. 5M ha). These popu-

lations display signs of stress or even decline related to biotic and abiotic stresses and their adaptive potential in the context of climate changes is uncertain. The genome of the pedunculate oak was sequenced recently, providing the blueprints to

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JenaU Two Evolutionary Ecology

PhD student position (m/f/d) in Evolutionary Ecology of Color Polymorphisms in Grasshoppers

We offer a part-time position (65%, 26 hours per week), limited until 31 December 2025 (more than 3 years) and starting as soon as possible. Evaluation of applications will start on 21 May 2022 and will end when the position is filled. The position will be hosted by the Population Ecology Group at Jena University (Germany).

The project deals with the ecological and evolutionary consequences of a widespread color polymorphism in grasshoppers. Practical work includes behavioral experiments in the field and in the laboratory. The aim is to understand the individual behavioral strategies and the reasons for the maintenance of the color polymorphism. The project is supervised in the Population Ecology group, which provides a strong environment for evolutionary ecological work and has proven experience on work on grasshoppers. The project is embedded within the DFG-funded Collaborative Research Center (CRC) “A New Synthesis on Individualization: Niche Choice, Niche Conformity, Niche Construction”.

Your responsibilities: - You work on individual behavioral strategies in grasshoppers - You plan, perform and analyze behavioral experiments in the field and in the laboratory - You collaborate with other research groups of the Collaborative Research Centre - You write scientific publications for international peer-reviewed journals - You work on your own scientific qualification project (PhD)

Your profile: - Completed Master’s degree preferably with a biological focus - Very good knowledge of written and spoken English - Experience with field and/or behavioral ecology work and ability to

organize yourself - Knowledge of at least one statistical program (ideally R) - Proven experience in scientific writing

We offer: - Remuneration based on the provisions of the Collective Agreement for the Public Sector of the Federal States (TV-L) at salary scale E13 depending on the candidate’s personal qualifications, including a special annual payment in accordance with the collective agreement. - You will work in a DFG-funded Collaborative Research Center (SFB-TRR 212) - Independent work with intensive scientific supervision - Participation in diverse conceptual and quantitative research with an interdisciplinary character - Interesting and varied tasks on an international level and participation in international conferences - A Graduate Academy for doctoral candidates and postdocs; - A family-friendly working environment with a variety of offers for families: University Family Office ‘JUniFamilie’ and flexible childcare (‘JUniKinder’);

Candidates with severe disabilities will be given preference in the case of equal qualifications and suitability.

Are you eager to work for us? Then submit your detailed written application, preferably by email (as a single PDF file), stating the vacancy ID 122/2022 by 21 May 2022 to: Prof. Dr. Holger Schielzeth, Friedrich Schiller University Jena, Institut of Ecology and Evolution, Dornburger Str. 159, 07743 Jena, E-Mail: pop ecol@uni-jena.de

PhD student position (m/f/d) in Evidence Synthesis on the Evolutionary Ecology of Individualized Niches

We offer a part-time position (65%, 26 hours per week), limited until 31 December 2025 (more than 3 years) and starting as soon as possible. Evaluation of applications will start on 21 May 2022 and will end when the position is filled. The position will be hosted by the Population Ecology Group at Jena University (Germany).

The project deals with systematic meta-analyses on individual niche specialization within the DFG-funded Collaborative Research Center (CRC) “A New Synthesis on Individualization: Niche Choice, Niche Conformity, Niche Construction”. The project has a synthesis character within the CRC and is simultaneously quantitative and conceptual. It promotes a conceptual overview while strengthening quantitative understanding of individualized ecological niches. The project offers the opportunity to develop a unique scientific profile that is of high demand in within and outside academia. The work will be supervised in the Population Ecology Group Jena, which deals with evolutionary ecology issues and has proven experience with meta-analyses.

Your responsibilities: - ——— You work on individual niche specialization in the light of systematic literature analyses - ——— You perform comprehensive reviews of the published literature on selected topics - ——— You implement advanced statistical analyses - ——— You collaborate with other research groups of the Collaborative

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KU Leuven InsectSocietyEvolution

Graduate Position

KULeuven.CastePlasticityInSocialInsects

PhD position: The evolution of caste plasticity and caste dimorphism in insect societies

We invite applications for a 3-year fully funded PhD position on the evolution sociality in insects (FWO-FAPESP project) Specifically, the project will study the occurrence of social insect caste plasticity in function of reproductive role and the origin of queen-worker caste dimorphism across a range of primitively and advanced eusocial temperate and Neotropical ants, bees and wasps. Comparative genomics techniques, light sheet fluorescence microscopy (LSFM) brain imaging and behavioural experiments will be used to study shifting patterns in the evolution of behavioural plasticity in eusocial insects, including possible tissue trade-offs and changes in the modularity in brain gene expression patterns. In addition, we will investigate how the origin of queen-worker caste dimorphism was built on pre-existing gene regulatory networks in primitively eusocial ancestors. We are looking for a highly motivated candidate with an MSc degree (or equivalent) in Biology or a related field. The successful applicant should have a background in behavioural ecology or evolutionary biology, should be able to carry out both lab and field work, and should have a keen interest to learn techniques required for the execution of this project, including both brain imaging techniques & comparative genomics analyses. Prior experience in working with social insects and statistics are advantageous. The project forms part of a collaboration with Prof. Nascimento (USP-Ribeirão Preto, Brazil) and Prof. Oliveira (UAB

Barcelona Spain). This implies that while much of the work will be carried out in Leuven, there will be the opportunity to also carry out field trips to Brazil and Spain. We are a multidisciplinary lab (<https://bio.kuleuven.be/eeb/tw/>) working on questions related to social evolution and use social insects as our principal model system. The working language of the lab is English. KU Leuven is among one of the most prestigious universities in the world (48th in the ranking of THE 2019) and offers good employment conditions (<https://www.kuleuven.be/personeel/jobsite/en>). Leuven is a historic university city with a vibrant student life. Leuven is a 15-minute train ride away from Brussels International Airport and a 20-minutes train ride from Brussels itself (<https://www.kuleuven.be/english/living>).

If you are interested, please send an application as a single pdf file containing your CV, a 1-page motivation letter, your previous research activities, BSc and MSc grades, publications (if available), and the names and email addresses of two potential referees. Applications should be sent to the promoter Prof. Tom Wenseleers (tom.wenseleers@kuleuven.be), and co-promoter Dr. Cintia Akemi Oi (cintiaakemi.oi@kuleuven.be) with the subject [PhD application_NAME]. Application deadline & starting date: flexible, the position will remain open until filled. Do not hesitate to contact us if you would have any further questions.

Prof. Tom Wenseleers & Dr. Cintia Akemi Oi Laboratory of Socioecology and Social Evolution Dept. of Biology, KU Leuven, Naamsestraat 59, 3000 Leuven, Belgium <https://bio.kuleuven.be/eeb/tw/> Cintia Akemi Oi <cintiaakemi.oi@kuleuven.be>

Mainz Germany HistoricalPopGenetics

PhD student position open in Computational method development in historical population genetics

We offer a part-time position (65%), for 3 years and starting as soon as possible. Evaluation of applications will start on 15th June 2022 and will end when the position is filled. The position will be hosted by the Palaeogenetics Group at the Johannes Gutenberg University of Mainz, Germany (<https://palaeogenetics-mainz.de>).

The project aims to develop methods to reconstruct kinship relationships within historical cemetery popula-

tions. The approaches developed will then be applied to genome data of early medieval skeletal populations. Therefore, the PhD will be involved in the development of methods in the fields of statistical genomics, bioinformatics, mathematical genetics, populations genetics, and Palaeogenetics. The project is supervised in the Palaeogenetics group one of the international leading groups in the field of Ancient DNA Research. The project is DFG funded and in Cooperation with the University of Tübingen, Germany.

Your profile

Completed Master's degree (or Diploma), preferably within the field of biology, genomics, statistics, bioinformatics or mathematics Very good knowledge of written and spoken English knowledge in bioinformatics, evolution, and statistics As the PhD project is interdisciplinary it requires historical- archaeological interest as well as a scientific will to develop new methods for computer

We offer:

The candidate will become part of a team of internationally leading computer scientists, anthropologists and archaeologists/historians. Independent work with intensive scientific supervision Participation in diverse conceptual and quantitative research with an interdisciplinary character Interesting and varied tasks on an international level and participation in international conferences Remuneration based on the provisions of the Collective Agreement for the Public Sector of the Federal States (TV-L) at salary scale E13 depending on the candidate's personal qualifications, including a special annual payment in accordance with the collective agreement

Candidates with severe disabilities will be given preference in the case of equal qualifications and suitability. We aim to increase women in the field of research and teaching and therefore encourage female researchers to apply.

Are you eager to work with us? Then submit your detailed written application, preferably by email (as a single PDF file) to: Joachim Burger, Palaeogenetics group, Johannes Gutenberg Universität Mainz, Anselm-Franz-von-Bentzel-Weg 7, D-55128 Mainz, Germany, Email: anthro2@uni-mainz.de

"Després, Dr. Viviane" <despres@uni-mainz.de>

MasseyU Cricket Evolution

An ecologically friendly solution is required to manage an endemic cricket (*Hemidrus*) in New Zealand vineyards. A lack of knowledge of ground cricket (*Hemidrus*) ecology is currently hindering the development of successful, sustainable management tools. Using a range of ecological methods, the factors that determine the spatial and temporal distribution and abundance of this insect species will be investigated. This project will combine field work to estimate population densities and life history traits with studies of diet and olfactory responses to plant volatiles, in native and modified habitats.

This project is part of a collaboration between scientists at Massey University and The New Zealand Institute for Plant & Food Research Limited, with support from the New Zealand Wine Futures Fund and New Zealand wineries. A Wildlife & Ecology programme in the School of Natural Sciences (Massey University) is investigating the diversity of Orthoptera in New Zealand and seeking to understand their biotic and abiotic interactions within the ecosystems of Aotearoa. This involves an array of approaches including geometric morphometrics, ecological niche modelling, behavioural and population biology, genetics and chemical ecology.

The scholarship: A tax-free living allowance stipend of NZ\$30,000 per annum for 3 years, tuition fees to be confirmed.

Location: The successful applicant will join the School of Natural Sciences on the Manawatu campus of Massey University (Palmerston North, NZ), and will undertake field work based near vineyards in South Island, New Zealand in cooperation with Plant & Food Research staff. Massey University is a smoke-free work environment.

Research Group: Te Taha Tawhiti resides within the Wildlife & Ecology Group in the School of Natural Sciences. Lead researchers are Mary Morgan-Richards and Steve Trewick. Who we're looking for: You'll need a good first degree from an internationally recognised university (minimum upper second class Hons) or a Master's degree in an appropriate subject. You should have a background in Ecology/Biology/Evolution/Entomology, good statistics skills (preferably R) and an interest in insect-plant interactions. A good understanding of experimental design and ability to work outdoors, independently and as a part of a research team are welcomed, and prefer-

ablypast experience in conducting fieldwork. English language proficiency and excellent communication skills are required. You will be part of a vibrant research group at Massey University where you will contribute to regular lab meetings, and also to departmental seminars.

How to Apply: Expressions of interest should be submitted, along with a CV, to Prof Mary Morgan-Richards.

Kind regards

Steve

Prof. Steve Trewick Wildlife & Ecology Group - Evolutionary Ecology and Genetics Massey University, Private Bag 11-222, Palmerston North, New Zealand 4410 evolves.massey.ac.nz Tel: DD. 06 951 7842

Read our colourful book on evolutionary ecology in New Zealand

<https://sites.massey.ac.nz/wildlifenz/> fishpond

Steve Trewick <S.Trewick@massey.ac.nz>

MaxPlanckInst AncestralRecombGraphs

The Transmission, Infection, Diversification & Evolution Group (tide) is a Max Planck Independent Research Group at the Max Planck Institute for the Science of Human History.

We are looking for a Master student to work on the development of an R package for the manipulation and visualization of ancestral recombination graphs. Ancestral recombination graphs are used to represent the evolution of organisms in the presence of recombination or horizontal gene transfer. The package will likely extend the existing ggtree package for the visualisation of phylogenetic trees.

This work will benefit ongoing projects in our group and could result in a scientific publication. Candidates should have proficient skills in R programming. Previous experience or knowledge of phylogenetics would be appreciated but is not mandatory.

Interested parties are invited to contact Dr. Arthur Kocher at kocher@shh.mpg.de

Kind regards,

Dr. Dorit Wammetsberger Recruitment Manager

Max-Planck-Institut für Menschheitsgeschichte/ Max Planck Institute for the Science of Human History

Kahlaische Str. 10 07745 Jena, Germany

Fon: +49 3641 686936 wammetsberger@shh.mpg.de

“Wammetsberger, Dorit”
<wammetsberger@shh.mpg.de> “Wammetsberger, Dorit” <wammetsberger@shh.mpg.de>

MaxPlanckInst Jena HostDiseaseBehaviour

Parasitism and social behaviour in ants

We invite applications for a fully funded PhD position to work on the behavioural and chemical ecology of nematode infections in ants with the groups of Yuko Ulrich (ulrichlab.com) and Markus Knaden (ice.iwww.mpg.de/-228656/odor-guided-behavior) at the Max Planck Institute for Chemical Ecology in Jena, Germany.

Background: Parasites can affect virtually any aspect of host biology, including behavior. Effects range from manipulations of host behavior that increase parasite transmission to changes in host social behaviour (e.g., social distancing) that reduce transmission. Social insects and their parasites include some of the best-known examples of behavioral effects at both ends of this spectrum (1, 2), but the mechanisms driving these changes are rarely known.

Nematodes of the genus *Diploscapter* infect the postpharyngeal gland of ants (3), an organ involved in the spread of cuticular hydrocarbons among nestmates. Cuticular hydrocarbons play a central role in communication within ant societies: they are the basis for the formation of a “colony odor”, which is in turn used for nestmate recognition (i.e, self vs. non-self discrimination) (4). It is currently unknown whether nematode infections in the postpharyngeal gland can affect the ants’ nestmate discrimination ability, and if so, what the consequences on aggressive behavior, colony composition, and parasite transmission are.

Project Description: You will combine behavioural and chemical analyses to study the effect of experimental infections with *Diploscapter* nematodes in the clonal raider ant *Ooceraea biroi* (5), an emerging model for the study of social behaviour (6). You will investigate whether and how nematodes affect ant cuticular hydrocarbon profiles and the ability of ants to discriminate nestmates from non-nestmates, and how this in turn affects the transmission success of the parasite and the fitness of host colonies. Depending on your interests, this

project can develop to address more detailed questions on the sensory and nutritional aspects of the interaction between host and parasite, intergenerational effects of infections on the host, or comparative approaches using other ant-nematode species pairs. The project provides opportunities for internal and external collaborations.

Candidate profile:

- Master's degree (or equivalent) in biology or related field
- Proactive, dynamic, and curious
- Excellent communication and organizational skills
- Proficiency in written and spoken English
- Experience with behavioural assays or chemical analyses in insects are desirable but not necessary

Applications should be submitted online through the online portal of the graduate school (International Max Planck Research School, IMPRS): <https://www.ice.mpg.de/296548/current-call> by May 6, 2022. Informal inquiries about the position can be addressed to Yuko Ulrich (yulrich@ice.mpg.de).

The Max Planck Institute for Chemical Ecology provides a thriving, international, and multidisciplinary research environment, state-of-the-art facilities and equipment, and world-class colleagues working on evolutionary biology, and insect chemical ecology and neuroethology. The working language of the institute is English. For more information, please visit www.ice.mpg.de. The Max Planck Society is committed to equal opportunities and diversity (www.mpg.de/equal_opportunities). We welcome qualified applicants from all backgrounds.

References:

1. D. P. Hughes, F. Libersat, Parasite manipulation of host behavior. *Curr. Biol.* 29, R45-R47 (2019).
2. S. Cremer, S. A. Armitage, P. Schmid-Hempel, Social immunity. *Curr. Biol.* 17, R693-702 (2007).
3. G. J. Poinar, Nematode Parasites and Associates of Ants: Past and Present. *Psyche* 2012, (2012).
4. P. P. Sprenger, F. Menzel, Cuticular hydrocarbons in ants (Hymenoptera: Formicidae) and other insects: how and why they differ among individuals, colonies, and species. *Myrmecological News* 30, 1-26 (2020).
5. G. Alciatore et al., Immune challenges increase network centrality in a queenless ant. *Proceedings of the Royal Society B-Biological Sciences* 288, (2021).
6. Y. Ulrich, J. Saragosti, C. K. Tokita, C. E. Tarnita, D. J. C. Kronauer, Fitness benefits and emergent division of labour at the onset of group living. *Nature* 560, 635-638 (2018).

yuko ulrich <yulrich@ice.mpg.de>

Munster Evolutionary Genomics

Dear all,

Later this year, I will be recruiting a PhD student to investigate the genomic signatures related to the evolution of beetle sociality, here in Munster within the group of Erich Bornberg-Bauer at the Institute for Evolution and Biodiversity. The position will involve genome assembly as well as several comparative genomics and molecular evolution methods to investigate how sub- and eusociality arose in beetles, and how this compares to other transitions to sociality in insects.

I will post more details later but if you could help me identify some interesting candidates, that would be greatly appreciated. Any talented students who are interested in this project are welcome to contact me directly or refer to my website for more details on my work (bornberglab.org/people/harrison/).

Thank you and best wishes, Mark

Mark C. Harrison, Dr. Westfälische Wilhelms-Universität Münster Institute for Evolution and Biodiversity Evolutionary Bioinformatics Group Hilferstrasse 1a D-48149 Münster, Germany

Hilferstrasse 1a, Room 3 Tel: +49-(0)251 - 83-21508 Web: bornberglab.org/people/harrison/

Mark Harrison <m.harrison@uni-muenster.de> Mark Harrison <m.harrison@uni-muenster.de>

SLU Uppsala HoneyBeeImmunityEvolution

The Department of Ecology (SLU) is looking to recruit a PhD candidate, whom will be fully funded, to work on a research theme related to characterizing the immune system and responses of the honeybee to be able to understand trade-offs and adaptations happening in populations evolving resistance/tolerance to diseases both on the phenotypic and genetic level. Are you interested in understanding social insect immunity and host-parasite interactions in a scientifically and soci-

etally relevant field of honeybee health? Would you like to collaborate internationally and communicate with stakeholders? Then this PhD position should be of interest to you. Our doctoral education aims to develop your creative and analytical thinking and to strengthen your research, communication, and outreach skills. The position will be placed within the internationally distinguished honeybee research group where the successful candidate will be offered a stimulating context with colleagues who focus on various aspects of bee health and have an extensive collaborative network.

The goal of this project is to produce a comprehensive overview of the ecological immunity of honeybees by combining phenotypic and genomic measurements. The successful candidate is expected to carry out supervised research leading to a PhD thesis within this topic as well as taking PhD courses to the equivalent of 45 credits. This will involve characterize individual immunity across various life stages; setting up field experiments to examine and evaluate different behavioural and physiological traits of honeybees in relation to their biological performance specifically relating to disease resistance and tolerance; exploring immunity trade-offs that may potentially result from resistance in order to develop mitigation strategies to improve honeybee health and the resilience of beekeeping. RNA-seq will also be used to look at gene expression variation between phenotypes.

Qualifications: The successful applicant is required to have completed an MSc degree (or equivalent) in Biology / Ecology / Evolutionary Biology / Molecular Biology or similar subject. Skills in planning, executing, and reporting scientific studies, as well as experience with statistical analyses are meriting. The applicant should have the ability to work both independently and in a team. Proven ability to communicate excellently in written and spoken English is essential. A driving license is required. Experience working with honeybees and molecular assays /genomics will be considered of high additional merit. Application:

The written application shall contain:

A letter of motivation, describing the applicants previous academic and professional experience and motivation in relation to the project

* Curriculum vitae * Copy of degree incl. transcript of academic records * Copy of degree thesis * A list of two reference persons familiar with the applicant's qualifications. * Certified knowledge of the English language

We welcome your application no later than April 30th, 2022, apply via the website: <https://www.slu.se/en/about-slu/work-at-slu/jobs-vacancies/?rmpage=->

[job&rmjob=6487&rmlang=UK](https://www.slu.se/en/education/postgraduate-studies/) A person has basic eligibility for third cycle education if he or she has taken a second cycle qualification or has completed course requirements of at least 240 higher education credits, including at least 60 higher education credits at second cycle education. Upper secondary school grade equivalent to English B/English 6 is a basic requirement. Selection among applicants is made with reference to the written application including curriculum vitae, dissertation for masters or undergraduate degree, reference persons, certified knowledge of the English language and an interview. Personal merits will play a significant role in the recruitment process.

Please observe that applicant/s chosen to participate in an interview shall hand in certified true copies of certificates, diplomas and transcripts from previous studies at an internationally recognized higher education institution (university or university college) and transcripts in connection to the interview. If the applicant is a foreign citizen, we require a certified copy of the page in your passport with your personal data and photography.

Read more about the PhD education at SLU at www.slu.se/en/education/postgraduate-studies/ The Swedish University of Agricultural Sciences (SLU) is a world-class international university with research, education and environmental assessment within the sciences for sustainable life. Its principal sites are in Alnarp, UmeÅ¥ and Uppsala, but activities are also conducted at research stations, experimental parks and educational establishments throughout Sweden. We bring together

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TechU Dresden OrganismicMolecularBiodiversity

Dear colleagues,

we would be glad if you could announce our master's programme on evoldir

Course: TU Dresden, Germany, Master's Program "Organismic and Molecular Biodiversity" in October 2022.

Details of the program and enrolment can be found here: <https://tu-dresden.de/ihi-zittau/>

[studium/studienangebot/organismic-and-molecular-biodiversity?set_language=en](#) Kind regards

Christiane Ritz

Christiane Ritz <christiane.ritz@senckenberg.de>

TrentU ForensicGenomics

The project: An interdisciplinary project funded by NSERC Discovery Horizons aims to develop biomarkers to estimate time since death in participation with Canada's first human decomposition facility - REST[ES]. This posting is for a PhD student and the project will integrate a variety of genomic assays and machine learning approaches to uncover post-mortem time-dependent signatures.

The team: Consisting of anthropologists, chemists and population geneticists, the applicant will join an interdisciplinary team with access to the unique REST[ES] facility. The successful applicant will be based at Trent University (Ontario, Canada) and supervised by Drs. Aaron Shafer (TU) and Shari Forbes (UQTR / REST[ES]).

Qualifications: The PhD student must meet the requirements of the Environmental and Life Sciences OR Applied Modeling and Quantitative Methods Graduate Programs at TrentU. Basic programming skills (R / Unix) will be an asset; MSc and non-domestic applicants will be considered.

How to apply: Send a CV and 2 referee contacts to aaronshafer@trentu.ca. Anticipated start date is September 2022 or January 2023.

aaronshafer@trentu.ca

UBielefeld SpeciesInteractions

* Open PhD position in the Theoretical Biology group and NC³ at Bielefeld University, Germany. Application deadline May 4*

Dear evoldir community,

We are looking for a PhD student to join the Theoretical Biology group and the Collaborative Research Centre "A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution:

Niche Choice, Niche Conformance, Niche Construction (NC³, https://www.uni-bielefeld.de/fakultaeten/biologie/forschung/verbuende/sfb_nc3/)". The PhD project will focus on developing a modeling framework to investigate how species interactions (e.g. consumer-resource, host-parasite, or competitive interactions) are shaped by individual trait variation within species as well as by niche choice, niche conformance (closely related to phenotypic plasticity), and niche construction, the three key processes investigated by the collaborative research centre NC³. The PhD student will be part of a highly interactive research environment in the research centre, with seminars, retreats, research clouds, and in particular also collaborations with the empirical groups in the research centre.

Research tasks (95 %) - development of eco-evolutionary models - mathematical analysis of models - implementation in a programming language (e. g. R, C++, Python) - simulation studies - writing of scientific publications - collaboration with other research groups within the collaborative research centre

Other tasks (5 %) - organisation tasks in the research group and collaborative research centre

We expect: - a university degree (e.g. Master) in a relevant scientific discipline, e. g. biology, mathematics, physics, or bioinformatics - aspiration and ability to do a doctorate - programming skills in at least one programming language (e. g. R, C++, Python) - interest in both biological and mathematical questions - excellent command of scientific English, written and oral - motivation and communication skills to work as part of an interdisciplinary collaborative team

Preferred experience and skills: - experience with mathematical modeling - working knowledge of ecology and evolution

Please send your application including a motivation letter, CV, copies of certificates, and contact details of two references as a single pdf to meike.wittmann@uni-bielefeld.de and put the code Wiss22329 in the subject line. The application deadline is May 4, 2022.

For full details, see the official advertisement at: https://uni-bielefeld.hr4you.org/job/view/1375/-research-position-phd-student?page_lang=en Best wishes,

Meike Wittmann

Meike Wittmann Junior Professor of Theoretical Biology Bielefeld University, Faculty of Biology Postfach 10 01 31, 33501 Bielefeld, Germany Office: W4-101 Phone: +49 521 106 67627 meike.wittmann@uni-bielefeld.de <https://www.uni-bielefeld.de/fakultaeten/>

biologie/forschung/arbeitsgruppen/theoretical/ Meike Wittmann <meike.wittmann@googlemail.com>

ULausanne Two PlantEvolution

Two PhD positions in the Department of Ecology and Evolution, University of Lausanne, Switzerland

1. Experimental evolution at species range margins 2. Evolution of plant sexual systems

Two PhD position are open in John Pannell's lab in the Department of Ecology and Evolution, University of Lausanne, to study (1) the evolution of plant populations at and beyond species range margins or (2) the evolution of plant sexual systems.

Further details about the lab, including recent papers on which this project will build, can be found at: <https://www.unil.ch/dee/pannell-group>, or on writing to john.pannell@unil.ch.

Project 1: Experimental evolution at species range margins This project will use experimental evolution to test contrasting hypotheses for the effects of migration in either promoting or hindering adaptation in marginal populations. It will thus build on, and build bridges between, two strands in the lab: research on the demography, evolution and genomics of species range expansions and metapopulations; and the use of experimental evolution to address general questions in evolutionary biology. The project will involve establishing experimental populations at a number of sites across Europe and following their evolution over several successive generations, with the aim of building three mutually informative datasets to determine how admixture and selection in marginal populations affect (1) their demography (and population viability), (2) the quantitative genetics of morphological, life-history and physiological traits with an influence on local adaptation in marginal environments, and (3) the genomic architecture of responses to selection in different environments and in the context of different sources of admixture.

Project 2: Evolution of plant sexual systems The aim of this project is to advance our understanding of sexual-system transitions in plants, with a primary focus on evolutionary transitions between hermaphroditism and dioecy. The scope of the project can be partly tailored to the particular interests of the successful applicant and could involve a range of angles. We are currently particularly interested in using experimental evolution to

address questions concerning the quantitative genetics and genomic architecture of sexual-system transitions, including but not only sex chromosomes. The student's project could benefit from involvement in conducting and analysing results from an experimental evolution study that has been running for more than a decade. It could also include field observations and experiments, theoretical modelling and/or genomic analysis. There is scope to choose from a number of different study systems for empirical work.

Research scope and skills sought The student should have broad interest in evolutionary biology and a foundation in evolutionary biology, ecology and/or quantitative/population genetics, with an interest in quantitative and statistical analysis of large datasets. He/she should also have good written and oral communication skills. The project will involve close collaboration other lab members and project partners across Europe, and the successful candidate should thus both be self-motivated and have a collaborative spirit. Although not a requirement (the language of the lab and the research environment of the department is English), some knowledge of French would be an asset.

Host Department and University The Department of Ecology and Evolution hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and is close to the Swiss and French Alps.

Starting dates Both project could start from September 2022, but the starting dates are flexible and could potentially brought forward or delayed to accommodate the timing of an excellent candidate.

Applications Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications for both positions should be uploaded using the link below. Applications should include (1) a cover letter detailing your research interests, experience and motivation for applying, (2) a CV, (3) an example of previous research work (an article, preprint or master thesis chapter, and (4) the names of two referees. All applications received by the 15.05.2022 will receive full consideration.

Application link. <https://bit.ly/3KdR9ok> **University equality policy** The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.



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UMontpellier RainForestEvolution

PhD position in spatial components of tropical rain forest diversification, Montpellier, France

Project name: “Macroevolutionary determinants of Annonaceae species richness patterns”

Institutes and researchers involved: - Université $\frac{1}{2}$ de Montpellier (France) & IRD: Dr. Thomas Couvreur - Maastricht University (The Netherlands): Dr. Roy Erkens

Within the ERC funded GLOBAL project, we are seeking a highly motivated student to undertake a PhD (3 years) on the evolutionary and spatial determinants of Annonaceae species richness patterns across tropical rain forests.

Research Area and Project Description: The ERC Consolidator project “GLOBAL” aims to unravel the evolutionary history and diversification of tropical rain forests (TRF) at a global scale. The project focuses on the pantropical Annonaceae plant family, an important component of TRF worldwide with around 2550 species. During the project we will sequence nearly all species of the family. For each species, around 460 Annonaceae-specific exons and the angiosperm universal exons (353) will be sequenced. This dataset will provide one of the first robust and near-complete phylogenies of any major pantropical plant families to date. This dataset will be used to test numerous TRF evolutionary hypotheses at a global and local scales. GLOBAL is highly collaborative with numerous collaborators from across the globe, especially in tropical countries. This will provide opportunities for the PhD to interact with a wide range of researchers during the PhD.

The PhD will tackle questions related to the spatial aspects of Annonaceae evolution, testing major hypotheses of tropical plant distribution at global (eg “odd man out”) and local scales (e.g. what determines diversity at local levels?). The PhD student will have access to the full Annonaceae phylogeny (+2000 species; which will already be generated and dated), data on the distribution of Annonaceae globally (of which the student

will contribute in building), and a large morphological trait dataset.

Qualifications and Specific Competences: The applicant must have a recognized Master degree in evolution or ecology (or equivalent). The candidate should demonstrate a proven interest in evolutionary biology and/or spatial analysis of biodiversity. Experience with tropical biodiversity especially tropical rain forests is a plus. The candidate must have a proven record in one or several of the fields listed here: macroevolutionary diversification analyses using dated phylogenetic trees; spatial analyses of biodiversity (generate maps globally, estimate species richness); inferring species distribution ranges or species distribution modeling; experience in handling large datasets.

In addition, the applicant should have a good knowledge of programming languages such as R and/or Python (or a strong will to learn/master such languages). Finally, the student will have a good level of spoken and written English and good communication skills. International applicants who do not have English as their first language must prove strong English language writing skills and fluency. Knowledge of French is a plus, but not mandatory. The candidate should also have excellent organizational and communication skills.

Place of Employment and Work: The student will be based at the “Institut de Recherche pour le Développement” (IRD), UMR DIADE, DYNADIV team, 911 Avenue Agropolis, Montpellier, France. Montpellier is a pleasant Mediterranean town with a vibrant and internationally recognized research community, especially in evolutionary biology (University of Montpellier). The successful candidate will be enrolled at the Université $\frac{1}{2}$ de Montpellier (France) for the PhD diploma.

Start date: The position needs to start by October 1st 2022 at the latest.

Application deadline: May 16th 2022 (23.59 Paris time). You will receive an automatic response when you submit your application. If you do not, please email the application again.

Application procedure: A short list of applicants will be selected by a committee shortly after the deadline for applications. An interview will be planned for short listed applicants, only via zoom, planned for early June. The application must be in English and include a motivation letter, a 2-page max curriculum vitae, degree certificate, full list of publications (including in press, submitted, or in prep), names and email of two recommenders (no recommendation letter should be sent in the application; recommenders will potentially be contacted directly af-

terwards). All interested candidates are encouraged to apply, regardless of their personal background.

Contact: All questions about the project or the employment conditions, can be directly addressed to Thomas Couvreur, thomas.couvreur@ird.fr

For applications please send the below files (PDF format) to the following emails: annonaceae4ever@gmail.com.

- Updated CV

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UMontpellier Spatial Population Genomics

We (Raphaël Leblois, Arnaud Estoup, and François Rousset) propose a *fully-funded 3-years PhD position* starting in September 2022 at the CBGP in Montpellier on the *development, test and application of new methods for estimating local and recent demographic parameters from genomic data under spatialized models*.

The project is anchored, notably through its applications on real datasets, in a double context: (i) conservation biology (component of the DevOCGen project : <https://biodivoc.edu.umontpellier.fr/recherche/projets-consortium/projet-de-consortium-devocgen/>, 50% of the funding) and (ii) management of organisms of agronomic interest (INRAE component : <https://www6.montpellier.inrae.fr/cbpgp>, 50% of the funding).

A short summary of the subject is available at the end of this email. More detailed information, in french (but can be easily translated using e.g. DeepL), can be downloaded here : <https://filesender.renater.fr/?s=download&token=5ecf3c15-2ff4-4d21-921e-2423eed7e255> This project is multi-disciplinary at the border of several fields: population genetics, ecology, statistics and computer science. Minimal knowledge of all these fields and in-depth knowledge in one or more of them is expected. An important part of the project will involve the simulation of population genomics data and the analysis of these simulations. A strong taste for computational approaches

and programming is therefore required (C++, R).

We are therefore looking for a candidate who is highly motivated by methodological developments in population genetics/genomics, with a master's degree in evolutionary biology, bio-statistics or mathematical computing, and a strong interest in evolutionary biology and ecology.

The student will benefit from an extremely favorable work environment within the CBGP, the Montpellier scientific community, and the DevOCGen project (more than 20 researchers in 11 UMR, 6 bioinformatics and sequencing platforms, and 4 non-permanent funded researchers).

Interested applicants should send their CV and a half-page motivation letter

by May 26th to raphael.leblois@inrae.fr

Interviews will take place in early June.

Do not hesitate to spread this announcement around you and to contact us for more information,

Have a nice day,

Raphaël Leblois & Arnaud Estoup & François Rousset

raphael.leblois@inrae.fr

arnaud.estoup@inrae.fr

francois.rousset@umontpellier.fr

Short summary of the proposed thesis topic:

New developments for inferring local and recent population demographics from genomic data and applications for the management of threatened populations and organisms of agronomic interest.

The development of agro-ecological approaches for the management of pests and beneficials, as well as their vectors and antagonists, requires a better understanding of the local demographic functioning of their populations. Similarly, the management of threatened populations requires a detailed knowledge of the demographic and genetic status of these populations: population sizes, fragmentation, dispersal, inbreeding... Among the key factors to characterize, population densities/sizes and dispersal abilities, at a small geographical scale, as well as their variations over the recent past, are often poorly known but crucial to better understand the dynamics of these populations. Spatialized genomic data contain information on these demographic parameters, but current analysis methods do not allow for the use of all this information. Furthermore, the resulting demographic estimates often involve large spatial and temporal scales of limited practical interest. The goal of this project is to fill this methodological gap, by developing new

tools for estimating local demographic parameters, as well as their recent variations, from genomic data using spatialized demo-genetic models. In continuation of our current work on spatialized population genetic models and the development of simulation-based inference methods, the PhD student will focus on: (1) implement temporal changes of demographic parameters in our spatialized genomic simulator GSpace; (2) develop a set of new statistics summarizing the genomic information relevant for the inference of the parameters of interest; (3) couple them to powerful simulation-based inference methods; (4) test the level of spatio-temporal complexity that can be considered depending on the type and amount of data available. In order to validate their practical interest, these developments will be thought, tested and applied in two quite different contexts: (1) the study and management of

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UMuenster SticklebackTapeworms

The Institute for Evolution and Biodiversity at the University of Muenster, Germany, is seeking to fill the position of a

Doctoral Student (Ph.D position)

(salary level TV-L E 13)

for the externally funded project SFB/TRR 212 at the earliest possible date. We are offering a fixed-term position (65%) for 3 years.

Your tasks:

The position is part of the Collaborative Research Centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3), as granted by the German Research Foundation (DFG).

This PhD project deals with the ecological and evolutionary effects of parasite virulence. In this project, you will investigate the niche construction effects of a trophically transmitted tapeworm parasite (*Schistocephalus solidus*) on individual three-spined stickleback fish. The project aims to show how these effects cascade

from the individual to the ecosystem level and alter eco-evolutionary dynamics. The successful candidate will be involved in mesocosm experiments to investigate how parasite virulence affects individual trophic specialisation of the hosts. We also aim to identify the physiological and metabolic traits associated with these individual differences. The successful candidate will further take advantage of transcriptomic datasets to identify the immuno-physiological traits associated with host niche individualisation, and contribute to the development of computational models that will bridge the gap between individual, population, and community processes.

Our expectations:

Applicants should be highly motivated scientists of any nationality, who are interested in interdisciplinary work. They should have the equivalent of a master degree in biology, preferentially with a focus on evolution and ecology, or related fields. A background, and ideally some experience, in any of the following areas will be useful: fish handling and care, limnology, molecular skills, individual-based models, as well as a good understanding of statistics. Applicants should have excellent communication skills and be able to work both independently and as part of a multidisciplinary team. The working language of the Institute and the lab is English, and good proficiency in spoken and written English is a requirement.

Advantages for you:

The University of Muenster is a large vibrant university hosting a number of excellent scientific institutions (<http://www.uni-muenster.de/en/>). The Institute for Evolution and Biodiversity provides a stimulating research environment with a number of scientific groups researching diverse topics centred on different aspects of evolution. The successful candidate will join the team of Professor Joachim Kurtz, focussing on host-parasite coevolution and ecological immunology. As a part of the Collaborative Research Centre SFB/TRR 212 (https://www.uni-bielefeld.de/fakultaeten/biologie/-forschung/verbuende/sfb_nc3/), the project will involve intensive collaboration with consortium partners at the Universities of Muenster and Bielefeld. The town of Muenster itself has many students and presents a dynamic environment with many cultural and social events throughout the year (<http://www.muenster.de/en/>).

The University of Muenster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the

legal possibilities.

The University of Muenster is committed to employing more staff with disabilities. Candidates with recognised severe disabilities who have equivalent qualifications are given preference in hiring decisions.

Are you interested?

Then we look forward to receiving your application, written in English, in one single pdf file by 22 April 2022 at Dr. Jaime Anaya-Rojas (jaime.anaya-rojas@uni-muenster.de). Please note that we cannot consider other file formats. Applications should include 1) a cover letter with a statement of research interests and motivation (max. 1 page), 2) a CV including details about university degrees, research experience and publications, and 3) contact details of at least two referees.

Joachim Kurtz <joachim.kurtz@uni-muenster.de>

UNeuchatel ComparativeGenomicsButterflies

This is the final call to apply for the graduate position outlined below - the deadline is the 22nd of April.

The project is funded through a Swiss National Science Foundation Eccellenza Professorial Fellowship that was awarded to me and with which I will start the Biodiversity Genomics at the University of Neuchatel this year.

Project: Unravel the genomic architecture and evolutionary impact of chromosomal fusion and fission in Lepidoptera

Barriers to gene flow that lead to reproductive isolation are essential for speciation. Large-scale genomic rearrangements through chromosomal fusion and fission may represent such barriers, but the underlying genomic features and their contribution to speciation are poorly understood. This project aims to resolve the genomic architecture and evolutionary impact of chromosomal fusion and fission in one of the most karyological diverse groups of butterflies - Erebia. You will generate chromosome-scale genome assemblies and analyse them with comparative genomic and phylogenomic methods. The goal is also to assess the impact of these chromosomal rearrangements on rates of speciation. The prospective PhD student will be supervised by Kay Lucek and be part of the Biodiversity Genomics group at the University of Neuchatel in Switzerland.

Your profile: Enthusiastic, self-driven, responsible, and highly-motivated; excellent communication and interpersonal skills in verbal and written English; a strong work ethic. The ideal candidate brings strong conceptual thinking together with profound genomic and/or bioinformatic skills. Applicants should have a Master degree in evolutionary biology, genomics, bioinformatics, or close related fields. We offer you: A cutting-edge, four-year position fully funded by the Swiss National Science Foundation (SNSF), based at the Institute of Biology, University of Neuchatel, Switzerland. The Institute offers a vibrant and interdisciplinary research environment, combining a broad spectrum of research activities in life sciences, including evolutionary genetics, conservation, ecology and microbial biology. Salary and social benefits are provided according to University of Neuchatel rules. Neuchatel is an enchanting historic Swiss city, well connected and offering a broad range of cultural and recreational activities.

Starting date: The anticipated starting date is the 1st of August 2022, with some flexibility.

Application: Motivated applicants should submit (1) a one-page letter describing yourself, your career goals, and your match to the above-mentioned project, (2) a CV describing your education, publications, and relevant work experience, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information of two references. The application deadline is 22nd of April 2022. Please, send all the information in a single PDF to Kay Lucek (kay.lucek@unibas.ch). For further questions, please contact me @ kay.lucek@unibas.ch

Kay Lucek <kay.lucek@unibas.ch>

UNewSouthWales ParentalAgeAndFitness

Location: UNSW Sydney, Evolution & Ecology Research Centre and School of Biological, Earth and Environmental Sciences. UNSW is one of Australia's top research-intensive universities. The Evolution & Ecology Research Centre includes labs working on a range of topics in evolutionary ecology and genetics.

Project: I'm looking for motivated PhD candidates to investigate how parental age and environment affect offspring development and fitness. Two positions are available.

Despite over a century of research on the biology of age-

ing, one intriguing aspect of ageing - the widely observed tendency for older parents to produce offspring with reduced lifespan and fitness - remains poorly understood. Such effects could be a major source of variation in individual fitness, and could play a role in the evolution of ageing. Building on recent work by the Bonduriansky lab and others, this research will address the mechanisms mediating these effects, the roles of mothers vs. fathers, and the role of the ambient environment. This project will also contribute new theory on the evolutionary implications of such effects.

Applicants should be highly motivated, and should have a strong academic background (including writing and quantitative skills) and previous research experience (preferably including publications). PhD students in the Bonduriansky lab are expected to play a central role in developing their projects, and to be able to work independently on their research.

Both domestic and international students are eligible for these PhD positions. If interested, please send an email to Russell Bonduriansky (r.bonduriansky@unsw.edu.au) outlining your qualifications and why you are interested in this project. Please include a CV and contact details for two academic referees who could provide supporting letters. A subset of applicants will be invited to submit full applications to the UNSW Graduate Research School.

For information on graduate studies at UNSW, please see: <https://research.unsw.edu.au/graduate-research> r.bonduriansky@unsw.edu.au <http://www.bonduriansky.net/index.htm> r.bonduriansky@unsw.edu.au

UPadua EvolutionCorrection

Call for PhD students in Ecology, Evolution and Conservation at Padua University is open: apply by May 13, 2022

Start date: Oct 2022

PLEASE NOTE: Respect to my previous posting, I corrected the email address for the colleague prof. Telmo Pievani and updated the links. My apologies for the inconvenience.

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 CON-

SERVATION 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. 80 PhD students are enrolled at the Biology Department), post-docs and the over 80 faculty members of the Department.

Proposed research topics include: - Exploring species interactions in wetland restoration and their effects on ecosystem processes and services. Contacts: Prof. Laura Airoidi and Dr. Davide De Battisti, e-mail: laura.airoidi@unipd.it davide.debattisti@unipd.it - Studying gymnosperms to understand seed plants evolution: unraveling reproductive mechanisms in Ginkgo biloba L. Contact: Prof. Barbara Baldan, e-mail: barbara.baldan@unipd.it - The ecological role of dissolved oxygen oscillations in marine ecosystems. Contact: Dr. Alberto Barausse, e-mail: alberto.barausse@unipd.it - Evolutionary routes to endemism in alpine rockfoils. Contacts: Dr Francesco Dal Grande and Prof. Barbara Baldan, e-mail: francesco.dalgrande@unipd.it barbara.baldan@unipd.it - Effects of heatwaves on reproduction and behaviour in a model insect species. Contact: Prof. Clelia Gasparini, e-mail: clelia.gasparini@unipd.it - How the theory of evolution is evolving. Contact: Prof. Telmo Pievani, e-mail: dietelmo.pievani@unipd.it - Sexual selection in a changing world. Contact: Prof. Andrea Pilastro, e-mail: andrea.pilastro@unipd.it - Mate choice, personality, and evolutionary genomics in freshwater fishes. Contact: Prof. Gil Rosenthal, e-mail: gil.rosenthal@unipd.it - Environmental DNA application to monitor biodiversity and to detect alien species in freshwater and lagoon ecosystems. Contact: Prof. Lorenzo Zane, e-mail: lorenzo.zane@unipd.it

Based on the excellence of applications, from 3 to 4 PhD Scholarships will be funded. Details on the potential research projects are reported in https://dottorato.biologia.unipd.it/fileadmin/dottorato/-/Evolution_Ecology_and_Conservation_4_2022.pdf Furthermore, 2 additional PhD Scholarships will be funded for specific "priority research grants" on:

- Understanding resilience mechanisms in marine restoration. Contact: Prof. Laura Airoidi, e-mail: laura.airoidi@unipd.it - Environmental DNA application to coastal marine ecosystems for the preservation of ecosystem functions and services under climate change pressure and overfishing. Contact: Prof. Lorenzo Zane, e-mail: lorenzo.zane@unipd.it

Details on the priority research grants are available at: https://dottorato.biologia.unipd.it/fileadmin/dottorato/Priority_Research_Grants_4_2022.pdf Candidates are encouraged to carefully read the potential research projects and to e.mail the reference persons for further details. When applying, please also check the news at https://dottorato.biologia.unipd.it/fileadmin/dottorato/Important_notices_2022.pdf 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 <lorenzo.zane@unipd.it>

UPadua Evolution Ecology Conservation

Call for PhD students in Ecology, Evolution and Conservation at Padua University is open: apply by May 13, 2022

Start date: Oct 2022

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 stu-

dents (approx. 80 PhD students are enrolled at the Biology Department), post-docs and the over 80 faculty members of the Department.

Proposed research topics include: - Exploring species interactions in wetland restoration and their effects on ecosystem processes and services. Contacts: Prof. Laura Airoidi and Dr. Davide De Battisti, e-mail: laura.airoidi@unipd.it davide.debattisti@unipd.it - Studying gymnosperms to understand seed plants evolution: unraveling reproductive mechanisms in Ginkgo biloba L. Contact: Prof. Barbara Baldan, e-mail: barbara.baldan@unipd.it - The ecological role of dissolved oxygen oscillations in marine ecosystems. Contact: Dr. Alberto Barausse, e-mail: alberto.barausse@unipd.it - Evolutionary routes to endemism in alpine rockfoils. Contacts: Dr Francesco Dal Grande and Prof. Barbara Baldan, e-mail: francesco.dalgrande@unipd.it barbara.baldan@unipd.it - Effects of heatwaves on reproduction and behaviour in a model insect species. Contact: Prof. Clelia Gasparini, e-mail: clelia.gasparini@unipd.it - How the theory of evolution is evolving. Contact: Prof. Telmo Pievani, e-mail: telmo.pievani@unipd.it Sexual selection in a changing world. Contact: Prof. Andrea Pilastro, e-mail: andrea.pilastro@unipd.it - Mate choice, personality, and evolutionary genomics in freshwater fishes. Contact: Prof. Gil Rosenthal, e-mail: gil.rosenthal@unipd.it - Environmental DNA application to monitor biodiversity and to detect alien species in freshwater and lagoon ecosystems. Contact: Prof. Lorenzo Zane, e-mail: lorenzo.zane@unipd.it

Based on the excellence of applications, from 3 to 4 PhD Scholarships will be funded. Details on the potential research projects are reported in https://dottorato.biologia.unipd.it/fileadmin/dottorato/Evolution_Ecology_and_Conservation_3_2022.pdf

Furthermore, 2 additional PhD Scholarships will be funded for specific “priority research grants” on: - Understanding resilience mechanisms in marine restoration. Contact: Prof. Laura Airoidi, e-mail: laura.airoidi@unipd.it - Environmental DNA application to coastal marine ecosystems for the preservation of ecosystem functions and services under climate change pressure and overfishing. Contact: Prof. Lorenzo Zane, e-mail: lorenzo.zane@unipd.it

Details on the priority research grants are available at: https://dottorato.biologia.unipd.it/fileadmin/dottorato/Priority_Research_Grants_3_2022.pdf Candidates are encouraged to carefully read the potential research projects and to e.mail the reference persons for further details. When applying, please also check the news at https://dottorato.biologia.unipd.it/fileadmin/dottorato/Important_notices_2022.pdf 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 <lorenzo.zane@unipd.it>

UPadua GenomicFishSexDetermination

A PhD position on “Genetic/Genomic basis of sex determination in fish of aquaculture interest” is available at the Doctoral Course in Veterinary Science (Padua University).

Apply by May 13, 2022 Information about the application can be found at <https://www.dottorato.veterinaria.unipd.it/enrollment>
Start date: Oct 2022

GENETIC/GENOMIC BASIS OF SEX DETERMINATION IN FISH OF AQUACULTURE INTEREST

In teleost fish, sex determination mechanisms are extremely diverse ranging from the presence of evident heterochromatic sex chromosomes to simultaneous hermaphroditism. When genetic sex determination (GSD) is observed the underlying mechanisms might be diverse even between closely related species or within the same species. In several fish species of aquaculture interest, it would be of great benefit to have tools that allow sex identification during early developmental stages. It is the case of the flathead grey mullet (*Mugil cephalus*), whose roe is a highly sought seafood consisting of raw or dried female gonads. In some Mediterranean areas it represents an important product for the local economy. Genetic markers at the FSHR (follicle-stimulating hormone receptor) gene were recently identified in *M.c.* by means of whole-genome sequencing (Ferraresso et al., 2021). However, genetic screening of natural populations from different geographic origins showed an incomplete penetrance of this character underlying the possibility that also other genetic and non-genetic (environmental) factors may play a role in sex-determination of *M.c.* The project has 5 lines of possible development: 1) Genomic scan searching for additional markers of sex determination in *M.c.*; 2) Application of the existing markers for sex sorting in early fish developmental stages aimed at rearing only female individuals for “bottarga” production; 3) Genotype-assisted individual breeding in order to maximize the percentage of female offspring; 4) Extension of the population analysis to gain a wider geographic picture of the penetrance of the FSHR sex-associated markers; 5) Extension of the genetic/genomic

study to other mullet species (i.e. *Liza* spp.) that are relevant for “bottarga” production.

CITED REFERENCE Ferraresso S., Bargelloni L., Babucci M., Cannas R., Follesa M.C., Carugati L., Melis R., Cau A., Koutrakis M., Sapounidis A., Crosetti D., Patarnello T. (2021). Fshr: a fish sex-determining locus shows variable incomplete penetrance across flathead grey mullet populations. *iScience*, 24 (1), art. no. 101886. DOI: 10.1016/j.isci.2020.101886

FIVE PUBLICATIONS RELATED TO THE RESEARCH TOPIC FOR THE CANDIDATE INTERVIEW Geffroy B., Douhard M. The adaptive sex in stressful environments. *Trends Ecol. Evol.* 2019; 34: 628-640 Houston, R.D. et al. Harnessing genomics to fast-track genetic improvement in aquaculture. *Nature Reviews Genetics* 2020; 21, 7: 389-409 Moore E.C., Roberts R.B. Polygenic sex determination. *Curr. Biol.* 2013; 23: R510-R512 Palmer D.H., Rogers T.F., Dean R., Wright A.E. How to identify sex chromosomes and their turnover. *Mol. Ecol.* 2019; 28: 4709-4724 Ribas L., Liew W.C., Diçaz N., Sreenivasan R., Orbiçan L., Piferrer F. Heat-induced masculinization in domesticated zebrafish is family-specific and yields a set of different gonadal transcriptomes. *Proc. Natl. Acad. Sci. USA.* 2017; 114(6):E941-E950

Contact person Prof. Tomaso Patarnello Dept. of Comparative biomedicine and food science Viale dell'Università, 16 35020 Legnaro, Padova, Italy Tel: +39.049.827.2977 e-mail: tomaso.patarnello@unipd.it

Lorenzo Zane <lorenzo.zane@unipd.it>

UParis Saclay TransposableElementsAdaptation

[PhD advertisement Univ. Paris Saclay] ADAPTIVE ROLE OF TRANSPOSABLE ELEMENTS IN FRUIT TREES IN RESPONSE TO BIOTIC STRESS, deadline for application : 29 April 2022

We are seeking candidates for a PhD to join the Cornille's Lab (ECLECTIC group?: <http://moulon.inrae.fr/en/equipes/eclectic/>) working on the genomics and ecology of fruit tree-pest interactions at the laboratoire Génétique Quantitative et Evolution-Le Moulon at the Institut Diversité, Ecologie et Evolution du Vivant (<https://www.ideev.universite-paris-saclay.fr/en/>) at Université Paris Saclay (<https://www.universite-paris-saclay.fr/en> Ile-de-France, France) within the ANR

PLEASURE project (<https://anr.fr/Project-ANR-21-CE20-0005>).

Keywords: adaptation, fruit trees, epigenomics - methylation, gene expression, evolution, pests?

Objectifs The aim of the PhD project is to investigate the effect of TE insertion on gene expression in response to biotic stress in fruit trees, using a population genomics lens. To that aim, the PhD candidate will undertake a rigorous analysis of the impact of TE insertion polymorphism on gene expression in crop and wild populations of an emblematic fruit tree, the apple tree, for which a very large amount of genomic data is available. The PhD project is structured into two interconnected questions, that will be subsequently investigated, which rely on exposure of crop and wild apple populations to pest attack and the investigation of the involvement of TEs in this stress response: 1) What is the effect of TE insertion on gene expression in response to biotic stress in a context of fruit tree domestication? 2) What is the impact of DNA methylation variants in TE repression in response to biotic stress in the context of fruit tree domestication? ? Methods -populations genomics of transposable elements; -epigenomics (methylation marks); -bioinformatics (scripting in perl/python/shell, access to informatics clusters); -experiments in controlled conditions (aphid rearing, apple culture) -molecular biology (RNA and DNA extraction).

Profile and skills required? Knowledge in 1) evolutionary biology and population genomics is required (in gene expression analyses or on transposable elements evolution will be a plus) and 2) bioinformatics (writing scripts, e.g., in perl/python/R/shell, access to computing clusters). Knowledge of 3) epigenomics will be a plus. The candidate should not necessarily be familiar with tree or insect models.

Collaborations? The PhD candidate will take advantage of the collaborative network involved in the project: CNRGV (molecular biology expert), URGI (expert on TE annotation), GQE-Le Moulon (expert in population and comparative genomics, fruit tree biology).

Application. Two steps process: - Before the 28th April: https://www.adum.fr/as/ed/voirproposition.pl?site=PSaclay&matricule_prop=39544 - The candidate will be selected by the lab between the 28th April to the 9th May to defend the project at the Doctoral school Science du Végétal in June 2022.

Feel free to contact directly at amandine.cornille@cnrs.fr
Leader of the Ecological genomics of multi-species interactions group CNRS Researcher G?n?rique Quantitative et Evolution - Le Moulon? Universit? Paris-Saclay - INRAE - CNRS - AgroParisTech?

Institut Diversit? Ecologie et Evolution du Vivant |?12 Route 128 |?91272 Gif-sur-Yvette |?France phone : +33 6 72 44 85 55 |?+33 1 69 33 23 52? Twitter: @CornilleAmand or @PommierVerger Google Scholar profile :? <https://scholar.google.com/citations?user=EqIE2h8AAAAJ&hl=fr> Personal page :? <http://moulon.inrae.fr/personnes/acornille/> Group page:?? <http://moulon.inrae.fr/en/equipes/eclectic/> On the ESEB-STN network on the ecological genomics of coevolution: <https://eseb.org/prizes-funding/special-topic-networks/stn-current-networks/ecological-genomics-of-coevolutionary-interactions/> On the wild apple orchard project: [@PommierVerger](https://www.ideev.universite-paris-saclay.fr/en/the-orchard?or)

Amandine Cornille <amandine.cornille@gmail.com>

UppsalaU ConservationGenomics

Uppsala University. PhD position in Conservation Genomics - Apply by May 20

A PhD student position in Conservation Genomics and Immunogenetics is available at the Department of Ecology and Genetics, Uppsala University, Sweden.

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our ultimate goal is to conduct education and research of the highest quality and relevance to make a long-term difference in society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has over 54,000 students, more than 7,500 employees and a turnover of around SEK 8 billion. The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see www.ieg.uu.se. Project description/duties: Climate change is predicted to increase temperatures worldwide and increase climatic instability. This will significantly impact infectious disease dynamics, altering pathogen distribution and disease intensity. Ectotherms are particularly susceptible to thermal changes, as they are dependent on the ambient environment to regulate their physiological processes, including the immune response. This PhD position will investigate how climate warming will impact immunocompetence in the sand lizard (*Lacerta agilis*), a vulnerable, temperate species in Sweden. It will integrate experimental biology with

genomics, transcriptomics and epigenomics, applying population genetics and genome-wide association approaches. The selected candidate will mainly engage in large-scale population genomics and quantitative genetics analyses that require solid bioinformatics skills. The candidate will also conduct field work, immune challenge experiments and molecular lab work to produce additional datasets. Additional duties include active participation in the research group activities, training of junior group members in relevant techniques and engagement in collaborative projects.

Qualifications required: To be eligible for a PhD-student position the applicant must hold a master degree (or equivalent) within evolutionary biology, ecology, bioinformatics or a related field. The ideal candidate will be highly motivated and have a strong interest in evolutionary biology and conservation genomics. A high standard of spoken and written English is required.

Qualifications desired: Experience with genomic techniques and bioinformatic analysis is highly advantageous, as well as an enthusiasm for field work.

If you have any questions regarding the position, please contact Mette Lillie, mette.lillie@ebc.uu.se

For further information on the position and to apply, please visit the following site at Uppsala University: <https://www.uu.se/en/about-uu/join-us/details/?positionId=497892> The application deadline is 20 May, 2022.

Mette Lillie

Department of Ecology and Genetics

EBC, Uppsala University

Norbyvägen 18D

75236 Uppsala

Sweden

Email: mette.lillie@ebc.uu.se

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

UppsalaU PopulationGenomics

A PhD student position in Population genomics is available at the Department of Ecology and Genetics, Program in Plant Ecology and Evolution, Uppsala University, Sweden, with Martin Lascoux, Pascal Milesi and Henrik Hallingbäck (Forestry Research Institute of Sweden).

The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see www.ieg.uu.se. The Evolutionary Biology Centre to which the Department belongs is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University, which has been ranked very high among all European Universities in the subject of evolutionary biology. Our lab is part of the Program of Plant Ecology and Evolution that excels in many aspects of genetics and evolution and offers an inspiring international atmosphere. There are ample opportunities for interaction with PhD-students, PostDocs and researchers working on related topics. We are tightly linked to the Science for Life Laboratory (<https://www.scilifelab.se>) and have access to advanced laboratory infrastructure, high performance computing resources and bioinformatics support.

Project description: Climate change puts our forests at risk, and current forest biomass production is neither secure, sustainable nor sufficient to meet the future demands of the energy and process industry sector, nor well-placed to meet additional societal goals for forest biodiversity, recreation, and aesthetics. The recently funded 'TREES FOR ME' is a centre of excellence on fast growing broadleaves, i.e. poplar, aspen, hybrid aspen and birch, for sustainable forests, materials and energy. In total, 13 PhD students will be recruited to the centre. Within the Centre, Uppsala University, in close collaboration with the Forestry Research Institute of Sweden, will be more specifically responsible for developing genomics tools related to the establishment of genomic selection in birch breeding. This will require a fine-scale understanding of the genetic structure and the pattern of local adaptation in birch across Scandinavia. The project will be based on genome resequencing of extensive collection of birch trees along latitudinal gradients. The project will also benefit from the avail-

ability of range-wide collection of birch material, from previous resequencing efforts in birch and from international collaborations. In addition to contribute to the establishment of genomic selection these data will also be used to address evolutionary questions.

For further information on the position and to apply, please visit the following site at Uppsala University: <https://www.uu.se/en/about-uu/join-us/details/?positionId=492202> The deadline for application is June 1, 2022.

Martin Lascoux Department of Ecology and Genetics EBC, Uppsala University Norbyvägen 18D 75236 Uppsala Sweden Tel +46 (0) 18 471 64 16 Email Martin.Lascoux@ebc.uu.se <https://lascouxlab.wordpress.com> När du har kontakt med oss på Uppsala universitet med e-post innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: <http://www.uu.se/om-uu/dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/about-uu/data-protection-policy> Martin Lascoux <martin.lascoux@ebc.uu.se>

UQueensland Experimental Evolution

PhD Scholarship: The costs and consequences of antimicrobial resistance in microbial communities

Applicants are invited for a fully funded PhD position in the group of Dr Andrew Letten at the University of Queensland to study resource competition and antimicrobial resistance evolution in microbial communities.

Background: Ecological theory provides a powerful framework for understanding the competitive balance between sensitive and resistant bacteria, and therefore the evolution of resistance (Letten et al, 2021 Nature Eco Evo). The primary goal of this ARC funded project is to go beyond the theory and test how well we can predict the evolution and persistence of resistant bacteria in microbial communities under the highly variable environmental conditions typical of most microbial systems (from soils and water to the gut). This is critical not only for our fundamental understanding of microbial competition and evolution, but also ultimately for the identification and development of new ecologically-aware

strategies for managing resistance.

A wide variety of investigatory approaches fall within the scope of the project including high throughput screening and competition assays, molecular work, mathematical modelling, and computer simulations. The PhD student will have ample room to take the project in a more experimental or computational/theoretical direction depending on their interests and background. This is to say that highly motivated students that are primarily interested, or have a strong background, in either empirical or computational/theoretical research are both encouraged to apply. Similarly, the project is suitable to students coming from a microbiology or molecular background interested in ecological and evolutionary research, or those coming from an ecological or evolutionary background who are interested in bringing their knowledge to microbial systems.

A working knowledge of laboratory research, experimental evolution and/or mathematical modelling would be of benefit to someone working on this project. The applicant will demonstrate academic achievement in the field(s) of ecology, evolutionary biology, microbiology or molecular biology and the potential for scholastic success. A background or knowledge of R or Python programming and ecological and/or evolutionary theory is highly desirable.

The student will be based in the School of Biological Sciences at The University of Queensland, Brisbane, Australia. We are a research-intensive University and our School comprises more than 100 academic and post-doctoral research staff, and ~200 higher-degree research students. The student and project will benefit from the School's formidable research expertise in ecology, evolutionary biology and genetics, physiology, and mathematical, statistical and computational biology.

As a scholarship recipient, you'll receive:

- Living stipend of \$28,854 per annum tax free (2022 rate), indexed annually
- Tuition fees covered
- Single Overseas Student Health Cover (international applicants)

Please contact Dr Andrew Letten (a.letten@uq.edu.au) as soon as possible if you are interested (including a CV and a brief statement on your research background and interests). More information on the recruitment process here <https://graduate-school.uq.edu.au/project/costs-and-consequences-antimicrobial-resistance-microbial-communities> . Andrew Letten

Lecturer School of Biological Sciences The University of Queensland Brisbane QLD 4072 Australia

phone: +61 7 336 52454

www.andrewletten.net
<a.letten@uq.edu.au>

Andrew Letten

UToronto Fishgenetics

Genetics of Endangered and Invasive Freshwater Fishes in the Great Lakes Basin, University of Toronto

The Lovejoy and Mandrak labs (mandraklab.ca) have an opening for an MSc or PhD student for September 2022.

Diet overlap analysis is a conventional method for evaluating potential competition. Such analyses are typically undertaken by sacrificing fish and dissecting their stomachs to determine the contents. A common non-lethal method is to wash the stomach contents out through the mouth using gastric lavage. However, a major shortcoming of both methods is that it is often difficult to identify stomach contents owing to gastric acid breakdown, particularly if the prey does not have resistant body parts (e.g. exoskeletons). Recent advances of genetic methods suggest that stomach contents can be identified to species using a genetic metabarcoding approach (Mychek-Londer et al. 2020). The student will further develop and conduct stomach contents DNA and eDNA analyses to determine the diet of invasive and endangered fish species. The project includes Indigenous, provincial, and federal partners and is funded by GEN-FISH (gen-fish.ca). The successful candidate could also apply to the FishCAST NSERC Create program (fishcast.ca).

Candidates should have genetics laboratory experience, excellent written and oral communication skills, quantitative skills, and other relevant skills. The student will be enrolled in the graduate Department of Ecology and Evolutionary Biology (MSc) or Department of Physical and Environmental Sciences (PhD) and be based at the University of Toronto Scarborough.

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ2S+ persons, and others who may contribute to the further diversification of ideas.

The University strives to be an equitable and inclusive community, and proactively seeks to increase diversity among its community members. Our values regarding

equity and diversity are linked with our unwavering commitment to excellence in the pursuit of our academic mission.

Interested students should send a letter of intent, resume, unofficial transcripts, and a writing sample to

Nathan Lovejoy Department of Biological Sciences University of Toronto Scarborough
nathan.lovejoy@utoronto.ca

Nathan Lovejoy <nathan.lovejoy@utoronto.ca>

UtrechtU FungusInsectInteractions

UTRECHT UNIVERSITY. PHD POSITION FUNGUS-INSECT INTERACTIONS

Job description Infected animals often behave differently from healthy animals. These changes can involve precise manipulations caused by parasites to increase that parasite's chances to spread. How exactly manipulative parasites can alter host behaviour is largely unknown. Uncovering the parasite compounds and host pathways involved could have both medical and agricultural applications through the discovery of novel drugs and holistic methods to battle insect pests. The behaviourally tractable "zombie ant system" has the potential to expose the mechanisms underlying parasitic behavioural manipulation and fundamentally transform perceptions of parasite-host interactions and their behavioural ecology effects. Our research group uses these fungus-infected "zombie ants" as a model to study disease progression, related behavioural phenotypes, and the mechanisms underlying those phenotypes. We love to push the boundaries when it comes to available techniques for this novel model system, so we often find ourselves adopting and creating new tools to answer our research questions.

The nature of the research that you will be involved in is naturally integrative. As such, your work will involve a variety of tasks spanning the fields of molecular microbiology, genetics, genomics, and behavioural ecology:

- Apply gene-editing and other molecular microbiology and genetics technology to study the function of candidate manipulation compounds.
- Produce and analyse genomics and transcriptomics datasets to reveal host pathways involved in altered behaviours.
- Conduct infection and compound exposure experiments with a variety of invertebrate host organisms ranging

from established model systems to ant colonies collected from nature. - Use quantitative behavioural tracking software and conducting statistical analyses to study disease-related behavioural phenotypes. - Participate in yearly field expeditions to Florida (USA) to collect carpenter ant colonies.

Qualifications

You fit well within our research team when you are ambitious, creative, and highly motivated. Next to that, you have a strong interest in parasite-host interactions, fungal biology and/or insect behaviour. It works in your favour if you have already developed good working knowledge in experimental design and statistics.

We would also like you to bring the following:

- a Master's degree with a background in molecular biology, genetics, microbiology or a related field; - prior experience with genomics or transcriptomics data generation and analysis (ideally, but not necessary); - prior experience with insect handling, collecting and husbandry (ideally, but not necessary, at the very least you are not squeamish around insects); - programming skills or the willingness to develop them; - great oral and written communication skills in English.

Offer

- A full-time position for 4 years; - Enrolment in the PhD Programme Environmental Biology within the Graduate School of Life Sciences <https://www.uu.nl/en/research/institute-of-environmental-biology/-education/phd-programme-environmental-biology>
- A full-time gross salary starting at euro 2,443 in the first year and increasing to euro 3,122 in year four (scale P Collective Labour Agreement Dutch Universities (cao)); - 8% holiday bonus and 8.3% end-of-year bonus; - A pension scheme, partially paid parental leave, and flexible employment conditions <https://www.uu.nl/en/organisation/working-at-utrecht-university/terms-of-employment> based on the Collective Labour Agreement Dutch Universities.

In addition to the employment conditions laid down in the CAO for Dutch Universities, Utrecht University has a number of its own arrangements. For example, there are agreements on professional development, leave arrangements and sports. We also give you the opportunity to expand your terms of employment via the Employment Conditions Selection Model. This is how we like to encourage you to continue to grow. About the organisation

The Department of Biology < <https://www.uu.nl/en/-organisation/department-of-biology> > hosts a large number of research chairs, which are organized within two

institutes: the Institute for Biodynamics and Biocomplexity < <https://www.uu.nl/en/organisation/institute-of-biodynamics-and-biocomplexity> > (IBB) and the Institute of Environmental Biology

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UWarsaw 2 SmallMammalsPaleogenomics

Two PhD student positions available at the Laboratory for Paleogenetics and Conservation Genetics, University of Warsaw in small mammal paleogenomics projects led by Mateusz Baca, PhD.

Project 1 - "Paleogenomic analysis of small mammals in the reconstruction of species responses to climate change" more info: https://www.uw.edu.pl/wp-content/uploads/2022/03/job-offer_cent-12-2022-sonata-bis-10-baca-phd-student-en.pdf

Project 2 - "Reconstruction and calibration of genome-based phylogeny of the *Microtus* genus using the Middle Pleistocene genomes" more info: https://www.uw.edu.pl/wp-content/uploads/2022/03/job-offer_cent-13-2022-opus-20-baca-phd-student-en.pdf

If you're interested in sequencing genomes of modern and subfossil small mammals and reconstructing their evolutionary histories, phylogenetic relationships, and responses to past climate changes, we encourage you to apply for these scholarships!

Application deadline: 25 April 2022

Mateusz Baca <m.baca@cent.uw.edu.pl>

"Laboratory of Paleogenetics and Conservation Genetics, University of Warsaw" <m.molak@cent.uw.edu.pl>

UWolverhampton SkinkPhylogenetics

Fully funded PhD to study the "Phylogenetic relationships and biogeography of the sphenomorphin skinks"

Based at the University of Wolverhampton, UK. Application deadline is 29th April 2022. Open to UK and International applicants. The position comes with an annual salary of GBP15,608 + tuition fees+ research expenses.

Skinks are the most diverse family of reptile, comprising a quarter of all lizard species: 7-9 subfamilies/tribes, 168 genera and ca. 1,744 species. Of these, over a third of all species, in 32 genera, belong to the tribe Sphenomorphini (formally in the subfamily Sphenomorphinae sensu Shea, 2021 Zootaxa, 5067(3), 301-351). Despite this high diversity, internal evolutionary relationships within the Sphenomorphini have remained poorly studied and may not form a true (monophyletic) taxonomic group. The sphenomorphin skinks have a wide geographic distribution spanning major biogeographic barriers, occurring across Asia, Australasia and the Americas.

Western Melanesia including New Guinea sits at the crossroads of Asia, Australia, and the Pacific and is one of the most interesting, puzzling, and understudied hyperdiverse regions on Earth. Despite being highly diverse, most taxonomic groups have lacked research focus. The sphenomorphin skinks of Western Melanesia occupy a substantial proportion of the region's lizard diversity but little is still known about them. Nine genera of sphenomorphin skinks are known to occur in the Western Melanesian region (*Alpinoscincus*, *Fojia*, *Glaphyromorphus*, *Nubeoscincus*, *Ornithuroscincus*, *Palaia*, *Papuascincus*, *Prasinohaema*, *Sphenomorphus*) yet the number of species within these genera are known to be underestimated and their relationships largely unknown. This PhD project aims to provide a better understanding of the evolutionary relationships and historical biogeographic patterns among the sphenomorphin skinks, using cutting edge molecular approaches.

The project aligns with Dr Simon Maddock (University of Wolverhampton, UK) and Dr Fred Kraus' (University of Michigan, USA) recently funded NERC-NSF grant, "Origins and expansion of endemic biodiversity in western Melanesia and their relation to tectonic evolution", and it is expected that the successful applicant will develop (alongside collaborators) additional research questions relating to the origins of Western Melanesian sphenomorphin skinks, following the generation of initial results and the applicant's interests.

With the onset of high-throughput sequencing methods, previously unavailable molecular data are now accessible from museum specimens with recently developed archival DNA methods. These advancements enable us to address questions relating to poorly sampled taxa, and the PhD project will exploit this by generating novel sequence data for mi-

tochondrial DNA and ultraconserved elements (UCEs) (<https://www.ultraconserved.org> < <http://%28https//www.ultraconserved.org> >/) from historic museum samples as well as freshly collected samples. The PhD project will primarily be genetics based, however, it will also provide the successful applicant with the opportunity to undertake some fieldwork to collect sphenomorphin DNA samples (and specimens).

The successful applicant will be based at the University of Wolverhampton, UK, which boasts excellent laboratory facilities and has recently received an internal 1million research investment fund for bioscience research. The successful candidate will be expected to work closely with the postdoctoral researcher, the research assistant, and other project partners on Maddock and Kraus' joint NERC-NSF grant. The ideal candidate should have an interest in evolutionary biology and ideally be willing to undertake fieldwork in a challenging environment (provisionally Papua New Guinea). Additionally, the candidate should be reliable, patient, enthusiastic, committed to scientific research, able to work both as part of a team and individually and they should show sensitivity and adaptability to foreign cultures. Candidates with prior lab and field experience will have an advantage. The project would benefit from independent direction by the successful candidate depending on their interests and preliminary results.

The supervisory team will be led by Simon Maddock (University of Wolverhampton, UK) and will be co-supervised by Fred Kraus (University of Michigan, USA). Informal and formal enquiries should be directed to Simon Maddock (s.maddock@wlv.ac.uk). Interviews will be scheduled for the week commencing 6th June 2022.

The PhD candidate will be encouraged to apply for additional funding to support field and museum work (with Dr Maddock's support) to cover any additional costs

Specific requirements of applicants: > A first or upper second-class honours degree in biology or zoology, or a related field.

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UWolverhampton SkinkPhylogenetics LastCall

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UZurich

GenomicsPlantInsectCoadaptation

PhD position in genomics of plant-insect coadaptation
 A PhD position funded by the Swiss National Science Funds is available by 1st of July in my group at the Department of Systematic and Evolutionary Botany, University of Zürich, for a period of four years. The position is to study the genomic bases of real-time plant-insect coevolution. In the project, experimental coevolution will be performed to test predictions derived from the geographic mosaic of coevolution theory, using *Brassica rapa* and *Pieris rapae* as plant-pollinator-herbivore model system. The successful applicant will be studying the genomic bases of coadaptation in *Brassica* and *Pieris*, using genomic and phenotypic data. Analyses of selection, GWAS, and co-GWAS will be performed to identify loci that (co)evolve in the interacting organisms.

I am looking for a highly motivated PhD candidate to join my team working on evolutionary question in the context of plant-insect interactions. I offer a vibrant, collaborative work environment and high-quality supervision. Several of my past PhD students have published as first authors in the highest-ranking journals such as *Science*, *Nature Communications*, *New Phytologist*, *Functional Ecology*, etc.; many have consecutively attained PostDoc positions at renowned academic institutions. You should have a Master (or comparable) degree in any field of biology and a thorough interest in evolutionary biology; proficiency in English, both orally and written, is also required. Prior experience in bioinformatics, genomics analyses, GWAS, and scientific publishing is an advantage.

Our department is located in the university botanical gardens and houses modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zürich has a broad research coverage of organismal and molecular biology, and several research groups work on evolutionary topics (www.lifescience-zurich.ch). The city of Zürich also offers excellent quality of life as well as an attractive surrounding for outdoor sports.

If you are interested in the job, please send me by e-mail (florian.schiestl@systbot.uzh.ch) a letter describing your motivation, CV, copy of degrees, publications (manuscripts), and e-mail addresses of two academic referees, by 1st of May 2022 (the job will remain open until filled). Please send all documents in a single file. If you have any further questions, don't hesitate to contact me.

"Florian P. Schiestl" <florian.schiestl@systbot.uzh.ch>
 "Florian P. Schiestl" <florian.schiestl@systbot.uzh.ch>

Vienna PopulationGenetics

PhD positions in Population Genetics - apply by April 21

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:

- Did selfish DNA from Neanderthals infect our human genomes?
- Evolution from de novo mutations - influence of elevated mutation rates.
- Evolution of sex-specific neuronal signaling.
- Impact of para-mutations on the invasion dynamics of TEs.
- Inference of selection signatures from time-series data.
- Invasion dynamics of different TEs.
- Leveraging long-read sequencing for population genetics of TEs.
- Long-term dynamics of local *Drosophila* populations.
- Studying the evolution of gene expression with single cell RNA-Seq.
- Studying speciation during experimental evolution.
- Temperature adaptation in *Drosophila*: phenotypic adaptation.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by April 21, 2022 will be considered. Two letters of recommendation need to be sent directly by the referees.

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 Mathematik, Universität Wien & Institut für Populationsgenetik, Veterinärmedizinische Universität Wien

T +43 1 25077 4302

Julia.Hosp@vetmeduni.ac.at
lia.Hosp@vetmeduni.ac.at

Ju-

WSL Switzerland TreeAdaptation

WSL.Switzerland.AdaptationGenomicsForestTrees

The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is part of the ETH Domain. Approximately 600 people work on the sustainable use and protection of the environment and on the handling of natural hazards.

The Research Unit Biodiversity and Conservation Biology studies the impact of the environment and land use on the diversity of life. In the framework of the ERC Consolidator Grant, MyGardenOfTrees, the Evolutionary Genetics Group (<https://sites.google.com/view/evolgenetgroup>) offers for the duration of 3-years starting as soon as possible a position for a PhD Student in “Adaptation during range expansion in European beech. The Evolutionary Genetics Group is interested in understanding the roles of demography and natural selection in shaping the life-histories and the genetic composition of forest tree populations across the landscape. The group uses field experiments, statistical models, and individual-based computer simulations to answer fundamental evolutionary questions and to aid adaptive forest management decisions. MyGardenOfTrees (<https://www.mygardenoftrees.eu/>) is establishing an unprecedented species range-wide transplant experiment to assess the capacity of growth and regeneration of two forest tree species, European beech and silver fir, as well as their Mediterranean and oriental sister species. The experimental part of the project is based on participatory science and involves foresters all across Europe. Two PhD students will be engaged on this project work-

ing on complementary topics.

The current PhD position will focus on understanding the adaptive and demographic processes that have led to the range expansion of European beech (*Fagus sylvatica* L.) after the last glacial maximum. *Fagus sylvatica* is best considered as a species complex whose current range extends from Spain to northern Iran. Despite the large genetic diversity of beech populations in Minor Asia and on the Balkan peninsula, a single lineage has colonized most of Europe. Did the colonizing lineage have superior performance, and does it outperform other lineages still today? Could current beech die-back across Europe be partly attributed to the reduced genetic diversity due to the expansion load beyond ongoing unprecedented climate change? Could the introduction of other beech lineages and hybridization between them be used to adapt European beech forests to future climate change? The selected PhD student will investigate these questions using a combination of genomics (whole genome sequence data), common garden experiments (performed by foresters) and environmental data. The PhD project will involve roughly 15% field and lab work, 50% data analysis (and simulations), and 35% dissemination and thesis writing.

The ideal candidate holds a Masters degree in evolutionary biology, population genetics, bioinformatics, plant science or in a related discipline and has a keen interest in evolutionary biology, statistics and bioinformatics. Advanced knowledge in R and/or python are necessary and interests in database management is a plus. We are looking for a person who is motivated to pursue a scientific career and who is curious, creative, responsible and can work independently. Fluency in English and excellent written and oral communication skills are expected. The PhD thesis will be supervised by Dr Katalin Csilléry (WSL, leader of the Evolutionary Genetics Group), Prof Dr Yvonne Willi (University of Basel), Dr Christoph Sperisen (WSL), and will be in collaboration with the Genetic Diversity Center of the ETH Zurich. The PhD student will be based at WSL in Birmensdorf with short stays at the University of Basel. The PhD degree will be awarded by the University of Basel and the Zurich-Basel Plant Science Center’s PhD program in Plant science.

Applications, including a motivation letter, a summary of past relevant accomplishments, a CV, and the names and contact details of two referees should be sent to Michèle Bucher, Human Resources WSL, by uploading the requested documents through the WSL webpage: <https://apply.refline.ch/273855/1312/pub/1/-index.html> Applications via email will not be considered. The position remains open until filled. Katalin Csilléry, [katalin.csillery\(at\)wsl.ch](mailto:katalin.csillery(at)wsl.ch), Tel. +41 44 739 23 43, will be happy to answer any questions or offer further infor-

mation. The WSL strives to increase the proportion of women in its employment, which is why qualified women are particularly called upon to apply for this position.

Katalin Csilléry, Group Leader, Evolutionary Genetics Group, Biodiversity and Conservation Biology Unit
Swiss Federal Research Institute WSL, Zürcherstrasse

111, 8903 Birmensdorf, Switzerland Office: Bi MG E floor, Tel:

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BotanicGarden Berlin PlantEvolution

Dear EvoDir community,

the Botanic Garden Berlin looks for an experienced plant taxonomist/systematist to lead the research group “plants” at the Botanic Garden Berlin. You’ll find the job announcement here (in German only): https://www.fu-berlin.de/universitaet/beruf-karriere/-jobs/wiss/59_ze-botanischer-garten-botanisches-museum/BG-Bo-Berlin—Leitung-Pflanzen.html If you know of any interested colleagues, we’d be pleased if

you could forward the information accordingly. Best wishes Eva

Dr. Eva Häffner Wissenschaftliche Koordinatorin
Botanischer Garten Berlin

Telefon: +49 30 838 59964 Mobil: +49 30 176 183 850
63 e.haeffner@bo.berlin

Freie Universität Berlin ZE Botanischer Garten und
Botanisches Museum Berlin Köpenicker Straße 6-8
10175 Berlin

#BoBerlin Internationales Wissenszentrum der Botanik
“Häffner, Eva” <E.Haeffner@bo.berlin> “Häffner,
Eva” <E.Haeffner@bo.berlin>

BrownU ResAssist WildlifeMetagenomics

We are seeking a Research Assistant in Molecular Ecology at Brown University.

Link to the job application: https://brown.wd5.myworkdayjobs.com/en-US/-/staff-careers-brown/jobs/details/Research-Assistant_REQ177255?q=REQ177255 *Job Description:*

The lab of Dr. Tyler Kartzinell at Brown University (www.kartzinellab.com) is seeking a Research Assistant to support research on the diets, microbiomes, and metagenomes of wildlife. The Research Assistant will devote ~80% of their time to specific research projects and the remaining ~20% time to general maintenance and lab support. The Research Assistant will be welcomed as a full lab member and be expected to attend lab meetings and to contribute to a supportive and interactive lab atmosphere. The Research Assistant will interface with varied research facilities including the Brown University Genomics Facility, Brown University Herbarium, Brown Center for Animal Resources and Education and diverse collaborators on our NSF-funded projects around the world. This is a unique opportunity to become deeply involved in exciting research at the interface of ecology, genetics, and conservation. As such, it is well-suited for a college graduate seeking additional experience before graduate school.

The ideal start date will be May or June 2022, with some flexibility possible for the successful applicant. This is a fixed term position with a current end date of April 30, 2023, however this may be extended based on funding and performance.

Responsibilities

- Executing standard molecular biology laboratory protocols involving DNA extraction, PCR, gel electrophoresis, and similar procedures. Keep organized records of research samples and experiments. Collaborate with postdocs and students in the lab when requested by the Principal Investigator.
- General lab maintenance, such as preparing reagents and keeping equipment functional.
- General lab support, such as obtaining purchase orders and placing orders to ensure supplies are kept in stock in coordination with the Principal Investigator.

Qualifications

- Bachelor's degree in life science (biology, molecular biology, ecology, or related sciences).
- Undergraduate research experience or previous experience working in a laboratory setting.
- Basic molecular ecology techniques including sample preparation, DNA extraction, PCR.
- Excellent organization, record-keeping, task-prioritization, and ability to communicate with a diverse team of people.
- Ability to self-motivate and work independently.
- Ability to think critically and solve problems.
- Ability to complete tasks in a timely manner.
- Ability to learn new skills quickly.
- Ability to organize datasets and perform general lab maintenance and support.
- Demonstrated ability to support a community of diverse perspectives and cultures in an inclusive environment.

All offers of employment are contingent upon successful completion of a background check.

Recruiting Start Date:

2022-03-22-07:00

Job Posting Title: Research Assistant

Department: Institute at Brown for Environment and Society

Grade: Grade 7

Worker Type: Employee

Worker Sub-Type:

Fixed Term (Fixed Term)

Time Type: Full time

Scheduled Weekly Hours: 37.5

Position Classification: Onsite

Submission Guidelines:

Please note that in order to be considered an applicant for any staff position at Brown University you must submit an application form for each position for which you believe you are qualified. Applications are not kept on file for future positions. Please include a cover letter and resume with each position application.

Vaccination Requirements:

In order to maintain 90% or greater universal vaccination rates on campus, all newly hired employees at Brown University must receive the final dose of the COVID-19 vaccine before they begin work, unless they are approved for a medical or religious exemption. All employees must also receive a COVID-19 booster within thirty (30) days of becoming eligible. For more information, please visit the Healthy Brown site.

Still Have Questions?

If you have any questions you may contact employment@brown.edu.

EEO Statement:

Brown University is an E-Verify Employer.

Brown University is committed to fostering a diverse and inclusive academic global community; as an EEO/AA employer, Brown considers applicants for employment without regard to, and does not discriminate on the basis of, gender, sex, sexual orientation, gender identity, national origin, age, race, protected veteran status, disability, or any other legally protected status.

Tyler Kartzinel Peggy and Henry D. Sharpe, Jr. Assistant Professor of Environmental Studies Brown University

— / —

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>

Caltech Tech FunctionalGenetics

The Parker lab at Caltech is searching for a functional genetic technician to generate evoldir@evol.biology.mcmaster.ca the study of behavior and chemical ecology. The successful applicant will work with the Principal Investigator and lab members (graduate students and postdocs) to establish and maintain engineered beetle lines created using CRISPR/CAS9 gene editing and transposon-mediated lab at Caltech is searching for a functional genetic technician transgenesis technologies.

The position requires competence in molecular biology techniques for the design and construction of plasmid vectors and sgRNAs for insect genome engineering. The position also demands careful screening and husbandry of insect cultures. Necessary bioinformatic skills can be acquired through training in the Parker lab (<https://www.beetles.caltech.edu/>)

Job Duties:

- Molecular biology methods (DNA/RNA extraction, PCR, cloning, DNA synthesis).
- Design and synthesis of sgRNAs and transformation vectors for gene editing and transgenic manipulation of rove beetles.
- Screening and husbandry of transgenic and mutant rove beetles to

- establish stable genetically modified lines.
- Work with genomic and transcriptomic data for the above tasks.
- Maintenance of genetically modified beetles.
- Work with postdocs and students on design and engineering of project-specific genetic constructs.

Basic Qualifications:

BS in a biology-related field with a minimum of 2 years of relevant work experience. Demonstrated molecular biology experience.

Preferred Qualifications:

Experience with insect genetic manipulation. Experience with plasmid design and construction. Experience with insect transgenesis. Experience with insect rearing/husbandry.

Required Documents:

Resume

Apply: <https://phf.tbe.taleo.net/phf03/ats/careers/v2/viewRequisition?org=CALTECH&cws=37&rid=-6514> For more info contact: joep@caltech.edu

Joe Parker, Ph.D. California Institute of Technology Division of Biology and Biological Engineering 1200 E. California Blvd. MC 216-76 Pasadena, CA 91125

Tel: +1 626 395 8729 <https://www.beetles.caltech.edu/> "Parker, Joseph" <joep@caltech.edu>

ClemsonU MolecularGeneticsTechnician

The Clemson University Center for Human Genetics and the Greenwood Genetic Center have been awarded a five year Phase I COBRE in Human Genetics grant to understand the genetic, genomic, and epigenetic mechanisms by which molecular genetic variation affects transcriptional and other molecular networks in health and disease. The Research Core of the COBRE in Human Genetics is seeking a Molecular Genetics Technician to support the genomics research of Research and Pilot Project Leaders and their laboratories. Ideally, the successful applicant will have previous molecular biology and genomics experience, including (but not limited to) basic molecular biology and next generation sample and library preparation for Illumina short read and Pacific Biosciences long read sequencing. However, this is not required and training in these techniques will be provided. Salary will be commensurate with credentials

and experience.

Enquiries should be addressed to Dr. Trudy F. C. Mackay, Self Family Endowed Professor and Director of the Center for Human Genetics, Clemson University, Self Regional Hall, 114 Gregor Mendel Circle, Greenwood, SC 29646 (tmackay@clemson.edu). Applications must include a cover letter explaining the qualifications for this position and the names of three references. The position is available immediately. Clemson University is an equal opportunity employer.

To apply, go to jobs.clemson.edu and apply for job ID 106592.

TRUDY F. C. MACKAY, PhD, FRS

SELF FAMILY ENDOWED CHAIR OF HUMAN GENETICS

DIRECTOR, CENTER FOR HUMAN GENETICS

PROFESSOR OF GENETICS AND BIOCHEMISTRY

Center for Human Genetics

Clemson University

110 Self Regional Hall

114 Gregor Mendel Circle

Greenwood, SC 29646

w 864-889-0522

c 919-604-6531

tmackay@clemson.edu

Trudy Frances Charlene Mackay
<tmackay@clemson.edu>

CornellU 2 ResTech CnidarianEvolution

Research Technician in the Babonis Lab at Cornell University

In the Babonis Lab, we use the dynamic processes of embryogenesis and tissue morphogenesis to understand how novel traits arise. We seek to hire a highly motivated junior research technician (postbac) and a senior technician (lab manager) to work in a research lab dedicated to studying the cellular, molecular, and developmental biology of cnidarians (corals, sea anemones, jellyfish).

Primary responsibilities for the technicians will be to support ongoing research in the lab and to oversee

maintenance of the animal colony (sea anemones, tube anemones, and corals). Animal maintenance includes preparing seawater, maintaining animal-safe conditions, cleaning animal dishes, feeding/preparing adults for spawning, and caring for embryos. This portion of the research requires the ability to carry 5 gallons of water (~40 lbs) over short distances. The technicians will also assist in the generation and phenotypic analysis of mutations produced by genome editing (CRISPR/Cas9) in sea anemones. Analyses associated with this research include extracting genomic DNA, performing PCR and gel electrophoresis, molecular cloning, and basic DNA sequence analysis. The technicians will analyze phenotypes in wildtype and mutant animals using in situ hybridization, immunofluorescence, and RNA extraction for quantitative PCR. Many of these techniques will require the use of microscopy (light, confocal, and electron microscopy). An additional portion of the work will involve general lab maintenance, including: ordering and organization of consumables, assisting in the training of incoming students and postdocs in relevant techniques, and summarizing data, preparing figures, and reporting results at lab meetings. Specific duties will be coincident with experience.

Both positions are full-time (39 hrs/wk), one-year appointments with the possibility of extension annually based on continued available funding and successful work performance. Review of applications will begin May 1, 2022 and the positions will remain open until filled.

For additional details and to apply, visit:

Junior tech position (postbac): https://cornell.wd1.myworkdayjobs.com/en-US/-/CornellCareerPage/job/Ithaca-Main-Campus/-Lab-Research-Technician—Dept-of-Ecology—Evolutionary-Biology—Technician-III_WDR-00030793-1 Senior tech position (lab manager): https://cornell.wd1.myworkdayjobs.com/en-US/-/CornellCareerPage/job/Ithaca-Main-Campus/Sr-Lab-Technician-Lab-Manager—Dept-of-Ecology—Evolutionary-Biology—Technician-IV_WDR-00030794-1 Leslie Babonis <lsb257@cornell.edu>

NatHistMuseum Luxembourg CuratorEcology

Job: NatHistMuseum.Luxembourg.CuratorEcology

The National Museum of Natural History of Luxembourg is hiring a replacement for a retiring Curator (senior researcher) in Ecology. We encourage all interested parties to apply, especially if you have experience in research on invasive species. People with molecular experience are welcome. The detailed job description can be (in French) under <https://tinyurl.com/45kzjj32> or in English below. It is a strict requirement that applicants have to be EU nationals and that they are fluent (written and spoken) in one of the three administrative languages of Luxembourg (Luxembourgish, French or German). The deadline for applications is the 27th of May 2022. The email address of a person taking general enquiries can be found on <https://tinyurl.com/45kzjj32>. If you decide to apply via the website given above, you need to postulate as an “Employé; $\frac{1}{2}$ ”. Hope to see you soon in Luxembourg!

Job advertisement Who is recruiting? National Museum of Natural History - Collections and Research - Ecology Section The National Museum of Natural History is a cultural and research institute located in the Grund. Its Collections and Research department studies and documents natural heritage, geodiversity and biodiversity in general and ecology and exotic species in particular.

Tasks Contribute to the museum’s activities and projects related to biodiversity and ecology; Design and implementation of scientific research projects in the field of biodiversity and ecology; Invasive alien species: monitoring species, coordinating and feeding the neobiota.lu internet portal, representing the Museum in national and European working groups on invasive alien species; Creation of a network of applied research actors in the field of biodiversity protection and ecology to ensure knowledge transfer; Exchange of expertise with museum sections and external institutions; Exchange and analysis of data from different species groups; Organisation of national and international scientific conferences and symposia; Writing of reports, practical guides and scientific publications; Accompanying university students in their final studies (bachelor, master, doctorate, postdoc) in the framework of the Museum’s projects; Organisation of and contribution to exhibitions at the Museum; Organisation of and participation in the Mu-

seum’s awareness-raising and popularisation activities. Profile Technical skills

Excellent project management skills in the field of ecology and biodiversity research at national and international level; Excellent knowledge of native species and habitats, including methods of species recording in the field, with a focus on species ecology and habitat management, in relation to maintaining species populations and target habitats; Good knowledge of invasive alien species; Good knowledge of statistical data analysis, GIS and the use of the Recorder-Lux database; Proficiency in writing scientific reports and publications; Very good writing and speaking skills; Experience in managing working groups and in supervising final year university projects (master, bachelor, doctorate) and postdocs; Experience in acquiring external funding; Knowledge of national and European legislation and regulations in the field of nature protection; Good oral and written knowledge of one of the three administrative languages of the country and of English.

Assets

Possession of a PhD in natural sciences (ecology, biology, environmental sciences); Additional experience in a museum context in the fields of: collections, environmental education, scientific communication and popularisation, exhibitions, etc; Basic knowledge of the other two administrative languages; Good knowledge of office tools (Word, Excel, Outlook, Powerpoint, Skype, Zoom, InDesign); Mastery of the management of a CMS such as Wordpress.

“Alain.FRANTZ@mnhn.lu”
<Alain.FRANTZ@mnhn.lu>

NorthEasternU TeachingBioinformatics

Job: Assistant/Assoc Teaching Professor of Bioinformatics at Northeastern

Review of applications begins on April 15

About the Opportunity

The successful applicant will have the knowledge to develop and teach Bioinformatics courses at the Master's level. The person in this position reports to the Director of the Biotechnology and Bioinformatics Programs.

Responsibilities:

Assistant /Associate Teaching Professor is sought to teach full time in the College of Science Bioinformatics Professional Science Master's (PSM) Program. This position is located at the Northeastern University Boston Campus. The Bioinformatics PSM degree program is designed to allow students to pursue advanced training and excel in bioscience while simultaneously developing highly valued business.

The Assistant/Associate Teaching Professor will teach six (6) courses per academic year in the Bioinformatics Program. This role will work on growing the enrollment in the Department's Professional Master's program in Bioinformatics, and work with the Program Director and the Dean's Office to expand the range of concentrations offered. Teaching responsibilities are subject to modification based on the program's needs and at the Director of Bioinformatics Programs' discretion based upon time commitment of the service requirement. This unique position seeks to integrate professional practice into the classroom, specifically with respect to the Bioinformatics and Data Science market in Biotech and Pharma.

Teaching responsibilities include the following: review and learning of key teaching points within existing instructor guides, and a willingness to support high-quality teaching and standards through preparation of lectures based on course materials provided; effective facilitation of rich, respectful debates and discussions in an in-person or online class; timely review and grading of assignments with appropriate coaching and feedback to the students; consistent connection with students and their performance; adherence to Northeastern's policies.

Qualifications:

Candidate must have a Ph.D. in Biotechnology, Bioinformatics, Cellular Biology, or related field by the appointment start date, and commitment to teaching excellence at the university level. Candidates with expertise in Genetics or Evolution with considerable bioinformatics experience are welcome to apply. Candidate should possess relevant programming languages as well as a thorough understanding of leading computational approaches to bioinformatics. Position requires excellent communication skills and the ability to work productively and successfully interact with students, faculty, staff, and industry partners. Demonstrated industrial experience in the biotechnology industry desirable, but not required.

Diversity at Northeastern:

Northeastern University is an equal opportunity employer, seeking to recruit and support a broadly diverse community of faculty and staff. Northeastern values and celebrates diversity in all its forms and strives to foster an inclusive culture built on respect that affirms inter-group relations and builds cohesion.

All qualified applicants are encouraged to apply and will receive consideration for employment without regard to race, religion, color, national origin, age, sex, sexual orientation, disability status, or any other characteristic protected by applicable law.

To learn more about Northeastern University's commitment and support of diversity and inclusion, please see www.northeastern.edu/diversity . Apply Here:

https://northeastern.wd1.myworkdayjobs.com/en-US/careers/job/Assistant-Associate-Teaching-Professor-Bioinformatics_R103927 Review of applications begins on April 15

For more information contact Kevin Broadbelt: <https://cos.northeastern.edu/people/kevin-broadbelt/>

"Lotterhos, Katie" <k.lotterhos@northeastern.edu>

PennsylvaniaStateU SymbiosisEvolutionMicrobiome

Several Positions on Reproductive Symbiosis, Gut Microbiome, and Evolution

A lab manager, postdoc, or research professor position is available to work on the evolutionary genetics of animal-bacteria-phage symbioses and animal microbiomes/viromes in the lab of Seth and Sarah Bordenstein

at Penn State University in University Park, PA. Key focal areas include functional genetics of selfish reproductive symbioses in insects, computational analyses of microbiome/virome variation across humans, and the microbiology of host speciation.

Current Lab Research Directions:

- Genetics and mechanisms of the competition between Wolbachia endosymbionts, bacteriophage, and host sexual reproduction using transgenics, cell biology, reproductive biology, microscopy, and multi-omics
- Patterns and causes of human microbiome and virome variation using multi-omic data, statistical tests, epidemiology, social sciences, machine learning, and wet lab experiments
- Functional genetics of bacteriophage lysis in animal endosymbionts using protein purifications, enzyme assays, cell culture, and transgenics
- Microbiome-assisted speciation of hosts and phylosymbiosis

Additional Information:

The full position description and application link with relevant papers are here: <https://jobrxiv.org/job/-pennsylvania-state-university-microbiome-center-huck-institutes-of-the-life-sciences-departments-of-biology-and-entomology-27778-research-positions-on-symbiosis-and-the-microbiome-sciences/> The Bordenstein lab (<https://lab.vanderbilt.edu/bordenstein/>) is moving to Pennsylvania State University at University Park in the summer of '22 to direct the Microbiome Center in the Huck Institutes of the Life Sciences and join the Departments of Biology and Entomology in the Eberly College of Science and College of Agricultural Sciences. Pennsylvania State University is an innovative hub of life science research with 16 National Academy of Science members, 24 campuses, numerous outdoor adventures, a thriving life sciences enterprise with centers and institutes, and 18 disciplines ranked in the top ten nationally for research expenditures.

Applications:

If interested, please email inquiries to s.bordenstein@psu.edu in a single pdf with (i) a cover letter that summarizes start date and the relevant experience / specific reasons for interest in the research position; (ii) a CV that includes contact information for three+ references (name, position, mailing address, telephone number, and e-mail address); and (iii) 1st authored publications, posters, and lectures.

s.bordenstein@psu.edu

PurdueU GenomicsLabManager

Genomics Laboratory Manager

Job Summary

The Genomics Laboratory Manager will provide management, oversight, supervision, and maintenance of research labs in Department of Forestry and Natural Resources on the Purdue University campus, including genomics lab (PFEN 141), tree physiology lab (PFEN 158), and forest ecology, silviculture & soils lab (PFEN G041). In this role, you will be responsible for oversight of all activities taking place in afore mentioned labs. Additional duties will include:

Curate collections of biological samples (e.g., animal tissue, seeds, etc.) and the raw, unpublished research data produced by students or visiting scientists (e.g., DNA sequence, GIS, phenology, etc.) in a logical, effective, and accessible manner

Train students and visiting scientists how to use/search the databases and find biological samples in the freezers

Assist with bioinformatic analyses of nucleotide sequence data using R or other platforms

Ensure proper maintenance and coordinated use of laboratory equipment

Maintain inventories and order supplies

Train and oversee departmental personnel, students and visiting scientists in proper and safe methods, techniques and procedures for use of specific research equipment

Maintain compliance with relevant federal, state and university safety regulations for the laboratories and relevant animal use regulations for departmental animal care facilities

Ensures quality control within labs

Prepare and maintain common use chemicals and biologicals

Monitor freezers and respond/react to failures in a timely fashion

Coordinate personnel activity, manage projects, assist with and conduct specific research projects

Help design experiments and research

Participate in the development and implementation of policies along with faculty directors of the labs

Perform other organizational and administrative duties as assigned

Required: Bachelor's degree in wildlife, fisheries, forestry, biology, chemistry, biochemistry, molecular biology, or related field 2 years of general laboratory experience (or MS degree plus one year of experience) Immersive research experience Strong organizational and communication skills Skills with equipment and protocols used in chemical and molecular analyses Ability to diagnose/troubleshoot equipment failures Knowledge of purchasing procedures knowledge of BSL-2 safety procedures and associated work Knowledge of relevant safety procedures Computer skills (e.g., MS Office, R and other statistical analyses, etc.) Basic skills in pipeline analyses of genomic and transcriptomic sequence data

Preferred: Experience with supervision of technical personnel Experience with various computational platforms (e.g., Mac, PC, Unix, etc.)

Additional Information: Purdue will not sponsor an employment related visa for this position A background check will be required for employment in this position FLSA: Exempt (Not Eligible For Overtime) Retirement Eligibility: Defined Contributions Waiting Period Purdue University is an EOE/AA employer. All individuals, including minorities, women, individuals with disabilities, and veterans are encouraged to apply

Prof. Andrew DeWoody Depts. of Forestry & Natural Resources and Biological Sciences Purdue University West Lafayette, IN, USA dewoody@purdue.edu 765-491-6109

RBG Kew ResLeader FungalEvolution

Research Leader - Comparative Fungal Biology

<https://careers.kew.org/vacancy/research-leader-comparative-fungal-biology-481146.html> The Royal Botanic Gardens, Kew (RBG Kew) is a leading plant science institute, UNESCO World Heritage Site, and major visitor attraction. Our mission is to understand and protect plants and fungi for the well-being of people and the future of all life on Earth. We are working to end the unprecedented extinction crisis and to help create a world where nature is protected, valued by all and managed sustainably. We will achieve these goals by drawing on our leading scientific research, unrivalled collections of plants and fungi, global network of

partners, inspirational gardens at Kew and Wakehurst, and our 260 years of history. Join us on our journey as protectors of the world's plants and fungi.

Reporting to the Senior Research Leader in Comparative Fungal Biology, you will be an outstanding and inspiring scientist with a relevant PhD and post-qualification experience in fungal biology and evolution, comparative genomics, metagenomics, and/or phylogenomics. You will be responsible for leading your own research group, providing day-to-day supervision for post-docs, PhD students, Future Leader Fellows, and integrating the team's activities broadly throughout Kew Science.

We are looking for someone with innovative ideas seeking to develop their career as an independent researcher, leader and mentor, with interest for teaching and outreach. We want you to have a collaborative outlook to support and enhance Kew's mycological research, working with all relevant stakeholders across Kew Science, and to engage with the broader strategic landscape of Kew as a whole.

Please upload a research plan with your application form.

The salary will be 38,200 per annum.

This role is based at Kew with the option of regular home working, subject to operational requirements.

Our fantastic benefits package includes opportunities for continuous learning, a generous annual leave entitlement, flexible working to help you maintain a healthy work-life balance, an Employee Assistance Programme and other wellbeing support such as cycle to work scheme and discounted gym membership. We also offer a competitive pension, an employee discount scheme and free entry into a wide range of national museums and galleries, as well access to our own beautiful gardens at Kew and Wakehurst.

If you are interested in this position, please submit your application through the online portal:

<https://careers.kew.org/vacancy/research-leader-comparative-fungal-biology-481146.html> We are committed to equality of opportunity and welcome applications from all sections of the community. We guarantee to interview all disabled applicants who meet the essential criteria for the post.

Dr. Ester Gaya Senior Research Leader | Comparative Fungal Biology Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK Tel.:+44(0)208 332 5381 Email: e.gaya@kew.org

Ester Gaya <ester.gaya@gmail.com>

RBG Kew ResLeader FungalEvolution DeadlineExtended

Research Leader - Comparative Fungal Biology

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Ester Gaya <ester.gaya@gmail.com>

RBG Kew ResLeader PlantEvolution

Research Leader - Comparative Fungal Biology

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Dr. Ester Gaya Senior Research Leader | Comparative Fungal Biology Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK Tel.:+44(0)208 332 5381 Email: e.gaya@kew.org

Ester Gaya <ester.gaya@gmail.com>

RZSS Edinburgh Zoo Conservation Genetics Biobank

RZSS WildGenes Biobank Coordinator

Location: Royal Zoological Society of Scotland - Edinburgh Zoo

About Us

The charity that owns both RZSS Edinburgh Zoo and RZSS Highland Wildlife Park are looking for committed, compassionate and conservation-minded individuals to join our expert staff team. RZSS aims to connect people with nature and safeguard species from extinction, a mission that sees us work both here in Scotland and in over 20 countries around the world. From inspiring the next generation about wildlife in our parks to protecting chimpanzees in the Ugandan rainforest; looking after some of the world's most endangered species to saving the Scottish wildcat, RZSS is making a huge difference and we need your help to continue to grow.

The role

The Royal Zoological Society of Scotland's WildGenes team are looking for a Biobank Coordinator. Based at Edinburgh Zoo, the post will involve the archiving of genetic material for the long-term preservation of DNA from animals in zoo collections, processing donations and loans from zoos in the UK, and providing samples to conservation researchers across Europe. Our biobank is one of the four biobank hubs within the European Association of Zoos and Aquaria network as well as being a member of the Cryoarks initiative (www.cryoarks.org), a UK based partnership that is standardising approaches to biobanking within the university, zoo and museum sectors. A key part of the role will be supporting the management of these existing partnerships as well as the day-to-day running of the facility so we can safeguard genetic samples for the benefit of conservation research both now and into the future. It is a part-time 3-year fixed term role working 22.5 hours per week.

Who we are looking for

The successful candidate will hold a BSc in a relevant scientific discipline plus job experience in a relevant role. Ideally, they will have knowledge of standard molecular genetic laboratory techniques and the preservation of DNA as well as excellent communication skills for working with project partners including those in the university, zoo and museum sectors.

Salary

The position sits within Band C (£21,747 - £24,923 Per Annum for FT equivalent position)

Interested?

For full information on how to apply, please visit the RZSS vacancy page and follow the instructions: <http://www.rzss.org.uk/job-vacancies/> Closing date: Sunday 1st May 2022

Invitation to interview will be by email/phone during the 3rd week of May 2022.

For any questions and queries, please email Dr Alex Ball

at aball@rzss.org.uk quoting Biobank Coordinator as the subject.

Our mission is to connect people with nature and safeguard species from extinction.

The RZSS strives to be an equal opportunities employer. Registered Charity SC00406

Alexander Ball <aball@rzss.org.uk>

Senckenberg Bioinformatician

For over 200 years the Senckenberg Gesellschaft für Naturforschung represents one of the most relevant institutions investigating nature and its diversity. Currently, scientists from more than 40 countries conduct research in the fields of biodiversity, earth system analysis and climate change in seven Senckenberg Institutes across Germany.

Following its mission to analyse and document biodiversity in earth system dynamics - to serve science and society, Senckenberg fosters curiosity-driven and application-oriented research. In Senckenberg at Frankfurt we seek to fill the position of a

Bioinformatician (m/f/d)

(full time)

This position is funded by a five-year project designed to combine cutting edge technology for studying both the anatomical and genomic basis for evolutionary novelties in molluscs, and test whether genomic novelties are more strongly associated with armour and shell morphology or rather physiological adaptations that allow the invasion of new niche spaces.

Your job would be to provide bioinformatics capacity especially in de novo genome assemblies of mollusc species.

Your tasks:

Genome assembly and annotation of mollusc species that are sequenced via the LOEWE TBG and external partners using state-of-the-art sequencing technologies and compute infrastructure Support other members of the research group working on morphological features to identify specific research questions Perform independent research in collaboration with other members of the research group, the LOEWE-TBG, Senckenberg Ocean Species Alliance, and external collaborators on molluscan genomics Perform comparative analyses of resulting genomes including for phylogenomics

Your profile:

Master degree or equivalent training and experience in bioinformatics / computational biology, genomics or a related area; a PhD degree in these fields is an advantage but not strictly required Experience with shell scripting and Unix tools Previous experience in genomics, genome assembly and/or annotation using non-model organisms, preferably molluscs Familiarity with measures of genome assembly data quality and completeness, troubleshooting, screening data for contamination Genuine curiosity and interest in nature, the oceans and their inhabitants, and especially molluscs What can you expect?

An interesting and challenging task in a dynamic and stimulating team of researchers, technicians and communicators Excellent benefits and work-life balance: Flexible working hours - dual career service - leave of absence due to family reasons - parent-child-office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt - leave of 30 days/ year

Senckenberg supports equal opportunity for men and women and places an emphasis on fostering career opportunities for women and under-represented groups. Qualified women and other under-represented groups are strongly encouraged to apply. Equally qualified applicants with disabilities will be given preference.

Senckenberg is a globally connected institute. The working language within this project is English. Frankfurt is a vibrant, international, culturally diverse city and one of the world's travel hubs. We welcome candidates from all nations and will provide support with your relocation process.

Location: Frankfurt am Main

Volume of employment: 100 % full-time position (40 weekly working hours)

Type of contract: Employment shall start as soon as possible and will be limited for a two-year contract

Would you like to apply?

Please submit two documents as email attachments:

download and complete the information form for this position from <http://sosa.senckenberg.de>. This form will be considered anonymously and will be used for the initial short-listing process a single pdf including a cover letter and your CV (not anonymous), including names and contact details of three professional references. The one-page cover letter should address your fit to the advertised position as described above. Use the code created for the form for "blind review" also in the cover letter and in the file name Please submit two files (see above), mentioning the reference of this

job offer (#01-22014) until 11 May 2022 by e-mail to: recruiting@senckenberg.de.

For more information, please contact Prof. Dr Julia Sigwart (julia.sigwart@senckenberg.de).

Mit freundlichen Grüßen / Yours sincerely

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung

(Rechtsfähiger Verein gemäß § 22 BGB)

Senckenberganlage 25

60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG)

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales

- 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting)

- 1478 Gajcevic, Isabel

- 1564 di-Biase, Maria

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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>

StanfordU LifeSciTech EvolutionaryGenomics

The Petrov lab in the Department of Biology at Stanford University, (<http://petrov.stanford.edu/>) has a position for a full-time research assistant at the Life Science Technician I level with interests in genomics, evolutionary, or molecular biology.

The main responsibilities of the successful candidate will be performing high-throughput DNA extractions and library preparation for next-generation sequencing. These duties will largely be carried out using existing protocols, though protocol optimization and use of new

lab equipment is expected. One year or more full-time lab experience and experience with handling samples in high throughput formats (plate-based) is preferred. Please include your CV with GPA and a cover letter with a description of your research interests and career goals.

The full position description and application link are here: <https://careerssearch.stanford.edu/jobs/-life-science-technician-1-16488?et=1INEfr2p3> Life Science Technician 1 in School of Humanities and Sciences, Stanford, California, United States < <https://careerssearch.stanford.edu/jobs/life-science-technician-1-16488?et=1INEfr2p3> > This position is represented by SEIU Local 2007 and the collective bargaining agreement between the university and SEIU Local 2007 governs the terms..... careerssearch.stanford.edu Tuya Yokoyama

Tuya Yokoyama <osmo3@stanford.edu>

TrinityU TeachingEvolBehavior

One year lecturer- Animal Behavior, Trinity University <https://www.trinity.edu/human-resources/-employment-opportunities/faculty/38526> <https://www.trinity.edu/human-resources/employment-opportunities/faculty/38526>

UAberdeen FieldWork ClimateAdaptation

Paid summer entomological field work in Norway and Finland The Lancaster Lab within the University of Aberdeen School of Biological Sciences (Aberdeen UK) is looking for a short-term research technician (3 months) to join our team to investigate ecological and evolutionary processes associated with range shifts caused by climate change. As climates are warming, many species, and particularly insects, are moving to higher latitudes that have become newly suitable. To better understand this process, our team will be travelling to Norway and Finland in summer 2022 to conduct latitudinal sampling transects of the rapidly-range expanding insect species, the blue-tailed damselfly (*Ischnura elegans*). Fieldwork

will be conducted by a postdoctoral research associate and 1-2 research technicians (this post). The job requires field sampling (capturing damselflies by net), and taking field data and samples to a high quality and precision.

Good identification skills are a plus, as is the ability to occasionally work long hours in the field under various weather conditions. Previous fieldwork experience a plus. Job open to UK and EU applicants.

Salary will be approx. $\dot{i}_{\frac{1}{2}}$ 20,000 pa with placement according to qualifications and experience; travel expenses will further be covered.

We aim to have someone in post by May 20, 2022, and the first review of applications will be April 15, 2022.

Please send informal enquiries or CV and cover letter to Lesley Lancaster, e-mail:lesleylancaster@abdn.ac.uk

Lesley Lancaster <lesleytherese@gmail.com>

UAmsterdam EvolutionaryEcology

At the Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, we seek to appoint an early career assistant professor for a tenure track in the area of Evolutionary Ecology in rapidly changing environments.

At IBED, we investigate how species relationships determine the structure and stability of biological communities, and how the integrity of these communities is influenced or compromised by processes such as species extinction, the introduction of non-native invaders, and the growth of harmful species. Within EPB, our research comprises fundamental and applied investigations at the level of individual variation, population genetics and community dynamics, to understand the process of speciation, the evolution of resistance, the evolution of endangered and invasive species, and evolution in the face of climate change. Specifically, we are working on evolutionary questions related to plant communities, plant-herbivore, herbivore-herbivore, predator-herbivore and host-pathogen interactions, both within and between species.

We are looking for candidates that can complement the research program of the department of Evolutionary and Population Biology (EPB, see<https://ibed.uva.nl/content/research-departments/epb/epb.html>) at IBED, that covers a broad range of topics related to the

eco-evolutionary dynamics of species interactions in challenging environments. The ideal candidate will also strengthen collaborations between existing research lines within EPB as well as within IBED, and link fundamental research on evolutionary ecology with applied areas such as (urban) planning, nature conservation or pest management and values public engagement and outreach.

As for education, the EPB Department is involved in the educational programs of the BSc-programs (i) Biology and (ii) Future Planet Studies, and the MSc-programs (i) Ecology and Evolution and (ii) Future Planet Ecosystem Science, and teaches courses in the fields of behavioral and physiological biology, (field) ecology, neurobiology and evolutionary biology, among others.

More specific information on the job profile, salary and qualification requirements can be found in this link: <https://vacatures.uva.nl/UvA/job/Tenure-Track-Assistant-Professor-in-Evolutionary-Ecology-in-Rapidly-Changing-Environments/746023102/>. If you have more questions about this vacancy, you can contact Astrid T. Groot, Head of the Department of Evolutionary and Population Biology (EPB), a.t.groot@uva.nl.

Do you recognize yourself in the job profile? Then we look forward to receiving your application by 20 May 2022. Please note that applications can only be done online through the link above. The University of Amsterdam is actively promoting to increase diversity and inclusion at the faculty level. Even though this position is open to all early-career scientists in the field of evolutionary ecology, we especially encourage early-career scientists from underrepresented minorities to apply, and in case of equal suitability priority will be given to these scientists.

Prof. dr. Astrid T. Groot Department head Evolutionary and Population Biology (EPB) Institute for Biodiversity and Ecosystem Dynamics (IBED) University of Amsterdam Visiting address: Science Park 904, 1098 XH Amsterdam Postal address: P.O. Box 94240, 1090 GE Amsterdam Room nr. C3.210 +31 20 525 5400 a.t.groot@uva.nl Personal website Department website

Astrid Groot <a.t.groot@uva.nl>

UBirmingham Bioinformatics

University of Birmingham UK - Data Analyst in Bioinformatics and Biostatistics - School of Biosciences - 99486 <https://bham.taleo.net/careersection/-external/jobdetail.ftl?job=220000PH&tz=-GMT%2B01%3A00&tzname=Europe%2FLondon>

Background

To undertake data analysis of multi-omics datasets generated by the Environmental Genomics Group within the research fields of environmental change, evolution and ecotoxicology.

Summary of Role

Analyse data generated with high throughput sequencing technologies within specified research grants and contribute to writing research outputs Analyse and interpret research findings and results with the support of a project leader Contribute to undergraduate and postgraduate student supervision Support research in the group through expert analytical support

Main Duties/Responsibilities

Carry out bioinformatics data analysis on transcriptomics, genomics, methylomics and ATAC Seq data generated from experimental exposures Develop appropriate pipelines or skilfully use existing pipelines for multi-omics data analysis Analyse and interpret data, applying biostatistics on high throughput multi-omics posters Contribute to satellite projects in the field of ecotoxicology, metagenomics and metabarcoding Support the work and development of PhD students in research related work Provide guidance, as required, to support staff and any students who may be assisting with the research Develop research objectives and proposals for own or joint research, with assistance of a mentor if required Apply knowledge in a way that develops new intellectual understanding Present research outputs, including drafting academic publications or parts thereof, for example at seminars and as posters Contribute to public engagement activities of benefit to the College and the University, often under supervision of a project leader Undertake management/administration arising from research Deal with problems that may affect the achievement of research objectives and deadlines Decide in consultation with the principal investigator as appropriate, on the most appropriate way of undertaking the specified research activities Decide in consultation with

the principal investigator as appropriate how to analyse and interpret the data from the specified research activities Decide in consultation with the principal investigator as appropriate what knowledge to draw on and how to apply it to develop new intellectual understanding Promotes equality and values diversity acting as a role model and fostering an inclusive working culture Person Specification

PhD-degree or near completion in bioinformatics, computational biology or biology with demonstrated computation skills. Alternatively a Master in one of the fields mentioned is acceptable if accompanied by a demonstrated hands-on experience of at least 3 years. Demonstrated skills in biostatistics Literacy in machine learning is preferred A short postdoctoral experience is preferred but not required Analytical capability Ability to identify analytical tools most suitable to the researchability to communicate complex information clearly Ability to work both independently and as a teamability to assess resource requirements and use resources effectively Understanding of and ability to contribute to broader management/administration processes Contribute to the planning and organising of the research programme and/or specific research project Knowledge of the protected characteristics of the Equality Act 2010, and how to actively ensure in day today activity in own area that those with protected characteristics are treated equally and fairly

Informal enquires to Dr Luisa Orsini, email:l.orsini@bham.ac.uk

Luisa Orsini <l.orsini@bham.ac.uk>

UCalifornia Berkeley LabManager PupfishCichlidEvolution

The Martin Fish Speciation Lab seeks an enthusiastic and detail-oriented part-time laboratory manager for research on the rapid evolution and ecological diversification of new fish species. Primary responsibilities will involve caring for laboratory pupfish and cichlid colonies, molecular genetics, behavioral data collection, and specimen curation in the Museum of Vertebrate Zoology. Tasks include daily feeding and maintenance of the fish colonies, maintenance of recirculating aquatic systems, DNA extractions and genomic library preparation, curation and dissection of preserved fish specimens, behavioral observations, and training undergraduate researchers. Interest in ichthyology, evolution, genomics,

and ecology is highly desirable. This position would be excellent preparation for graduate school and there will be opportunities to pursue independent research interests.

Pupfishes present a rare opportunity to investigate the recent origins of a spectacular adaptive radiation and the evolution of novel niches (e.g. scale-eating) localized to a single Bahamian island despite thousands of similar Caribbean environments. Our lab also investigates Cameroon crater lake cichlids, one of the most celebrated examples of sympatric speciation in nature, and the role of gene flow in their diversification.

Education and Experience Required:

We are seeking applicants with strong attention to detail who are thorough, well-organized, and able to work collaboratively with other researchers. Preferred qualifications include a B.S. or B.A. in Biology (or related field) and either some molecular training or experience with animal care. However, no previous research experience is necessary; on-the-job training will be provided for all tasks. The successful applicant will enjoy caring for animals in a low-stress and flexible work environment. Those with a passion for aquarium fishkeeping and possible interest in applying to graduate school are strongly encouraged to apply. For more information on our research, please check out our website <<http://ib.berkeley.edu/labs/martin/>> . Salary:

This will initially be an hourly position with the possibility for a permanent staff position after one year. Salary is \$20 per hour plus benefits. Work schedule is flexible and includes some weekend fish care responsibilities, but is expected to be approximately 20 hours per week.

Start Date: Late spring or summer 2022 (or sooner if desired). This position is for one year with the potential for a permanent staff position after one year.

To apply, please email Chris Martin (chmartin@berkeley.edu) within the next two weeks with your resume/CV, GPA, and describe why you are interested in this position, career goals, and any past research or animal care experience.

The position is listed here: https://careerspub.universityofcalifornia.edu/-/psp/ucb/EMPLOYEE/HRMS/c/-HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=-HRS_APP_JBPST&Action=U&FOCUS=-Applicant&SiteId=21&JobOpeningId=-33668&PostingSeq=1 However, please reach out to me directly before applying through the portal. Applications will be reviewed on a rolling basis starting next week.

Christopher Martin Assistant Curator of Ichthyology, Museum of Vertebrate Zoology Assistant Professor, Department of Integrative Biology University of California, Berkeley <http://ib.berkeley.edu/labs/martin/> @fishspeciation

chmartin@berkeley.edu

UCalifornia Irvine LabTechManager Genomics

The Lee lab in the Department of Ecology and Evolutionary Biology at the University of California, Irvine invites applications for an Assistant specialist (technician/lab manager). Our group studies how the widespread genetic parasites, transposable elements, influence genome function and evolution through epigenetic mechanisms. Toward this end, we combine functional genomics, computational biology, experimental genetics, and evolutionary biology.

Our lab is part of the Department of Ecology and Evolutionary Biology (<https://ecoevo.bio.uci.edu/>), the Center for Evolutionary Genetics (<https://evogen.bio.uci.edu/>), and Center for Complex Biological Systems (<https://ccbs.uci.edu/>). More information about our research interests can be found at <http://grylee.science/> Requirements for the position include: - a B.S. in Biology or related degree - at least one-year independent experience with standard molecular biology techniques (e.g., DNA/RNA extractions, PCR, qPCR) in a research laboratory setting - experience and demonstrated ability to execute complex protocols (e.g., Next-generation sequencing library preparation) - attentive to details and strong organizing skills - strong communication skills - can work independently as well as collaboratively - be comfortable working with fruit flies

Preferences will be given to candidates with experience with functional genomics or Drosophila genetics.

Responsibilities of the position include - execute and optimize molecular biology experiments for genomics studies - maintain Drosophila culture and make genetic crosses - maintain laboratory equipment and inventory (including ordering supplies) - assist projects of other members of the lab when necessary

The initial appointment is for one year with potential extension and/or renewal based on work performance and availability of funding support.

Qualified candidates should submit curriculum vitae along with the names and contact information of three references to the following recruitment URL: <https://recruit.ap.uci.edu/JPF07080> Please contact Grace Lee (grylee@uci.edu) for any questions. Informal inquiries are welcome.

The University of California, Irvine is an Equal Opportunity/Affirmative Action Employer advancing inclusive excellence. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, protected veteran status, or other protected categories covered by the UC nondiscrimination policy.

Grace Yuh Chwen Lee <grylee@uci.edu>

UCalifornia LosAngeles LabTech ConservationGenomics

The California Conservation Genomics Project is hiring a lab assistant in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles.

For more information and to apply, please visit <https://hr.mycareer.ucla.edu> and search for Requisition # 36047

Description: The Conservation Genomics Lab Technician will primarily support the laboratory research requirements of the CCGP, a state-wide initiative that seeks to assemble a large multispecies genomic data set for California's wild taxa. The incumbent is to assist in the processing of tissues and DNA extracts and generate genomic libraries for next-generation sequencing in a high-throughput research setting. In addition, in collaboration with the Associate Director, the incumbent is to troubleshoot to ensure the project progresses. Previous experience in a molecular biology laboratory is essential. Incumbent is to help with similar research tasks supporting related projects. Incumbent is responsible for some general lab management, including equipment maintenance and supply stock ordering. To learn more about the CCGP, please visit <https://www.ccgproject.org>. Skills:

1. Demonstrated experience in basic molecular biology benchwork.
2. Experience in DNA isolation and quantitation.
3. Experience in PCR and whole-genome library prep.

4. Experience working with non-model organisms.
5. Competence in common computer programs (e.g., Microsoft Office, or other word processing and spreadsheet programs).
6. Experience with development and/or use of relational databases.
7. Demonstrated excellence in organization, attention to detail, and keeping thorough and up-to-date records.
8. Ability to manage several tasks, keeping all on track and organized.
9. Ability to maintain cooperative working relationships in the laboratory.
10. Effective communication skills (verbal and written).
11. Ability to follow and enforce laboratory safety guidelines.

Erin Toffelmier <etoff@ucla.edu>

UColorado Boulder InvertZoologyCollectionsManager

The University of Colorado Boulder Museum of Natural History invites applications for an Invertebrate Zoology Collections Manager position! We seek an individual with interests in non-insect invertebrates to guide the continued growth and management of the physical collections and associated resources including archives and paper records, databases, images, and genomic resources. The collections manager will work with the Curator of Invertebrate Zoology to develop policy and procedures, grow the collection, write grant proposals, participate in informal and formal teaching and training, assist with shared administrative duties, and help develop and implement a long-term collections strategy consistent with American Association of Museums accreditation requirements, standards, and the best methodologies.

We are looking for candidates who have

- Proficiency with the taxonomy, nomenclature, preparation, dry and fluid preservation of invertebrate specimens and their DNA.
- Experience managing zoological collections, including cataloging and accessioning specimens, processing loans, acquiring applicable permits and licenses to ensure legal compliance with regulations pertaining to biological collections, and a working knowledge of standard methodologies curation standards.
- Data management skills, including specimen digitiza-

tion, data workflow design, data cleaning and migration, and facilitating data integration with national and global biodiversity data aggregator services (e.g., GBIF, iDigBio). - Ability to write successful collections improvement grant proposals, and experience developing collections policies and protocols. - Ability to manage projects, students, and volunteers. - Ability to interface professionally with the university, public, governmental & research communities. - Attention to detail and accuracy. - Excellent teamwork and communication skills.

A M.S. degree in relevant field (Biology, Zoology, or Museum Studies) with at least three years' experience working in zoology collections. This experience should include solid understanding of care and management of invertebrate collections.

The University of Colorado offers excellent benefits, including medical, dental, retirement, paid time off, tuition benefit and ECO Pass. The University of Colorado Boulder is one of the largest employers in Boulder County and offers an inspiring higher education environment. Learn more about the University of Colorado Boulder.

The University of Colorado Boulder is committed to building a culturally diverse community of faculty, staff, and students dedicated to contributing to an inclusive campus environment. We are an Equal Opportunity employer, including veterans and individuals with disabilities.

To apply, please submit the following materials:

- A current resume. - A cover letter that specifically tells us how your background and experience align with the requirements, qualifications, and responsibilities of the position.

We may request references at a later time.

Please apply by April 14th, 2022 for prompt consideration.

Please apply through here: <https://jobs.colorado.edu/-jobs/JobDetail/?jobId=38066> Jingchun Li Curator of Invertebrate Zoology jingchun.li@colorado.edu

Jingchun Li <Jingchun.Li@Colorado.EDU>

UConnecticut ResTech TapewormPhylogenetics

The Caira, Jockusch and Wegrzyn labs at the University of Connecticut, Storrs are looking for a research technician to employ next-generation sequencing technology and associated bioinformatics in support of a project on tapeworm phylogeny. This position is suitable for recent graduates with some molecular research experience and an interest in gaining more in-depth experience before applying to graduate school, as well as individuals with an MS in biology or a related field.

Application deadline: April 20, 2022

The full position description and application link are here: <https://jobs.hr.uconn.edu/en-us/job/-496200/research-assistant-1> Elizabeth Jockusch <elizabeth.jockusch@uconn.edu>

UdelRosario Bogota VertebrateEvolution

The Department of Biology (<https://www.urosario.edu.co/Programa-de-Biologia/inicio/>), Faculty of Natural Sciences (FNC) at the Universidad del Rosario (Bogotá, Colombia) seeks applicants for one full-time tenure track professor in Vertebrate Zoology. Candidates are expected to have a PhD in Vertebrate Zoology including Organismal Biology, Ecology and Evolutionary Biology aspects. We seek candidates with a strong publication record working in any area of vertebrate biology, and on any vertebrate group, whose work emphasizes field-based studies within an evolutionary context. Possible research areas include (but are not limited to) phylogenetics, biogeography, adaptation, speciation, evolutionary genetics, genomics, and comparative morphology. Postdoctoral experience, success in obtaining third party research funding, training in collections and teaching experience will be of added value. The successful candidate is expected to engage in scholarly activities, mentor graduate and undergraduate students, investigate broad questions related to the origin and diversification of vertebrates,

and lead research projects. The position involves about 40% research, 20% academic service and 40% teaching, which will include about two courses per semester, including an undergraduate course on Vertebrate Zoology. It is also anticipated that the candidates will establish collaborations with professors and students from across the Biology Department and the Earth System Sciences program, and with other academic units at Universidad del Rosario.

Applications must be written in English and include: 1) a detailed CV with a complete list of publications and funding awarded; 2) reprints of three selected papers; 3) a Research Statement summarizing the candidate's experience, interests and an outline of the research plan that can be potentially developed at Universidad del Rosario (2 pages); 4) a Teaching Statement describing teaching experience and philosophy as well as pedagogic strategies (4-5 min video-english); and 5) two recommendation letters.

Monthly salary is competitive for both Colombian and international standards and will be determined by a University-wide point system, based on research and teaching experience. Publications in high-ranking journals are yearly recognized following the University financial incentives policy. Non-native speakers are encouraged to apply and will be given two years to strengthen their Spanish communication skills and take an exam at the Multicultural and Multilingual Center at Universidad del Rosario, or take an international DELE B2 exam. Non-native speakers who have obtained the BSc, MSc or PhD in Spanish speaking countries are exempt from these exams.

The ideal starting is July 2022, but other dates can be arranged. Please send your application by e-mail at f.cn@urosario.edu.co no later than May 30th 2022 indicating the position you are applying for. For questions about the positions and life in Colombia please contact Prof. Camilo Salazar (camilo.salazar@urosario.edu.co).

Universidad del Rosario is a prestigious Colombian University that typically ranks in the top five universities in the country and in the top 50 in Latin America. It was founded in 1653 and has a long tradition in the areas of Medicine, Law, Economics and, Social and Political Sciences. The Faculty of Natural Sciences (FNC) was founded in 2008, with the goal of creating strong undergraduate and graduate programs that excel in both teaching and research. At present, the FNC has 25 full time faculty members and incorporates the undergraduate programs of Earth System Science and Biology, a Master, and PhD Program in Natural Sciences. The FCN has a vigorous and growing research agenda and published over 90 international peer-reviewed articles

in 2021 (<https://www.urosario.edu.co/facultad-ciencias-naturales/Inicio/>).

Carolina Pardo-Díaz, Ph.D.

Decana

Facultad de Ciencias Naturales

Universidad del Rosario

Bogotá, Colombia

Tel. (+571) 2970200 ext. 4032

Carolina Pardo Díaz <cabardia@gmail.com>

UI Idaho Conservation Genomics

Research Scientist Position in Conservation Genomics and Molecular Ecology

University of Idaho

We are excited to recruit a Research Scientist with expertise in Conservation Genomics and Molecular Ecology to join our research team at the University of Idaho (UI), Moscow Campus.

The Research Scientist will join a dynamic faculty, post-doc and graduate student team focused on conservation genomic and molecular ecology research projects across the Western US and around the world. Our team also has the goal of providing training for local and international students and outreach to managers and policy makers. We have already developed strong relationships and have current funded genomic projects with state, federal, tribal and international partners. This research scientist would work with the collaborating faculty listed below to conduct a variety of policy and management relevant projects in wildlife conservation and management, fish ecology and fisheries management, and environmental monitoring, and work with faculty to apply for future funding. Other responsibilities include student mentoring and training related to next-generation sequencing, transcriptomics, eDNA monitoring, diet metabarcoding and associated bioinformatic analyses. The research scientist will have access to UI resources such as genomics and computational core facilities and collaborative research groups in the Institute for Interdisciplinary Data Sciences (IIDS), the Institute for Modeling Collaboration and Innovation (IMCI) and the Idaho EPSCoR-NSF Genes by Environment (GEM3) program. Funding is available for 2 years

with the opportunity to start in Summer 2022.

Priority application deadline is April 26th and applications will be accepted until the position is filled. The UI is an equal opportunity and affirmative action employer committed to assembling a diverse, broadly trained faculty and staff. Women, minorities, people with disabilities and veterans are strongly encouraged to apply. For more information and application submission, see <https://uidaho.peopleadmin.com/postings/35585> Recruitment Team: Lisette Waits and Chris Caudill - Department of Fish and Wildlife Sciences and Bioinformatics and Computational Biology Program (BCB), College of Natural Resources, and Paul Hohenlohe - Department of Biology, BCB Program, College of Science Contact Lisette Waits lwaits@uidaho.edu with questions.

LISETTE WAITS Distinguished Professor Department Head Fish and Wildlife Sciences College of Natural Resources

lwaits@uidaho.edu 208-885-7823 875 Perimeter Drive MS1136|Moscow ID 83844-1136

www.uidaho.edu/cnr/faculty/waits “Waits, Lisette (lwaits@uidaho.edu)” <lwaits@uidaho.edu>

ULeicester UK Lectureship Population Genomics

We are seeking a Lecturer in Population Genomics to join the Department of Genetics & Genome Biology at the University of Leicester, UK.

This new post represents an exciting opportunity to conduct research and teaching in the field of population genomics and its application to problems including complex disease in humans. Your role will align with strategic priorities in the Department and the College of Life Sciences, while benefiting from the excellent interdisciplinary environment provided by the wider University.

You will conduct high-quality research in areas such as demographic history, admixture, adaptation, genotype-phenotype relationships and gene-environment interactions, using the tools of genomics at the population scale. Your research in population genomics will be expected to enrich human health research in Leicester, where there are opportunities to collaborate with outstanding researchers within the NIHR Biomedical Research Centre (BRC), the Leicester Precision Medicine Institute,

and the Centre for Ethnic Health Research working on genetic epidemiology and functional genomics across a range of diseases including cardiovascular, respiratory and infectious disease, diabetes, cancer and multiple long term health conditions. Colleagues also include geneticists studying non-model organisms including social insects, mammals and plants. Our accessible campus and collegiate atmosphere facilitates interdisciplinary collaboration with archaeologists and geographers in considering temporal and spatial contexts.

To support your work, you will generate funding through research grants. You will have the opportunity to supervise PhD students associated with several funded Doctoral Training Partnerships including BBSRC MIBTP, MRC Advanced Interdisciplinary Models (AIM), NERC CENTA2, and our Wellcome Trust Genetic Epidemiology & Public Health Genomics programme.

You will also form part of a team delivering innovative teaching across a range of undergraduate and postgraduate programmes in genetics, genomics, and bioinformatics. This includes delivering lectures, practicals and seminars, designing and marking assessments, and personal tutoring. You will enhance teaching and learning by contributing to the administration of modules and continually improving your own understanding and skills.

We will support you in developing your research and teaching career and, in turn, you will play a key role in ensuring our continued success and fulfilling our future ambitions.

About you: You are a researcher with a growing or established reputation, a high-quality publication profile and exciting and potentially fundable research ideas. You will also have excellent networking skills, which you will use to seek out opportunities for collaboration, both internally and externally. You will be capable of inspiring excitement for learning in our undergraduate and post-graduate students, and able to provide them with the very best experience, using your expertise and skill to ensure that all reach their potential.

Additional information: For full details and how to apply, visit: <https://jobs.le.ac.uk/vacancies/4550/lecturer-in-population-genomics.html> Informal enquiries are welcome, to: Prof Mark Jobling (maj4@le.ac.uk), Prof Chris Bayliss (cdb12@le.ac.uk) or Prof Jacqui Shaw (Head of Department, js39@le.ac.uk).

Closing date: 05 May 2022

“Jobling, Mark A. (Prof.)” <maj4@leicester.ac.uk>

UOregon ResAssist EcologicalGenomics

The Streisfeld lab (<http://streisfeldlab.weebly.com> < <http://www.uoregon.edu/~mstreis> >) in the Institute of Ecology and Evolution at the University of Oregon is looking to hire a research assistant to help with multiple projects on the ecological genomics of adaptation and speciation in plants (mostly *Mimulus*). The position involves a combination of laboratory and greenhouse work. Review of applications is ongoing, but the position will remain open until filled. Please contact me with any questions. Please see the full job ad, with instructions on how to apply and other details, here:

<https://careers.uoregon.edu/en-us/job/528775/-pro-tem-research-assistant> Matt Streisfeld
mstreis@uoregon.edu

< <http://www.uoregon.edu/~mstreis> >

Matt Streisfeld <mstreis@uoregon.edu>

UTexas Austin ResTech EvolutionaryMorphology

The Kemp Lab (<http://www.kemplab.com>) seeks to hire a research technician to contribute to an NSF-funded project on the long-term stability of adaptive radiations, using the fossil record of Caribbean *Anolis* lizards as a model system. The successful candidate will perform data collection on a large dataset of high-resolution X-ray chromatography (CT) scans for use in downstream analyses of morphological diversification and extinction in changing environments.

Prior experience analyzing CT data is required, and prior experience with natural history collections and reptile osteology is preferred.

The Kemp Lab is actively involved in K-12 outreach, and several educational modules will be developed as part of this project. Thus, candidates with an interest in K-12 education are highly encouraged to apply.

A cover letter is required for this position and should describe the applicant's interest in the position and out-

line their skills and experiences that directly relate to this position.

For more information, and to apply: https://utaustin.wd1.myworkdayjobs.com/UTstaff/job/UT-MAIN-CAMPUS/Research-Engineering-Scientist-Assistant---Kemp-Lab_R_00019400 We will begin reviewing applications on May 16 until the position is filled.

Melissa E. Kemp, PhD Assistant Professor, Department of Integrative Biology The University of Texas at Austin
mkemp@austin.utexas.edu www.thekemplab.com
mkemp@austin.utexas.edu

WellesleyCollege TeachingEvolution VisitingLecturerPositions

The Biological Sciences Department at Wellesley College is conducting a search for several visiting lecturers (part-time or full-time) to teach lectures and labs for several introductory organismal biology, and introductory cellular and molecular biology courses, biostatistics and ecology. Strong interest in undergraduate teaching is preferred.

We are preparing for in-person instruction during the AY '22-'23. Ideal candidates will have a minimum of a Master's degree in a relevant field. Teaching these courses will offer an excellent opportunity for a current/recent graduate student or post-doc to obtain teaching experience at an elite liberal arts institution in a department with dedicated faculty.

Please consider this opportunity even if you are not in the area since Wellesley College offers subsidized faculty housing for visiting lecturers at more than 0.5FTE...and the fall in New England is stunning!

Interested candidates should contact the department chair, Yui Suzuki (ysuzuki@wellesley.edu), with questions and/or send 1) a cover letter, 2) curriculum vitae and 3) contact information for 3 references to him directly.

Wellesley College is an Affirmative Action/Equal Opportunity Employer committed to Inclusive Excellence, and we encourage persons of all genders, persons of color, and persons with disabilities to apply. The college is committed to enriching its educational experience and its culture through the diversity of its faculty, administration, and staff.

Andrea Sequeira, PhD (pronouns she/her) Gordon and Althea Lang '26 Professor of Biological Sciences Wellesley College, Wellesley MA 02481 Biology Department

FB page <https://www.facebook.com/wellesleybiology/>
 Andrea S Sequeira <asequeir@wellesley.edu>

Other

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ASN SSB SSE EvolutionMeetings AssistMeetingOfficer

Evolution meetings - Assistant Meeting Officer

The Society for the Study of Evolution (SSE), on behalf of the Joint ASN/SSB/SSE council, seeks a member of one or more of our societies to help plan and run our annual scientific conference - the Evolution meetings (<https://www.evolutionmeetings.org>). The meetings are coordinated by a Chief Meeting Officer (CMO), an academic who oversees all aspects of the meeting and who is responsible for final decisions about schedules, activities and venues, in consultation with a tri-society Joint Meeting Committee (JMC) and the larger ASN/SSB/SSE Joint Council. The CMO also acts as the principal liaison with a Professional Conference Organizer (PCO), whose responsibilities include executing the logistics of conference management, interactions with vendors and service providers, and helping identify and negotiate contracts with future meeting venues. Joint CMOs are also possible.

We are currently seeking an Assistant Meeting Officer who will help the CMO(s) with organization, including interfacing with society councils and other stakeholders, producing the scientific program, and providing

academic insight to help guide the work of the PCO. Specific duties will be determined by the CMO and the JMC, in consultation with the AMO. Assistants normally serve a 3-year term and, if interested, may transition into the lead CMO role at some point, with approval of the JMC. Helping run our meetings is an important and valuable service to our societies and our field which is largely a volunteer effort, but the AMO will be given a stipend of \$5000/year in appreciation. All meeting attendance costs will also be covered, as well as any other costs associated with carrying out meeting responsibilities.

The time commitment is variable but is expected to average a few hours/week, ramping up at certain times depending on particular tasks and in the month preceding the meeting. Much of the time is spent in electronic communication and virtual meetings, but there are also some duties at the conference.

This position is best suited to someone who has attended several of our recent meetings, has academic organizational and leadership experience, enjoys teamwork, and would find it rewarding to serve the societies by fostering dynamic and high-quality meetings. We welcome expressions of interest; please email these to <mailto:evolution.meetings@gmail.com> with 'AMO position' in the subject and include any relevant experience and a CV. These will be reviewed on a rolling basis with the goal of filling this position by summer 2022, with working starting then on the 2023 meeting (to be held

in Albuquerque, NM from June 21-15). There are no geographic restrictions, nor citizenship or residency requirements, but attendance at the 2023 and subsequent meetings is expected and in-person attendance at the 2022 meeting would be an asset.

About the annual conference: The Evolution meeting is the joint conference of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists. The conference is held in a different location every year, primarily in the United States but occasionally in other countries. Recent and future locations include Portland OR, Providence RI, Cleveland OH, and Albuquerque NM. The meeting is the premier opportunity for sharing research on evolutionary biology. The conference attracts between 1500-2000 attendees and includes more than 1,000 oral presentations, 400-500 posters, a diverse array of social events, and a variety of workshops. It runs for approximately 5 days (depending on satellite events) in mid-late June. Evolution 2022 will be our first hybrid meeting, with options for virtual and in-person participation, and we anticipate this continuing in future years. Evolution has an enforced meeting Code of Conduct and a strong commitment to promoting equity and inclusion. More information is available on the conference web site: <http://www.evolutionmeetings.org>, including complete programs from recent meetings. Conferences are run on a break-even basis with careful attention given to minimizing registration costs for attendees.

Howard Rundle <hrundle@uottawa.ca>

CallBiodiversityProposals FrenchFoundation

Dear Sir, Madam,

I am contacting you about a new call for proposals that the French Foundation for Biodiversity Research launched today to fund three innovative projects relating to the synthesis of ideas and concepts and/or the analysis of existing data. The main aim of these projects should be to improve scientific knowledge of biodiversity and demonstrate how we can use this knowledge to better protect it. The submitted projects can deal with any topic related to biodiversity, in the fields of natural sciences and/or human and social sciences.

More information can be found here <https://www.fondationbiodiversite.fr/en/actualite/call-for-proposals-frb-cesab-2022-opening-of-the-call/> Don't

hesitate sharing the information in your network.

[signature_701717591]

Marie-Claire Danner

SCIENCE OFFICER

IPBES TSU FOR THE ASSESSMENT OF SUSTAINABLE USE OF WILD SPECIES

CHARGÉE DE COMMUNICATION

CESAB (CENTRE DE SYNTHÈSE ET D'ANALYSE SUR LA BIODIVERSITÉ)

+33 (0)6 71 66 46 58

FRB-CESAB : 5 rue de l'école de médecine, 34000 MONTPELLIER

Marie-Claire DANNER <marie-claire.danner@fondationbiodiversite.fr>

DonalHickey HasPassed

Donal Hickey passed on April 7th after a short battle with cancer.

Donal has always been a good, true and loyal friend to me ever since I started off at the University of Alberta as a young PhD student. Donal, after completing his PhD with Dick Lewontin, started off his career at Brock University, then moved on to the University of Ottawa and then Concordia University. Ever since I have known him he was a friend and a mentor to all that knew him. He was a valued member of the Genetics Society of Canada and served as its President. He published regularly in a career that spanned almost 50 years.

I still use his simple and clear explanation of how transposable elements can be deleterious and yet still spread in a population in my undergraduate classes. This explanation will now be tinged with fond memories of a great scholar.

Brian Golding

FlowCytometry For GenomeSize

Hi,

Does anyone know a company (or any research organisation) that can estimate plant genome size via flow cytometry based in the UK.

Many thanks, Mark

Dr Mark A. Chapman M.Chapman@soton.ac.uk +44 (0)2380 594396

Biological Sciences University of Southampton Life Sciences Building 85 Highfield Campus Southampton SO17 1BJ

Mark Chapman <markchapman4774@gmail.com>

Phillippines FellowshipTeachingEvolution

Other:EvolBiol.6monthTeachingFellowshipPhillippines

Teach General Biology and Research methods at a private high school in the Phillipines and help develop and catalog an intertidal invertebrate biodiversity project.

We, Science Corps, are looking for 1 broadly trained evolutionary biologist, with a recent PhD (up to four years after graduation), for a fully paid fellowship to help build science capacity at our partner location, CVIF in Jagna, Bohol, Phillipines . The Central Visayan Institute Foundation (CVIF) is a private highschool that serves as a host location for Science Corps Fellows. This summer and Fall 2022, CVIF is looking for a PhD level evolutionary biologist to teach Biology and help the research team at the school use MinION sequencing to produce a gene bank for phylum Mollusca from the Bohol Sea (as baseline data).

Science Corps is a small group of scientists running a non-profit that sends recent PhD graduates to teach science abroad. Fellows travel to partner institutions to develop science curriculum, teach in secondary school classrooms, and build community-based research projects. In addition to building science capacity at these host locations, we also aim to offer fellows a life-changing experience.

They are given the opportunity to spend time in beautiful locations, immerse themselves in different cultures, and learn from their host educators-all while making positive contributions to these communities.

The deadline for this specific fellowship opportunity for an evolutionary biologist in the Phillipines is June 30th, but we still encourage you to contact us if you would like to be considered for a later appointment.

To find out more about us and apply, please go to

<https://science-corps.org> Stephen Harris
<harris.stephen.e@gmail.com>

Seminar ESEB STN Speciation Apr12

Dear colleagues,

The next session of the monthly online seminar series organised by the ESEB-funded STN network «— Integration Of Speciation research—» (for more info—: [<https://speciation-network.pages.ist.ac.at/>]) will be held on Tuesday the 12th of April 2022, 9 am CET.

This session will be the first of a series of three addressing the general topic of how to understand the relative importance of different barriers to gene flow and outline best practices to measure them, with a focus on phenotypes and traits.

The first session on this general topic will focus on “What is reproductive isolation: promises and pitfalls in measuring reproductive barriers”. We will welcome as speakers Anja Westram (Nord University, Norway) and Daniel Ortiz-Barrientos (University of Queensland, Australia). The session will last 1.5 hours, with the first hour dedicated to the two talks from our speakers and questions, and the last half-an-hour dedicated to a more general discussion.

To attend the session live, please follow the link below :
Webinar link:

[<https://gu-se.zoom.us/j/61007486919?pwd==bXYyY2l6UjU5UG5tNUNuNVdnUXZiZz09>] Passcode: 940593

Talks (but not the discussion session) are recorded and made available [https://www.youtube.com/channel/UCIEkDdE_5sDw70SQq78DIAA | here].

The IOS network does not only aim at scientific inte-

gration, but also integration of the community. A main objective on this front is to foster diversity and inclusion across the field. The seminar series and subsequent discussion is open to everyone, from students to established researchers and non-scientists alike. In order to maximise the geographic diversity of attendees, we will alternate between two time slots every other month: 5 pm CET and 9 am CET. Please help us to circulate this email to anyone who may be interested, especially those in countries that are typically underrepresented in scientific discourse.

The programme of the seminar series is announced by email, on Twitter (@Speciation.net) and on the IOS network website. People who wish to receive automatically the programme and other news from the IOS network can sign up to the network mailing list from the IOS website.

We look forward to seeing you there!

The STN IOS organising committee

Jonna Kulmuni (chair), Chris Cooney, Sean Stankowski, Carole Smadja (co-chairs), Sonal Singhal, Liz Scordato, Joana Meier, Richard Merrill, Konrad Lohse, Nick Barton and Roger Butlin.

Dr. Carole Smadja Directrice de recherche CNRS - CNRS Senior researcher Directrice adjointe de l'ISEM - ISEM Deputy director carole.smadja@umontpellier.fr
Tél : +33 (0)4 67 14 92 70

Institut des Sciences de l'Evolution de Montpellier - Institute of Evolutionary Science of Montpellier (ISEM) [<mailto:carole.smadja@umontpellier.fr>] [tel:+33 (0)4 67 14 92 70] [<mailto:carole.smadja@umontpellier.fr>] [<https://isem-evolution.fr/>] ISEM UMR 5554 cc065 Campus Triolet - Université de Montpellier - 34095 Montpellier Cedex 05 –

Carole Smadja <carole.smadja@umontpellier.fr>

SMBE Awards Nominations Applications Apr15

SMBE Awards 2022:

15 April deadline for nominations and applications

Dear SMBE Members,

Please be reminded of the deadline approaching for:

1. The SMBE Graduate Student Excellence Award provides a forum for young investigators to showcase their exemplary research at the annual meeting. We showcase the winners of this award at the Graduate Student Excellence Symposium, which will be part of SMBE Everywhere symposia in 2022. More details for the symposium will follow in the coming months.

Eligibility: Current graduate students and postdoctoral researchers who are members of the Society and who received their primary doctoral-level degree no earlier than July 2021 are eligible. Eligibility extensions can be granted for any career disruption or delay; such an extension should be requested in a cover letter. Approximately eight winners will be selected every year to cover the broad spectrum of research covered by SMBE.

How to apply: You must email a scientific abstract (not to exceed 300 words for body of abstract), title of proposed presentation, and your Curriculum Vitae to tosmbe@allenpress.com.

The deadline for applications for this award is 15 April 2022.

2. SMBE seeks nominations for 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 annual 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.

SMBE Mid-Career Excellence Award

This annual 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.

SMBE Lifetime Contribution Award

This annual 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.

SMBE Community Service Award

This special 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.

The materials should be compiled into a single PDF file, and should be emailed to

smbel@allenpress.com by or before 15 April 2022.

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

Early-Career Excellence Award**Mid-Career Excellence Award****Lifetime Contribution Award****Community Service Award**

Sincerely,

Harmit Malik, Past President James McInerney, President

Society for Molecular Biology & Evolution
smbel@allenpress.com

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

**SMBE Awards
Nominations Applications
Ext Deadline Apr 30**

SMBE Awards 2022: 30 April EXTENDED deadline

SMBE Awards 2022:

30 April EXTENDED deadline for nominations and applications

Dear SMBE Members,

Please be reminded of the EXTENDED deadline approaching for:

1. The SMBE Graduate Student Excellence Award provides a forum for young investigators to showcase their exemplary research at the annual meeting. We showcase the winners of this award at the Graduate Student Excellence Symposium, which will be part of SMBE Everywhere symposia in 2022. More details for the symposium will follow in the coming months.

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The deadline for applications for this award is 30 April

2022.

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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.

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smbe@allenpress.com by or before 30 April 2022.

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

Early-Career Excellence Award

Mid-Career Excellence Award

Lifetime Contribution Award

Community Service Award

Sincerely,

Harmit Malik, Past President James McInerney, President

Society for Molecular Biology & Evolution
smbe@allenpress.com

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

SMBE IDEA ProposalCall

SMBE IDEA (Inclusion, Diversity, Equity and Access) 2022 Proposal Call

SMBE, through the IDEA (Inclusion, Diversity, Equity and Access) task force, aims to address all forms of exclusion in our society. With this in mind, a budget of up to \$25,000 per year will be dedicated to initiatives that help reduce inequities in molecular biology and evolution research. The task force would therefore like to invite members of SMBE to propose initiatives that would take place in the year 2022/2023. Examples of initiatives could include, but are not limited to, workshops, symposia, training opportunities, stand-alone featured talks, or inequity data collection in particular groups, countries, or regions (to name a few).

Guidelines and instructions for proposals

- At least one of the organizers must be a member of SMBE. Please note that you can apply for a complementary SMBE membership by contacting the SMBE council.
- A short description (between half and one full page) of the proposed idea should be submitted by email to smbe.contact@gmail.com for review by 16th May 2022. This is the initial submission. Submissions should address how the proposal will help advance the goals of the SMBE IDEA task force.
- The initial submission should include the names and full contact information of all organizers and involved institutions. Universities/organizations providing additional financial support, if involved, should also be listed.
- Initial submissions will be reviewed and pre-selected by the IDEA task force, and candidates will be notified with a decision within 3 weeks after the initial submission deadline (by 6th June).
- If the initial submission is selected, organizers are expected to submit a full project plan by email to smbe.contact@gmail.com by 25th July 2022. This must include a budget and time plan, as well as relevance and expected short and long-term impacts of the initiative on inclusion, diversity, equity and/or inclusion. The IDEA task force commits to aiding organizers during the development of the project plan.
- Successful proposals will be notified by 15th August

2022.

- All deadlines are 5pm local time.

Additional information

- To promote the submission of initiatives, the task force will host an open workshop (open to all SMBE members and not restricted to those who submitted an initiative) on "How to design project proposals" during the SMBE IDEA symposium (at the annual SMBE conference) on the 11th and/or 12th of July (date to be confirmed).
- Organizers should submit a report (~2 pages) of the activity to the SMBE IDEA committee within 3 months of its completion.

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

On behalf of the SMBE IDEA task force

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

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

smbe.contact@gmail.com

SMBE Nominations Apr15 LastCall

Dear Colleagues,

Last call for SMBE leadership nominations - due April 15!

We are writing to solicit nominations for SMBE President-Elect, Secretary and 2 Councilors whose terms will begin on January 1, 2023. All of these positions are for a duration of three years.

As the society grows and thrives, council members play important roles in guiding its development and in soliciting and implementing programs that support our members, while enriching opportunities for young scientists from around the world, and overseeing our two excellent journals (MBE and GBE) as well as our annual meeting, regional meetings, and satellite meetings.

Nominations will be reviewed by the nominations committee* who will then put forward a slate of two candidates for each position for membership vote. Past and current council members are at this URL: <https://www.smbe.org/smbe/ABOUT/>

Council.aspx Please send nominations with a brief statement in support of your suggestion (self-nominations are welcome) to Justin Blumenstiel <jblumens@ku.edu> and Nadia Singh <secretary.smbe@gmail.com>.

*Nota bene: we ask the nominators to confirm explicitly that the person they are nominating has already confirmed their willingness to run for office.

Please send your nominations by Friday, April 15, 2022.

We look forward to hearing from you!

Sincerely yours,

Nadia Singh Secretary of SMBE, on behalf of the Nominations Committee*

and

Justin Blumenstiel Chair of Nominations Committee *The Nominations Committee is composed as follows: Justin Blumenstiel (Chair), University of Kansas, United States Andrea Betancourt, University of Liverpool, United Kingdom Tal Dagan, Christian-Albrechts University of Kiel, Germany David Enard, University of Arizona, United States Jun-Yi Leu, Academia Sinica, Taiwan Aurora Ruiz-Herrera, Universitat Aut?noma de Barcelona, Spain Yonas Tekle, Spelman College, United States Nadia Singh (ex officio), University of Oregon, United States

Justin Blumenstiel Associate Professor Chair, Graduate Admissions Committee Department of Ecology and Evolutionary Biology University of Kansas Lawrence, KS 66045

jblumens@ku.edu

“No Drosophila female could conceivably lay two billion eggs in her lifetime”. Lewontin and Hubby. 1966.

jblumens@ku.edu

land. An overview over our past work can be found here: <https://www.youtube.com/watch?v=JaH6wjAYAiE>

Our current project investigates the effect of social interactions on the dispersal of Siberian jays. The work of the field volunteers will be to help with catching, radio-tagging and colour-ringing birds, sampling blood, conducting population censuses and behavioral observations, and managing data. This work will provide insights into a long-term study system and will be carried out in managed and pristine boreal forests. Our fieldwork may at times involve walking up to 15km per day.

Qualifications: 1) Bird ringing and mist-netting experience 2) Field work experience, preferably involving behavioural observations and experiments 3) Radio tagging and radio tracking experience is a plus 4) Ability to work in small teams and sociable personality 5) Driver's license (manual transmission) 6) Fluent in English

We will cover accommodation, travel expenses from and to the study site (up to 360 euros return), as well as on-site living expenses (food).

Applications, including a CV, letter of motivation (1 page), and the name of two referees, should be sent to Michael Griesser michael.griesser@uni-konstanz.de, preferably in a single PDF.

Applications received until 2. May 2022 will be given full consideration.

Michael Griesser Group Leader, Heisenberg Fellow Department of Biology University of Konstanz

<https://scholar.google.com/citations?user=IEIH0xkAAAAJ>

Michael Griesser
<michael.griesser@uni-konstanz.de>

UKonstanz FieldAssist LaplandBirds

2 Expenses-paid field assistant positions for a project investigating dispersal of Siberian jays in Swedish Lapland

For the upcoming field season (15.6.-1.10.2022), we are looking for 2 highly motivated, expenses-paid field volunteers to assist with our field project (principal investigator Dr. Michael Griesser, University of Konstanz). The study site is located near Arvidsjaur in Swedish Lap-

Webinar

Demystifying Graduate School Apr21

Dear colleagues,

The Rutgers Ecology & Evolution graduate program (<https://ecoevo.rutgers.edu/>) 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. Please join us! Or, if you have students who may be interested, I'd be grateful if you could forward our invitation.

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

The session will be Thursday, April 21st, from

2:30 - 4:00 pm EDT. Participants must register in advance at https://rutgers.zoom.us/webinar/register/WN_mh5RaGzvRYCX9ZWabLJ7Zg. We also have a flyer available at https://drive.google.com/file/d/1uID_t12PyVyXKE2PqzPvovPZGKvZC0J/-view?usp=sharing. This is the third event of this type that we have hosted, after high demand for our first events last year.

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 and hope to see you later this month.

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://pinskylab.rutgers.edu) <http://pinsky.marine.rutgers.edu> I recognize that at my institution, we learn, teach, and live on or near the ancestral homelands of the Munsee Lenape and Lenni-Lenape. I acknowledge my institution's role in histories of dispossession and recognize my own responsibility to our Indigenous connections.

Malin Pinsky <malin.pinsky@gmail.com>

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BoyceThompsonInst Cornell PlantCyanobacteriaSymbiosis

The Fay-Wei Li lab (fernway.net) at Boyce Thompson Institute & Cornell University is looking for two postdoctoral researchers to work on bryophyte-cyanobacteria symbiosis, funded by NSF Dimensions of Biodiversity grant.

Plant symbiosis with nitrogen-fixing cyanobacteria is a unique form of mutualistic association that has independently evolved in diverse lineages including a few species of bryophytes, ferns, cycads, and one small genus of flowering plants. Compared to other nitrogen-fixing microbes, cyanobacteria are generally less dependent on the plant host, and therefore could be an ideal partner for engineering symbiotic nitrogen fixation into crop plants. However, our current understanding of plant-cyanobacteria symbioses is limited. The phylogenetic diversity of cyanobionts has been largely unexplored, and very few studies have investigated variation in the symbiotic interaction. In addition, most genetic research has solely focused on the model cyanobiont *Nostoc punctiforme*, and the plant genes involved in symbiosis remain unknown. Hornworts one of the three bryophyte lineages are an ideal system to study cyanobacterial symbiosis, primarily because of the groundwork laid by our lab and collaborators. This project aims to investigate the phylogenetic, functional, and genetic dimensions of hornwort-cyanobacteria symbiosis.

Essential Job Functions:

The postdocs are encouraged to develop their own research questions as long as they are related to hornwort-cyanobacteria symbiosis. These could include:

1. Carry out microcosm experiments to examine hornwort-cyanobacteria symbiotic interaction and test selectivity and specificity.

2. Sequence and analyze hornwort and cyanobacteria genomes, and correlate the genomic features with symbiotic behaviors.

3. Identify the chemical signals exchanged between hornworts and cyanobacteria.

4. Characterize the genetic elements underlying the symbiosis.

Qualifications

1. Ph.D. in plant science, microbiology, bioinformatics, or related fields.

2. Ability to work independently and creatively.

Anticipated start date: June-September 2022

To Apply: Applicants should contact Fay-Wei Li (fl329@cornell.edu) and/or through this link: <https://recruiting.paylocity.com/Recruiting/Jobs/-Details/1054711> Fay-Wei Li <fl329@cornell.edu>

Brussels PDForPhD InvertEvolution

1 year research position (PhD or Post-doc) in Late Quaternary evolutionary dynamics of invertebrates in Antarctic lakes - apply by 29.4.22

Context The Royal Belgian Institute of Natural Sciences (Brussels) is recruiting a research assistant (PhD or postdoc level) who will be employed in the recently started project HabitAnt: Past and future habitability in Antarctic lakes: succession, colonization, extinction, and survival in glacial refugia, funded by BelSPO BRAIN-BE. The project is coordinated by Ghent University and also includes the University of Liege; at these partner institutions, a PhD student each has already been recruited.

The young researchers work will be organized to design three complementary sub-projects. Several project

tasks will be conducted in close collaboration between the respective research groups. Fossil DNA from lake sediment cores will be sequenced and used to develop molecular phylogenies of focal taxa to study the processes that contributed to the present-day diversity of organisms in Antarctic lakes. Studied evolutionary processes include long-term persistence of biota in glacial refugia, their extinction, colonization, diversification, and biological succession in response to past climate and environmental changes.

Job description The job is a supporting Antarctic research on the evolutionary history of lake invertebrates.

The job tasks include: - Analyses of recent lake sediment samples and determination of selected invertebrate groups (ostracods, rotifers, copepods). - Extraction of fossil DNA and the development of DNA libraries for high-throughput sequencing with a focus on invertebrates. - Construction of multi-gene molecular phylogenies. - Bioinformatics and statistical analysis of metagenomic and DNA amplicon datasets. - Usage of Antarctic databanks.

Profile: - Interest in Antarctic and evolutionary research of lacustrine organisms. - Willingness to sample under extreme circumstances.

Diploma: - Master or similar degree (for postdocs: also PhD) in biology, biochemistry or biotechnology.

Technical competencies: - Experience with determining freshwater invertebrates. - Genetic laboratory skills for DNA extraction from ancient samples and sample preparation for high-throughput sequencing. - Experience with bioinformatic analyses of eDNA or metabarcoding approaches. - Experience with phylogenetic analyses.

Generic competences: - Good organization skills. - Good social skills (as communication with different project partners is required). - Good skills in problem solving. - Good writing and presentation skills. - Willingness to participate in additional training courses (probably abroad), and to follow and implement novel technical advancements in high throughput sequencing and subsequent analysis.

Positive additional points are: - (For potential PhD students: interest to inscribe as PhD student at a Belgian university). - Interest in Antarctic freshwater fauna and evolutionary research. - Active knowledge of English.

We offer: - A full-time position as assistant for minimal 1 year with the possibility for extension after positive evaluation. - Salary according to the statutory pay scale grade SW1. - Free public transport between your home and the institute. - A dynamic, challenging, variable and stimulating research framework. - High-quality training

to develop hard and soft skills, and opportunities to participate in sampling campaigns to Antarctica and international scientific conferences.

Application: Please send your cv and motivation letter (preferably by email) before 30.4.22 to Royal Belgian Institute of Natural Sciences Isa Schon Vautierstraat 29 1000 Brussels ischoen@naturalsciences.be

The interviews will take place in the first week of May 2022.

Isabelle Schon <ischoen@naturalsciences.be>

ClemsonU Toxicogenomics

Postdoctoral position in Toxicogenomics at the Center for Human Genetics at Clemson University

The Center for Human Genetics at Clemson University invites applications for a postdoctoral position as part of the European Commission-funded PrecisionTox consortium, which encompasses collaboration between 15 institutions in Europe and the United States. This European-funded project seeks to identify biomarkers predictive of chemically induced adverse health effects in humans via the systematic use of distantly related animal species from across the tree of life and the highly interdisciplinary mix of genomics, metabolomics, evolutionary theory, quantitative genetics, data science, and toxicology. Within this project, our group focuses on allelic variants and genetic networks that determine variation in sensitivity to select environmental toxicants using the *Drosophila melanogaster* Genetic Reference Panel of sequenced inbred lines. This project fits within a larger interest in our laboratory to define the dynamics of the genotype-phenotype relationship in the presence of genome by environment interactions.

The successful applicant will have a record of research productivity in genetics/genomics, solid statistical skills, and expertise in whole-genome DNA and RNA sequencing and analyses. Previous experience with *Drosophila* is desirable but not required. The person in this position will have excellent verbal and written communication skills and the ability to function independently while at the same time being able to work as a member of a team.

The start date is January/February 2023, and the duration of support is for three years, with a competitive salary and benefits.

Applications should be addressed to Robert R. H. Anholt, Ph.D. (ranholt@clemson.edu), including a cover letter, curriculum vitae with a list of publications, and the names and contact information of three references. Apply at <http://apply.interfolio.com/106099>. Clemson University promotes a diverse and inclusive environment and welcomes applicants regardless of age, disability, gender, nationality, ethnicity, religion, sexual orientation, or gender identity.

TRUDY F. C. MACKAY, PhD, FRS

SELF FAMILY ENDOWED CHAIR OF HUMAN GENETICS

DIRECTOR, CENTER FOR HUMAN GENETICS

PROFESSOR OF GENETICS AND BIOCHEMISTRY

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CNRS UGrenobleAlpes EvolutionaryGenomics

2Y POST-DOC POSITION IN EVOLUTIONARY GENOMICS & MOLECULAR EVOLUTION CNRS, Univ. Grenoble Alpes, France

“Natural selection does not work as an engineer works. It works like a tinkerer - a tinkerer who does not know exactly what he is going to produce.” (F. Jacob, 1977).

Standing on the shoulders of François Jacob, among others, in our team we aim at understanding and predicting biological functions by rationalizing evolutionary properties that can be extracted from the immense resource of publicly available genome sequences.

Here, we are looking for a postdoc aiming at applying phylogenomics and co-evolution approaches to tackle the problem of the emergence and evolution of enzyme

functions. Specifically, the recruited researcher will investigate evolutionary properties of a specific class of enzymes that are involved in the biosynthesis pathway of the ubiquinone [1,2], a molecule that is key to the energy metabolism of bacteria and eukaryotes. The project, funded by the Agence National de la Recherche, consists in an interdisciplinary framework that combines comparative genomics (recruited postdoc), biophysical models of molecular dynamics (Isabelle André’s team, Toulouse Biotechnology Institute) and biochemical experiments (our team). A major goal is to provide predictions of natural, artificial and ancestral enzymes (enzymes resurrection) that will be experimentally tested.

The post-doctoral contract is for 2 years with extension possibilities. The recruited post-doc will benefit from a rich interdisciplinary environment provided i) by our computational group, which includes comparative genomics, machine/deep learning methods and biophysics, ii) by our team TrEE, which focuses on biology (from experimental evolution to biochemistry) and health questions and iii) Isabelle André’s team in Toulouse.

* Candidate’s profile: we are looking for a highly motivated young scientist with a strong background in computational biology, evolutionary genomics or mathematical methods, with a strong interest to investigate the evolution of biological functions.

* Starting date: 2022 - Position open till filled

* Contacts: sophie.abby@univ-grenoble-alpes.fr and ivan.junier@univ-grenoble-alpes.fr.

To apply, please send your CV, a motivation letter, and the names and contact information of two references to Sophie Abby and Ivan Junier. For more details, informal enquiries are also welcome.

* Links: TrEE comp bio group: <https://tree-timc.github.io/compbio/> TrEE team: <https://www.timc.fr/en/tree> Online position announcement : <https://jobrxiv.org/job/compbiotree-27778-postdoc-position-in-evolutionary-genomics-molecular-evolution/> * References: [1] Pelosi et al. “Evolution of Ubiquinone Biosynthesis: Multiple Proteobacterial Enzymes with Various Regioselectivities To Catalyze Three Contiguous Aromatic Hydroxylation Reactions”. mSystems, 2016. <https://doi.org/10.1128/mSystems.00091-16> [2] Abby et al. “Advances in bacterial pathways for the biosynthesis of ubiquinone”. Biochimica et Biophysica Acta (BBA)-Bioenergetics, 2020. <https://doi.org/10.1016/j.bbabi.2020.148259> Sophie Abby <sophie.abby@gmail.com>

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CornellU 2

PopulationStatisticalGenetics.html

<pre> The Wei Lab at Cornell University is looking for 2-3 postdoctoral fellows. The start date is flexible but can be as soon as possible.

We are looking for highly motivated postdoctoral fellows with a background in population and/or statistical and/or evolutionary genetics, strong statistical and programming skills, and an ability to perform independent research. Potential projects include, but are not limited to:

1. Inferring demographic history from genome sequences using ancestral recombination graphs.
2. Statistical methods for understanding the evolution of complex traits in light of admixture.
3. Methods for analyzing genomic time series data of SARS-CoV-2 and experimental evolution.
4. Inferring the relationship between dominance and selection.
5. Understanding the evolution of life history, including but not limited to aging, sexual reproduction, and variance in offspring number.
6. Detecting genes underwent selection due to infectious diseases in recently admixed populations.
7. Understanding the gene conversion landscape in human populations.
8. Algorithmic and data structure development in scaling methods to massive datasets.

As a postdoctoral fellow, you will have the opportunities to:

1. Collaborate closely with the PI and receive both low-level and high-level support on your research.
2. Mentor and collaborate with students at the graduate and/or undergraduate levels.
3. Develop your project ideas aligned with the direction of the lab.
4. Collaborate with other scientists from the Department of Computational Biology, the Cornell scientific community, and more broadly.
5. Grow your research program and plan for the next stages of your career.

Potential postdoctoral fellows are very much encouraged to get in touch. Generally, the most useful emails will touch on your background and previous work, how our research interests may intersect, your timeframe for seeking a position, and include a copy of your CV and the contact information of three references.

Contact: Prof. April Wei Cornell University aprilwei@cornell.edu <https://aprilweilab.github.io> April Wei <xw583@cornell.edu>

CornellU CnidarianEvolution

Postdoc Position in the Babonis Lab at Cornell University

Open until filled

The Babonis Lab in the Department of Ecology and Evolutionary Biology at Cornell University seeks to hire a highly motivated postdoc to work on the cellular, molecular, and developmental biology of cnidarians (corals, sea anemones, jellyfish). The Babonis Lab is interested in understanding the origin of taxon-specific traits (novelties) across levels of organization. Primary areas of interest in the lab currently include: the functional diversification of cnidocytes (stinging cells), the emergence of specialized animal secretory cell types, the evolution of stem cell identity, and the origin of novel genes. The Babonis Lab uses a broad range of taxa and techniques for interrogating the evolutionary and developmental drivers of novelty and provides a highly collaborative and interdisciplinary environment to support exploratory studies and maximize opportunities for discovery. For more information on our interests, visit: www.babonislabs.com. To qualify, applicants must have a Ph.D. (or be close to earning one) and expertise in molecular biology, genetics, and biochemistry. The ideal candidate will also have significant experience with transgenesis, functional genomics and genome editing (including CRISPR/Cas9 technology), gene delivery techniques (e.g. microinjection, electroporation), and expertise in DNA and RNA sequencing and analysis.

The position will be appointed initially for 1 year with the option to renew pending satisfactory performance and available funding. Salary is commensurate with NIH standards.

To apply, please visit <https://academicjobsonline.org/ajo/jobs/21484>. Please submit a current curriculum vitae, a 1-page statement of research interests detailing experience with the required and preferred techniques, and contact information for two professional references. Review of applications will begin May 1, 2022, and will continue until the position is filled.

Leslie S. Babonis, PhD (she/her) Assistant Professor

Curator of Marine Invertebrates Ecology & Evolutionary Biology Cornell University

E145 Corson Hall Ithaca, NY 14853
 babonislabs.com lsb257@cornell.edu

Eawag Lucern Aquatic Evolutionary Genomics

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology). Eawag conducts research, education and expert consulting to achieve the dual goals of meeting direct human needs for water and maintaining the function and integrity of aquatic ecosystems.

Eawag's Department of Fish Ecology & Evolution has an opening for a Postdoc in Evolutionary Genomics of Aquatic Ecosystems

The position, based in the group of Philine Feulner, is funded for 2 years within the project "The eco-evolutionary effects of predators in aquatic ecosystems". The project funded by the Swiss National Science Foundation is led by Blake Matthews (Eawag) and also includes a collaboration with Ryan Greenway (University of Konstanz). The Fish Genomics group of Philine Feulner focuses on evolutionary questions regarding the genetic basis of adaptation and speciation, and the influences of various evolutionary processes such as selection, drift, mutation, and recombination on genome evolution.

The project will investigate multiple stickleback populations in small to medium sized lakes across Southern Greenland, using a combination of existing whole genome data sets and new sequencing conducted throughout the project. The first major goal of the project is to infer demographic histories for different lake populations and explore to which respect colonization histories varied and influenced phenotypic variation across lakes. The second goal is to track initial evolutionary changes of stickleback from a recent experimental introduction of stickleback into six experimental ponds. This will involve existing sequencing data from the ancestors and new data sequenced from the first few generations. Within the larger project, which is also including a PhD position, the genomic data of the sticklebacks will be interpreted in the context of how stickleback evolve in response to both predation and prey community dynamics.

The candidate will be in charge of the analysis of next generation whole genome data of sticklebacks, the de-

velopment of bioinformatics pipelines and tools, and the interpretation and publication of the results. There will be opportunities to gain field experience in Southern Greenland, to develop their own research skills, and to assist in the supervision of Bachelors and Master students. Ideally, the candidate has a profound interest in Bioinformatics and Evolutionary Genomics and has earned a PhD in a relevant field of evolutionary biology, or bioinformatics. Excellent communication skills in English and ability and will to work in a team are essential. The group's working language is English and fluency in writing and speaking is required. Knowledge of German or French is not required.

The position is situated in the Department of Fish Ecology & Evolution: www.eawag.ch/en/department/-fishec/. The Department is part of Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB), which is located on the shore of Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science www.eawag.ch/forschung/cc/ceeb/. The postdoc will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science. The Fish Genomics group is also affiliated to the Institute of Ecology and Evolution of the University of Bern www.iee.unibe.ch, and the successful candidate will have a unique opportunity to take advantage of both these excellent academic environments. More information about the current research group and ongoing projects in both groups can be found at www.eawag.ch/en/department/fishec/main-focus/fish-genomics/ and www.blakematthewslab.com. Eawag is a modern employer and offers an excellent working environment where staff can contribute their strengths, experience and ways of thinking. We promote gender equality and are committed to staff diversity and inclusion. The compatibility of career and family is of central importance to us. For more information about Eawag and our work conditions please consult www.eawag.ch and www.eawag.ch/en/aboutus/-working/employment. We strongly encourage applications from researchers identifying as a member of a historically marginalized group.

Applications should include a cover letter with a concise statement about your previous education and research experience, your vision for the

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Hatfield UK Salmon Virus Evolution

We seek an ambitious and skilled postdoctoral scientist to undertake innovative research into combatting infectious disease outbreaks in animals.

Through close collaboration with global industrial partners and national government agencies, you will help pioneer how virus genomic sequencing approaches can be adapted and adopted to provide real-time information critical for informing interventions. You will become a key member of Dr Sarah Hill's research group during the 3-year post.

Key challenges will involve the design and refinement of rapid targeted and metagenomic genome sequencing approaches that can be used successfully within varied animal health, farming and aquaculture contexts. By combining newly generated virus genome sequences with detailed epidemiological, ecological, and industry data (including rarely available data on the network of individual host movements between farms), you will help gain high-resolution insights into the factors that drive virus transmission and the repeated emergence of new virulent strains. You will focus on explaining the transmission of two viruses within the production network of farmed Atlantic salmon.

Working in close partnership with the world's largest provider of animal health diagnostics will allow you to access samples and rarely available industry data from producers across the globe. Through funded visits to Norway and Scotland you will develop strong relationships with industry partners, which will enable you to see the impact of your work and help achieve the widespread adoption of the methods that you design. We will support you to travel to international and national conferences, and to access opportunities at the RVC and elsewhere that will enhance your professional career development. You will be encouraged to publish in high impact, international journals, including through collaborating with other researchers within the RVC community working on a range of emerging animal and human pathogens. Please see Dr Hill's Google Scholar profile for examples of her recent work, including collaborative publications in *Science*, *Nature* and *Lancet Infectious Diseases*.

The successful applicant will hold (or be about to receive) a PhD-level degree in a suitable subject, preferably in

virus genomics or genomic epidemiology. We are seeking candidates with either expertise focused on exploring novel sequencing methods, or candidates with a broader skill-set spanning both wet-laboratory sequencing and computational approaches.

We encourage interested candidates to contact Dr Hill (sahill@rvc.ac.uk), who would be very pleased to informally discuss this role further. Further information on the role and person specification is available at <https://jobs.rvc.ac.uk/vacancy.aspx?ref=PPS-0086-22>. "Hill, Sarah" <sahill@rvc.ac.uk>

HolarU Iceland Fitness Variation

Post-doctoral position on understanding the determinants of spatio-temporal variability of life-history traits in small populations

Holar University seeks a three-year post-doctoral fellow for an Icelandic Research Council (RANNIS) funded project. The goal is to study spatial and temporal variation in fitness, using data collected in a longitudinal study of sixteen small, isolated populations of Arctic charr found in lava caves, which we have followed since 2012.

The project is led by Assoc. Prof Camille Leblanc and Prof Bjarni K. Kristjánsson. It is part of a large collaboration across Holar University, Iceland (Prof. Skúli Skúlason), University of Edinburgh (Dr. Kasha Strickland, Dr. Elizabeth Mittell), University of St. Andrews, Scotland (Dr. Michael Morrissey) and University of Jyväskylä, Finland (Assoc. Prof. Katja Räsänen).

The phenotype is an important determinant of the dynamic interactions between ecological and evolutionary processes. However, to date, there is limited understanding of how spatio-temporal variation in phenotypes is related to fitness in the wild. Our study uses longitudinal data across a unique system of sixteen isolated small populations of Arctic charr (*Salvelinus alpinus*) inhabiting lava caves near lake Mývatn, Iceland. Individual-based data has been collected from these populations since 2012. This study system allows us to ask questions about the interplay between phenotypic traits (e.g. growth and morphology) and fitness (reproductive success and survival) and how ecological factors shape this relationship in space and time.

We are looking for a highly motivated postdoctoral can-

didate with strong quantitative skills, which will be applied to this unique study system. The post-doctoral fellow has the opportunity to: 1) use molecular tools to establish genetic pedigrees and assess reproductive success; 2) use mark-recapture data to estimate survival; and 3) combine these with individual-based phenotypic data to understand the interplay between ecological, phenotypic and fitness variation. The postdoctoral fellow will have opportunities to develop the focus of their work and will be encouraged to further develop their research career by opportunities in developing spin off projects, and through student supervision.

Location: The candidate will be based at the Dept. of Aquaculture and Fish Biology (DAFB - <http://holaraquatic.is>) at HÍlár University (HU, North Iceland). The candidate is also encouraged to spend time at the institutes of the collaborators. HU is situated in the beautiful village of HÍlár (Skagafjörður), with offices and research laboratories in the nearby town Sauðárkrúkur. DAFB is an active research centre, where the postdoc is part of a dynamic international team of graduate students and faculty. The beautiful natural setting and central location in North of Iceland, allow both outdoor and cultural activities.

Requirements: The candidate must hold a PhD degree in Ecology or Evolution or a related discipline. The ideal candidate should have a strong interest in evolutionary ecology and strong quantitative skills. A background in bioinformatics and/or analysis of quantitative genetic and/or long-term data sets would be an advantage. The candidate should have shown ability to publish their own findings, enjoy working in a dynamic group, and have experience with fieldwork. The candidate should be able to work independently as well as a part of a team.

The working language is English. A valid driving license is a requirement.

This is a 100% position for three years. Salary is in accordance with the current collective wage and salary agreement between the relevant union, and the Minister of Finance in Iceland. Rights and obligations follow the Act 70/1996 on the Rights and Obligations of Civil Servants.

Applicants should send an application letter, labelled with their name, with a statement of research interests and relevant experience (max. 2 pages), curriculum vitae with a list of publications, copies of academic qualifications and the names and e-mail addresses of three referees, as a single pdf to bjakk@holar.is. The deadline for application is May 1.

For further information contact Dr Bjarni K.

Kristjánsson (bjakk@holar.is) or Dr. Camille Leblanc (camille@holar.is).

Bjarni K. Kristjánsson, þáttgjafi

HÍlárskólinn í HÍlár / HÍlár University

Fiskeldis og fiskalífræðingadeild / Department of aquaculture and fish biology

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INRA Rennes Population Genetics

*Theoretical impacts of reproductive modes on the dynamics of genetic diversity of invasive populations and application on the case of the aquatic invasive plant, *Ludwigia grandiflora* subsp. *hexapetala*.*

*Post-doc position*at INRAE, L'institut Agro, UMR ESE in Rennes (west coast of *France*), 18-month position.

*Keywords:*population genetics, invasive species, reproductive modes (clonality, allogamy, autogamy), demography, spatial structure, dispersal.

Context:

Invasive species are good opportunities to understand how para- and peri-patric populations contribute to the biological evolution of organisms. Reproductive modes are key component to understand and predict the success of invasive species, with deep consequences on their demography, dispersal, genetic and phenotypic evolution and adaptation to the new habitats. Understanding the impacts of reproductive modes, demography and dispersal on the genetic diversity of a newly introduced species colonizing new areas will help predicting evolutions of invasive populations and inferring the ecological and evolutionary processes driving their biology.

The ANR Clonix2D project¹ is an international, collaborative project aiming at understanding the evolutionary consequences of partial clonality on genetic diversity and its structure during colonization events using a multidisciplinary approach involving mathematical modelling, simulations, and population genomics using various model species across the eukaryotic domain.

We developed demogenetic models and methods to understand, track and predict the evolution of partially clonal, polyploid populations colonizing new areas. We currently use these mathematical models to infer the ecological and evolutionary processes ongoing on the major aquatic invasive populations of *Ludwigia grandiflora*/ subsp. *hexapetala* (Lgh) colonizing western Europe watersheds. We demonstrated that this decaploid *Ludwigia*/ species reproduces using both sexuality and clonality and mates through a self-incompatible with at least one self-compatible type capable of selfing. We recently acquired a huge genotyping dataset on 37 populations over the Loire watershed, including temporal and parentage sampling on fewer populations.

We propose a postdoc position for 18 months to explore the ecological and evolutionary processes ongoing in these partially-clonal polyploid invasive populations, using their current genetic diversity and structure.

Conditions:

The recruited applicant will join the genetic, ecology and evolution group of INRAE/Institut Agro group working on theoretical and applied population biology in Rennes (France) with direct collaboration with Solenn Stoeckel (Demecology, IGEPP²) and Dominique Barloy (Evolutionary ecology of systems perturbed by biological invasions and xenobiotics, ESE³) for 18 months, daily available for group discussions, analyses and co-writings. Monthly gross salary from 2 800 euro to 3 000 euro, depending on professional experience, including vacation. Our team and Rennes research community constitute a friendly, open, inclusive, egalitarian and efficient environment to tackle ecological and evolutionary studies about invasive species, reproductive modes and the dynamics of genetic diversity within species, with skilled people in genetics, ecology, mathematical modelling and computing sciences., collaborative analyses

Duties:

The candidate will actively contribute to the analysis, interpretation and publication of the existing equations and datasets, specially developed and acquired for this project.

These datasets include i/ the numerical outputs of the adaptable mathematical and simulation models, ii/ the already-acquired *Ludwigia grandiflora*/ genotyping dataset across western Europe, and iii/ additional already-acquired genotyping datasets on partially clonal and potentially allo- and auto-gamous species across the eukaryote domains (publicly available, or in col-

laboration within the project with partners studying algae, fungi, tree species, recently spreading into new areas). We expect the postdoc to integrate their work in the living, friendly and established collaboration between Ifremer MARBEC (Sophie Arnaud-Haond) and University of Kansas (Maria E. Orive), and with ANR Clonix2D project partners, including Universidad Austral de Chile (Marie-Laure Guillemin), INRAE Nancy (Fabien Halkett), University of Alabama at Birmingham (Stacy Krueger-Hadfield), INRAE Bordeaux (Stéphanie Mariette) and CNRS Roscoff (Myriam Valero). We propose to use the *Ludwigia*/ dataset as an application of a more general study of the impacts of reproductive modes on the dynamics of genetic diversity in invasive populations using mathematical and simulation outputs of our own customisable developments, and, in a second step, to extend the

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Koblenz Populations Genetics

University of Koblenz, Institute for Integrated Natural Sciences

Postdoctoral or PhD Position in Population Genetics

Application deadline: 15th May 2022

The Department of Zoology, Institute for Integrated Natural Sciences, at the University of Koblenz, invites applications for a

Postdoctoral or PhD Position.

In case of appropriate experience, the position can also be filled as a PhD position.

Preferred starting date: July 1st 2022

Duration: 3 years

Salary: German salary scale (TV-L 13, 100% PostDoc, 66% PhD)

We invite applications from highly motivated candidates with a keen interest in population genetics. The position is available within the externally funded project “Condition, dispersal, and population connectivity of two butterfly species in agricultural landscapes”. Using two

species with contrasting dispersal ability, we will explore constraints on dispersal in traditional and modern agricultural landscapes. We will use an integrated approach combining field collections, common garden experiments, GIS analyses, and fine-scale landscape genomics.

Our department works mainly in the fields of evolutionary ecology and conservation biology. For further information please visit:

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

The successful candidate will (1) hold a Ph.D. or M.Sc., preferably in population genetics, (2) have experience with molecular genetic laboratory work, population and landscape analyses, and (3) be capable of doing field work. Experience with ddRADseq and SNPs will be advantage. Excellent English communication skills are essential.

The University of Koblenz is an equal opportunity employer.

To apply, please provide (i) a letter of motivation including a statement of your research experience, (ii) a scientific CV including publication list (if any) and copies of relevant certificates, (iii) names and contact details of two academic referees. Applications should be submitted electronically as a single PDF file to bewerbung-k21@uni-koblenz.de before May 15th 2022. Please mention your name and the call number (25-2022) in your application and in the header of your email.

For any enquiries please contact Prof. Dr. Klaus Fischer via e-mail:

klausfischer@uni-koblenz.de

For the official advertisement see: <https://www.uni-koblenz-landau.de/de/uni/organisation/stellen/wissenschaftliche-stellen>

Prof. Dr. Klaus Fischer

Institut für Integrierte Naturwissenschaften

Abteilung Biologie

Universität Koblenz-Landau

Universitätstraße 1

D-56070 Koblenz

klausfischer@uni-koblenz.de

Phone: +49-261-287-2238

Klaus Fischer <klausfischer@uni-koblenz.de>

Konstanz Taxonomy Species Delimitation

Postdoctoral position in Taxonomy, Species Delimitation & Evolutionary Biology

University of Konstanz, Department of Biology, Chair of Zoology and Evolution

Konstanz, Germany.

Earliest starting date: June 1st, 2022 or later

Description

A fully funded post-doctoral scholar position for 2 years will be available after the 1st of June at Prof. Axel Meyer lab to work on DFG funded work related to species delimitation in sympatric and allopatric populations of live-bearing fishes. The project aims at integrating whole-genome resequencing data and phenotypic data to conduct species delimitations applying coalescent-based integrative taxonomic approaches and to validate these by contrasting their outcome to empirically determined degree of reproductive isolation among species pairs. We seek applicants with a background in some of the following areas: evolutionary biology, taxonomy, phylogenetics and field research. We encourage applicants with bioinformatic skills.

The Meyer Lab at the Department of Biology at University of Konstanz, is interested in the origins of adaptations, speciation, and phylogenomics of fishes, in particular the cichlid fish adaptive radiations from Nicaragua and Africa. A total of three research groups two of which are headed by Junior Group Leaders make up the evolutionary biology group (15 members total in the lab).

The University of Konstanz and the Department of Biology are among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the southern border between Germany and Switzerland. The University of Konstanz and the Department of Biology are among them most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the southern border between Germany and Switzerland. Appointments are initially for three years and it comes with a competitive

salary, and excellent health and retirement benefits.

Qualifications

Required: PhD in Taxonomy, Ecology and Evolutionary Biology or Genetics/Genomics.

Preferred: Experience working with genomic data, a strong conceptual background in evolutionary biology, experience with field work.

Application Instructions

To Apply Submit the following documents to julian.torres-dowdall@uni-konstanz.de: - One page Cover Letter - C.V. - A relevant publication or manuscript in preparation - Contact information for 2 References

Applications will be considered until the position is filled.

Informal inquiries about the position are encouraged: julian.torres-dowdall@uni-konstanz.de

Julian Torres-Dowdall <julian.torres-dowdall@uni-konstanz.de > Axel Meyer <axel.meyer@uni-konstanz.de >

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

Julian Torres Dowdall <julian.torres-dowdall@uni-konstanz.de>

Krakow EvolutionaryPhysiology

Polish Academy of Sciences INC Krakow Poland.EvolEcolPhysiol

Postdoc position in the project "Integrating effects of anthropogenic and natural stressors across the organism's life cycle" at the Institute of Nature Conservation Polish Academy of Sciences in Krakow, Poland in collaboration with KU Leuven, Belgium.

The aim of the project is to understand how environmental stressors: native and invasive alien predators, increased temperature and seasonal time constraints influence key life history traits in aquatic invertebrates (bluetail damselfly) through changes in physiology and behaviour.

Requirements: - PhD in biology or ecology (PhD defence

not earlier than 7 years before the year of employment in the project; this period does not include breaks related to maternity leave) - Strong motivation for project work - Experience in field and laboratory work on animals - Experience in laboratory analysis of biochemical parameters - Publication record in leading ecological journals (at least five articles published within last five years) - Advanced skills in statistics in R environment - Fluency in English, written and spoken - Additional attribute: experience in and enthusiasm for working in an international team; valid driving license.

Responsibilities and job description: - Preparing field equipment and laboratory installations for experiments - Animal field sampling - Rearing experiment in climate chambers - Measurements of life history, behavioural (INC PAS in Krakow, Poland) and physiological traits (Univ. in Leuven, Belgium) - Involvement in work during irregular working hours (as field work and lab experiment require) - Attendance in national and international conferences/workshops - Collaboration with other group members - Running statistical analyses and writing manuscripts of scientific publications.

Required documents (combined in one PDF file): - Cover letter - Scientific curriculum vitae (including a list of publications) - Scan of Doctorate diploma - Contact details of two academics who can provide a reference.

I have funding from the National Science Centre, Poland (grant no. 2019/33/B/NZ8/00521) Contract of employment: full time for up to 15 months Starting date of employment: May/June, 2022 Application due date: 1 May, 2022 Salary: monthly gross salary ca. 8 000 PLN, ensuring a pretty good standard in Poland (average wage in Poland: +/- 5 700 PLN gross) Principal investigator: Dr hab. inÂ¿. Szymon Âniegula, <http://www.iop.krakow.pl/-pracownicy,102,szymon.sniegula.html> The posting is here, https://www.iop.krakow.pl/files/344/-call_post_doc_eng_2022_3.pdf To apply, please send combined in one PDF file documents to szymon.sniegula@gmail.com with 'postdoc 2022' in the subject heading.

Applications will be reviewed starting 1 May, 2022, and will be accepted until the position is filled.

Please contact Szymon Sniegula (szymon.sniegula@gmail.com) if you have any questions about the position.

Szymon Sniegula <szymon.sniegula@gmail.com>

KU Leuven PolarSeascapeGenomics

POSTDOCTORAL FELLOW IN POLAR SEASCAPE GENOMICS at KU Leuven, Belgium - Extended call

The KU Leuven invites scholars to apply for a 12 months postdoctoral fellowship on polar seascape genomics at the Division 'Ecology, Evolution and Biodiversity Conservation' (KU Leuven).

The research profile focuses on advanced expertise in seascape genomics to investigate research questions at the interface of marine evolution and global change biology. More specifically the candidate will determine the ecological and evolutionary interdependency of populations by studying the genetic structure, connectivity and adaptation of polar fish in the environmental context of the Southern Ocean and Arctic Sea. You genotype fish taxa with high throughput genomic tools and analyse connectivity and adaptation patterns with individual- and population-based statistical models. The study will result in advice on the conservation management of polar fish fitting in a context of ocean-wide resource management. The position is funded by the Federal Government and the European Union. The appointment is expected to start on July 1, 2022.

Marine science offers excellent prospects for a career, especially during the United Nations Decade of Ocean Science for Sustainable Development 2021-2030. We are looking for a motivated and internationally oriented colleague with an excellent research record.

The Division 'Ecology, Evolution and Biodiversity Conservation' hosts 10 professors active in ecology, evolution and ecosystem services. The Laboratory of Biodiversity and Evolutionary Genomics (LBEG) focuses on marine ecology and evolution, and collaborates closely with staff at the Royal Belgian Institute of Natural Sciences, associated to the project. Research assignment

The candidate is expected to further develop the analysis of high-throughput (RADseq) genotypes with bioinformatic and biostatistical tools, and prepare high quality scientific publications. You will be supported in your research by colleagues skilled in molecular tools and bioinformatic pipelines, and in the oceanographic and biological context of polar research.

Education The candidate has the option to take part in the teaching program at the KU Leuven to a limited extent.

Service Scientific, societal and internal services are an integral part of the assignment.

Requirements * PhD in Marine Science, Oceanography, Molecular Ecology or related disciplines. * Intermediate to excellent programming skills. * Experience with polar environments is an asset. * The quality of your research is proven by publications in leading international top 25% journals. * International research experience is an important advantage. * Your spoken and written English is excellent. The official administrative language at KU Leuven is Dutch.

Offer * We offer employment in an intellectually challenging environment. KU Leuven is a research-intensive, internationally oriented university that carries out both fundamental and applied scientific research. Our university is highly inter- and multidisciplinary focused and strives for international excellence. * We offer state-of-the-art access to data banks, statistical expertise and computational facilities. * KU Leuven offers a remuneration according to the grade of postdoctoral fellow, and free public transport or a bike allowance between home/work. * You will work in Leuven, a historic, dynamic, sustainable and vibrant city located in the heart of Belgium, within twenty minutes from Brussels. Leuven is located less than two hours from Paris, London and Amsterdam.

Interested? More information on the content of the job can be obtained from prof. Filip Volckaert (KU Leuven) at phone +32 16 32 39 72 and email filip.volckaert@kuleuven.be. The website of KU Leuven - LBEG is <https://bio.kuleuven.be/eeb/lbeg>. Application format and deadline Please apply no later than May 30, 2022 via the online application tool (KU Leuven academic jobs - <https://www.kuleuven.be/personeel-jobsite/jobs/60097059>). We request a motivation letter, CV, summary of your PhD thesis, a short commentary on your 5 most significant publications, evidence of accomplished skills and competences, and contact details of 3 reference persons with full addresses. Interviews will be organized in June 2022.

KU Leuven places foremost importance on research integrity and ethical conduct and will therefore ask you to sign an integrity statement upon appointment. KU Leuven is committed to creating a diverse environment and are therefore equal opportunity employers. They explicitly encourage candidates from groups that are currently underrepresented at the university to submit their application. KU Leuven seeks to foster an environment where all talents can flourish, regardless of gender, age,

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Laramie Wyoming WildlifeDataScientist

Laramie_Wyoming.WildlifeDataScientist

The Merkle Research Group (<https://merkleresearchgroup.org/>) at the University of Wyoming is seeking a Wildlife Data Scientist to work at the interface of data science and the ecology and conservation of animal movement. The scientist will develop and publish independent research in collaboration with the Wyoming Cooperative Fish and Wildlife Research Unit and our state, federal, and NGO partners. The scientist will also provide data science service to multiple units at University of Wyoming including the Merkle Research Group and Wyoming Geographic Information Science Center.

Research themes can be geared to the scientist's interests but must center on the ecology and conservation of animal movement. The scientist will have the opportunity to play a strong role in leading data science activities (e.g., GIS workflow development, R package development, database development and management) relative to several research and conservation programs within the Merkle Research Group. Further, the scientist will play a leadership role in developing a wildlife ecology component to the University of Wyoming's brand-new School of Computing.

Minimum qualifications include: 1) PhD in wildlife ecology, quantitative ecology, Information Technology, computing, or related field; 2) Proficient with R and ArcGIS; 3) Strong career interest in developing connections between data science and ecology; 4) Experience with managing and analyzing remote sensing and GPS collar data; 5) Excellent written, verbal, and interpersonal communication skills; and 6) Excellent peer-reviewed publication record for career stage.

Desired qualifications include: 1) Experience working with interdisciplinary teams; 2) Experience coordinating analytical teams; 3) History working with field biologists and wildlife managers; 4) Knowledge of various database programs and web mapping protocols (e.g., SQL Server, C#, JavaScript, Shiny).

The following documents are required to apply: online

application form (link below), detailed cover letter, CV, and contact information for four work-related references. The Wildlife Data Scientist will be employed by the University of Wyoming. We envision this position to be relatively long-term, and we have 3-yrs of funding secured. The person must relocate to Laramie, WY. Salary will be approx. \$55,000 depending on experience and includes full University of Wyoming benefits. The preferred start date is September 2022. Review of applicants will begin 4 May 2022. Please direct questions related to this position to Dr. Jerod Merkle (University of Wyoming) at jmerkle@uwyo.edu. Use the following link to apply: https://eeik.fa.us2.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/220406. Jerod Merkle <jmerkle@uwyo.edu>

LMU Munich SymbioticStress

Postdoctoral position: "Stress tolerance of symbiotic and free-living organisms"

We seek applicants with interests and background knowledge in the fields of Comparative Genomics, Bioinformatics, Population Genomics, Evolutionary Biology or Fungal Ecology to perform post-doctoral research in order to understand stress tolerance in symbiotic taxa, relative to their free-living relatives, using comparative transcriptomic and ecophysiological approaches.

Applicants should have the ability to work independently and publish their results in well-respected peer-reviewed journals. Applicants are required to have effective communication skills, both oral and written, and should be able to work and integrate in a team. Experience with bioinformatics for genomic/transcriptomic analyses is required. R-programming and analytical skills are considered advantageous. Experience with fungi or algae is desirable, and candidates possessing this experience will rank higher. Advantageous are skills in python or another programming language. Essential are German language skills and excellent manuscript writing skills. Applicants should have a doctorate in the field of bioinformatics, population genetics, genomics or comparable.

Salary and benefits are in accordance with a public service position in Germany (collective agreement TV-L E13, 50%). The contract shall start as soon as possible and will be limited to 12 months, with a possibility for extension depending on performance. Equally qualified

handicapped applicants will be given preference.

Our major research areas are population genetics, systematics and ecology of symbiotic fungi. The main study systems of our group are the model lichen lungwort (*Lobaria pulmonaria*) and other species of the Peltigerales. Lungwort is an epiphytic lichen which has been studied extensively regarding its ecology and dispersal biology. Extensive genome sequence datasets are already available for lungwort, including multiple assembled and annotated genomes of the mycobiont and of its primary photobiont, the green alga *Symbiochloris reticulata*. Our group has recently sequenced, assembled and annotated the genomes of several additional lichen symbionts.

The greater Munich area hosts two large Universities and several large research institutes. Faculty of biology of the LMU is characterized by a vibrant, international research environment setting the stage for fruitful collaborations. The candidate's workplace will be located near the premises of the beautiful Botanical Gardens of Munich in the Nymphenburg area.

With its beautiful old town, green spaces such as the forests along the Isar river, English Garden, Nymphenburg castle, numerous beer gardens and active night life, arguably, Munich is one of the cities with highest life quality in Germany. An interesting feature of Munich is its location proximate to the Alps, providing interesting opportunities both for biological studies and for various recreational activities.

Applications consisting of a CV, publication list, possible starting date, and a short statement of research interests (maximum 1 single-spaced page in length), names and contact information of up to three references should be prepared in a single pdf file and sent by email to Silke Werth, werth@bio.lmu.de. Review of applications will start on April 15th 2022, but applications will be accepted until a suitable candidate has been found.

Information on the research environment at University of Munich can be found here: www.en.biologie.uni-muenchen.de Information on relocation to LMU can be found here: www.en.uni-muenchen.de/about_lmu/-contact/int_office/index.html Prof. Dr. Silke Werth LMU Munich Systematics, Biodiversity and Evolution of Plants Menzingerstraße 67 80638 Munich Germany Phone: +49 89 17861 207 Silke Werth <werth@bio.lmu.de>

Werth <werth@biologie.uni-muenchen.de>

LundU PlantGenomics

LundU.PlantGenomics&Bioinformatics

Post-doctoral Fellow Position

Lund University, Sweden

<https://lu.varbi.com/en/what:job/jobID:499575/> We are looking for a postdoctoral fellow

We are accepting applications for a two-year postdoctorate fellow position in bioinformatics and plant genomics to 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. The candidate will use traditional and advanced machine learning-based approaches. In addition, the project will collaborate with researchers in other disciplines, including medicine, biostatistics, and paleogenomics.

See the link above for full details.

Review of applications begins on mid-May 2022.

Overview:

Candidates are expected to have an interest in plant biology alongside strong computational skills with a background in statistics, computer science, and/or a related field. Candidates are also expected to have experience with plant genomics. The candidate will work jointly with Dr. Eran Elhaik, Prof. Allan Rasmusson (Lund University) and Prof. Laura Grenville-Briggs (Sveriges lantbruksuniversitet (SLU), Alnarp).

If you have questions about the position, please email me, but apply on the website, not by email.

Kind regards,

Eran Elhaik, Ph.D. Assoc. Professor in genomics

Lund University Faculty of Science Department of Biology SE 223 62 Lund Visiting address: S-223 62 Lund
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Tel: +46 46-222 9419 Fax: +46 46-222 44 25
eran.elhaik@biol.lu.se <http://www.eranelhaiklab.org/>
Eran Elhaik <eran.elhaik@biol.lu.se>

NHM London Machine Learning Cranial Suture Evolution

Postdoctoral Research Associate - Machine Learning and Computer Vision for Cranial Suture Evolution through the Synapsid-Mammal Transition

We are currently advertising for a 2-year Postdoctoral Research Associate in Machine Learning and Computer Vision at the Natural History Museum, London. The Natural History Museum is one of the world's top museums and is internationally recognised as a leader in the study of the natural world through its collections and its role as a centre of excellence in scientific research and in the presentation of natural history through exhibitions, public programmes, publications and the web. This post will be based jointly in the Department of Life Sciences at the Natural History Museum (primary institution) and the School of Engineering at London South Bank University, working with PI Anjali Goswami, Co-Is Enrico Grisan, Alana Sharp, and Arkhat Abzhanov, and PDRA Heather White. The successful applicant for this post will be responsible for developing machine learning and computer vision tools for the automated extraction of cranial suture morphology and skull shape from 3D meshes for living and fossil specimens spanning the past and present diversity of synapsids, the clade that today is represented by mammals

This post is funded by a Leverhulme research grant that will focus on the evolution of cranial sutures through the synapsid to mammal transition. The mammal skull performs numerous critical functions, from prey capture and feeding to protecting the brain to fighting. These functions impose enormous pressures which are buffered by the skull's shock absorbers: cranial sutures. These highly variable joints between skull bones are intimately linked with ecology and development, but their complex 3D anatomy makes them tricky to capture using traditional methods. As a result, we know almost nothing about their macroevolutionary patterns. Bridging imaging, machine learning, cranial function and evolution, this project will reconstruct suture evolution and its role in one of the most important events in the history of life: the rise of mammals. The successful candidate will work closely with the PIs, Co-Is, and an evolution PDRA in developing these methods and applying them to a new cranial dataset for synapsids. They will be expected to lead on scientific publications describing these new

methods, including open access, user-friendly tools, and present at conferences, as well as promote the project at various outreach events at the NHM and outside the museum as the opportunity arises. We provide a friendly, flexible, and collaborative environment to accommodate and support diverse circumstances, backgrounds, and needs.

Main Responsibilities

- * Develop novel machine learning and computer vision tools for automated extraction of cranial suture morphology from 3D meshes
- * Lead or contribute to development and refinement of tools for automated capture of skull shape data from 3D meshes
- * Develop tools applicable to surface and micro-CT scans
- * Write well-documented code and produce user-friendly tools for open access dissemination
- * Work closely with project team, including Evolution PDRA, PI, and Co-Is for delivery of the full project
- * Lead and contribute to research publications
- * Present results at scientific conferences
- * Travel to work with collaborators as needed
- * Contribute to future research proposals

Person Specification

Essential:

- * PhD in Computer Vision, Machine Learning, or a relevant subject, completed or submitted by the time of starting this position.
- * Experience with 3D data and models
- * Experience developing ML models in R or Python
- * Ability to work independently, but also as part of a team
- * Demonstrated ability to complete a research project(s)
- * Track record of publications in international peer-reviewed journals
- * Strong communication skills; experience in presenting research at conferences

Desirable:

- * An interest in natural sciences and evolutionary biology
- * Experience with morphometric analyses in R
- * Experience in presenting research results to the public

Salary: 38,797 (Full time, 24 month fixed term contract)

Deadline, Wednesday, April 20, 2022, 5pm BST (GMT+1)

Interviews expected week of May 2

To apply

If that sounds like you, please apply online on the Natural History Museum's careers portal: https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail_2394.aspx You should upload the following documents:

- * A comprehensive curriculum vitae giving details of relevant achievements in recent posts as well as your

education and professional qualifications. * A covering letter that summarises your interest in this post, providing evidence of your ability to match the criteria outlined in the role competencies.

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NMNH Smithsonian FormFunctionSpiderEvolution

Postdoctoral Fellowship: Combining Functional Data with 3D Morphometrics to Understand the Evolution of Spider Chelicerae (“Jaws”)

Drs. Hannah Wood and Jeff Shultz are seeking a 2-year Postdoctoral Fellow. The appointment has the possibility to extend one year, for a total of three years. The Fellow will be primarily based at the National Museum of Natural History, Smithsonian Institution, in Washington DC, working with Hannah Wood, but will also collaborate closely with Jeff Shultz at the University of Maryland, College Park. The ideal applicant will have a strong interest in morphology and evolution, strong capabilities to work and learn independently, and a proven publication record.

This Postdoctoral Fellowship is funded by the National Science Foundation and has the goal of examining the evolution of cheliceral form and function across spiders using several different methodologies: 1) gathering UCE sequence data and phylogenetic analysis; 2) micro-Computed-Tomography scanning and 3D-morphometric analysis; 3) histological sectioning; 4) high-speed videography of cheliceral strikes; 5) comparative phylogenetic techniques.

There is flexibility in tailoring this position to the applicant’s research interests. Ideally though, the Postdoctoral Fellow will have experience or a strong interest in learning how to analyze and process 3D shape data from micro-Computed-Tomography scans. The Fellow will have some freedom to develop their own projects, although ideally their research interests will align with the goals of the project, that of using phylogenetics and functional morphology to understand morphological diversification. Applicants can come from a variety of backgrounds, but we are particularly interested in

those with a strong interest in functional morphology and evolution.

Responsibilities include: - Initiate and perform research on the morphology, function and evolution of spider chelicerae (“jaws”), and writing up the results of this research for publication in peer-reviewed journals. - Collaborating with other personnel involved in the project, which includes PIs, graduate and undergraduate students, and interns at both NMNH and UMD. - Participating and presenting at scientific conferences. - Participating in outreach activities, such as interacting with the public at NMNH and developing activities for children at “Bug Camp”, and acquiring mentoring experience. - Career development with the goal of building a strong CV and job application profile.

Starting salary is \$61,915, and includes benefits for Smithsonian non-federal Trust hires and built-in salary increases each year. The position can begin as soon as the NMNH hiring process is complete - typically taking 3 months.

To be considered, send an email to Hannah (woodh@si.edu) or Jeff (jshultz@umd.edu) that includes the following attachments: 1) a cover letter expressing your interest and your qualifications for the position, 2) your curriculum vitae, and 3) names and contact information of 2-3 professional references.

To receive full consideration, submit your application by April 20, 2022; however, we will consider applicants until the position is filled.

Please email Hannah Wood (woodh@si.edu) or Jeff Shultz (jshultz@umd.edu) with any questions or concerns about this position.

Hannah M. Wood Research Entomologist Department of Entomology National Museum of Natural History Smithsonian Institution

WoodH@si.edu

Norway eDNA Bioinformatics

Postdoctoral Research Fellow in Bioinformatics of eDNA
A position as Postdoctoral Research Fellow in bioinformatics of eDNA is available at the Arctic University Museum of Norway, UiT. The appointment is for two years. The workplace is at UiT in Tromsø, $\frac{1}{2}$. You must be able to start in the position no later than 6 months after receiving the offer. You will conduct research as a part of the newly established Norwegian Centre for Arctic Ecosystem Genomics (ArcEcoGen) and will be part of the methodological development working group.

The position will focus on developing new methods for processing and annotating DNA metabarcoding data. Our group has been analysing modern and ancient environmental samples using DNA metabarcoding for many years. We have a large collection of datasets corresponding to these samples, and a great deal of expertise on how to process them modularly. We now want to take advantage of this data collection to develop an efficient machine learning-based system capable of establishing cleaning and annotation rules for multiple broad taxonomic groups conditional on the ecosystem studied. The rules and annotations proposed by the system can be compared with those established empirically. While the architecture of the system remains to be defined in collaboration with the person recruited, it should be based on a database that can archive all the raw data and their annotation, and on, for example, a machine learning system backed up by this database. The position holder will also participate in teaching, outreach, and assistance to the ArcEcoGen members. It is expected that the position holder will participate in research group collaboration and professional networks nationally and internationally and will also be encouraged to obtain external funding from national and international funding agencies (e.g. RCN/EU).

<https://www.jobbnorge.no/en/available-jobs/job/-223609/postdoctoral-research-fellow-in-bioinformatics-of-edna> See also other positions here: <https://uit.no/research/arcecoegen> Prof. Inger Greve Alsos The Arctic University Museum of Norway UiT - The Arctic University of Norway NO-9037 Tromsø, $\frac{1}{2}$ Norway Telephone: +47 77 62 07 96 Telefax: +47 77 64 51 05 Email: inger.g.alsos@uit.no NOTE THAT WE ARE RECRUITING 9 POSITIONS: https://uit.no/research/arcecoegen#news_768037 <http://en.uit.no/ansatte/inger.g.alsos>

<http://ecogen.no/>
<https://www.iceagent.no/> <http://svalbardflora.no/>
<https://orcid.org/0000-0002-8610-1085> Inger Greve Alsos <inger.g.alsos@uit.no> Inger Greve Alsos <inger.g.alsos@uit.no>

OkinawaInstSciTech 4 Evolution html

<pre> The Marine Macroevolution Unit at the Okinawa Institute of Science and Technology (OIST) is looking for a postdoc or staff scientist in Ichthyology. Position is for 3+ years (dependent on progress) and start date is flexible. <https://www.oist.jp/careers/postdoctoral-scholar-or-staff-scientist-ichthyology> We seek a highly motivated, expert researcher with a deep knowledge of fish biodiversity, including but not limited to systematics, taxonomy, and ecology. The researcher will pursue groundbreaking projects on ichthyological topics, such as the origins of the Indo-Pacific biodiversity hotspot, diversification of fish groups, description and characterization of species and communities, and/or the influence of environmental and ecological factors on fish biodiversity.

Responsibilities: - Lead innovative projects focused on the ichthyological interests of the Marine Macroevolution Unit. - Publish results in high-quality journals. - Present at national and international conferences.

Qualifications: (Required) - PhD in Ichthyology, Ecology and Evolutionary Biology, Organismal Biology, Fisheries, Systematics or related field with dissertation focused on fishes. - Deep experience and understanding of fish biodiversity and taxonomy, with expertise in at least one major clade. - Interest in biodiversity, macroecology, and/or systematics questions. - Experience with specimens and museum collections, including imaging, preservation and dissection. - Familiarity with various descriptive and quantitative methods in Ichthyology (e.g. systematics, Phylogenetic Comparative Methods, CT imaging, geometric morphometrics, community metrics, etc.). - Willingness to develop knowledge about clades, areas, and events of interest to the unit if outside of past experience (e.g. paleoichthyology, evolutionary development). - Willingness to learn new methods as needed. - Willingness to collaborate with other units in the Marine Science and Ecology at OIST and other labs outside. - Willingness to travel to museum collections or field sites. - Good spoken and written English skills, includ-

ing relevant scientific terms and concepts. Japanese is not required but classes are provided to OIST employees and their families.

(Preferred) - Proficiency in phylogenetic comparative methods and image processing. - Proficiency in quantitative methods (e.g. Systematics, Phylogenetic Comparative Methods, geometric morphometrics, CT scan data, etc). - Proficiency in R or other programming language. - Proficiency in molecular phylogenetics. - Track record of publications demonstrating broad interests in fishes, including descriptive, systematic, and macroevolutionary.

Term: Full-time, the postdoctoral position (PhD <5 years) is initially for one year and can be extended to 2 more years based on performance and mutual agreement. The staff scientist position (PhD>5 years) is initially for one year and can be extended further based on performance and mutual agreement.

Benefits:

- Relocation, housing and commuting allowances - Annual paid leave and summer holidays - Health insurance (Private School Mutual Aid <http://www.shigakukyosai.jp/>) - Welfare pension insurance (kousei-nenkin) - Worker's accident compensation insurance (roudousha-saigai-hoshou-hoken)

Submission Documents: Single PDF with Title "Last-Name_FirstName_PositionArea" including:

- Cover letter including brief statements of research interests and interest in the unit (3 pages max). - List of top three representative publications (or manuscripts in prep) with one paragraph summary of key findings and scientific value for each. - Contact information for 3 recommendations (will be contacted after first evaluation) - Full CV including publication list. * Prior to the start of employment all new hires are required to successfully complete a background check. Personal information including employment history and academic background should be submitted to third-party administrators after a conditional offer of employment.

Application Due Date: June 1, 2022 for full consideration. Applications will continue to be screened until the position is filled.

How To Apply: Apply by emailing your Submission Documents to:

Lauren.Sallan[at]oist.jp

(Please replace [at] with @ before using this email address)

Declaration:

— / —

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OklahomaStateU ModellingDisease

Post-doctoral position in statistical modelling of infectious diseases and biodiversity

Applications are invited for a Postdoctoral Research Associates in to join the Stephens lab in the Department of Integrative Biology at Oklahoma State University. The position is associated with a project funded by NIH "Spillover of Ebola and other filoviruses at ecological boundaries."

The successful candidate will build statistical models of large-scale disease dynamics and biodiversity, primarily spillover and outbreak risk for Ebola and other African filoviruses, participate in database development, and develop project workflows in R. Knowledge of statistical modelling, machine learning (such as boosted regression trees), GIS, proficiency with R and experience either with macroecological analyses or statistical analyses of disease dynamics are required. Additional skills such as knowledge of disease ecology, Ebolavirusecology and evolution, economic or biodiversity analyses, mathematical modelling, phylodynamics or phylogenetic comparative methods in general are welcome but not essential.

Required qualifications are a Ph.D. in ecology, evolutionary biology, statistics, economics, epidemiology or closely related fields. Candidates with a past record of publication in disease ecology, macroecology, or economics will be given preference. Candidates must have excellent English writing and verbal communication skills, as well as an established record of productivity (i.e., at least one previous peer reviewed publication). The position will initially have a duration of one year, with possibility of extension to a second year depending on satisfactory performance and funding availability. Compensation will include \$53,760 for 12 months of salary, as well as health insurance and other benefits.

Send all inquiries to Patrick Stephens at (patrick.stephens@okstate.edu). To apply, please submit a (1) cover letter addressing how your expertise meets the position requirements, (2) a CV, (3) one representative publication, and (4) contact info (phone and email) for three references to Patrick Stephens (patrick.stephens@okstate.edu). In the subject line of

your e-mail, please include your name and the name of the position (i.e., "Application for Statistical Modeling of Spillover Risk: LASTNAME"). Applications received by May 16, 2022 will receive full consideration. However, recruiting will continue until the position is filled so applications received after this date may still be considered. We value the diversity of perspectives that a team made up of individuals with varied backgrounds will possess and encourage applications from members of groups underrepresented in STEM.

Oklahoma State University, as an equal opportunity employer, complies with all applicable federal and state laws regarding non-discrimination and affirmative action. Oklahoma State University is committed to a policy of equal opportunity for all individuals and does not discriminate based on race, religion, age, sex, color, national origin, marital status, sexual orientation, gender identity/expression, disability, or veteran status with regard to employment, educational programs and activities, and/or admissions. For more information, visit <https://eeo.okstate.edu>. "Stephens, Patrick" <patrick.stephens@okstate.edu>

RBG Kew Fungal Evolution

Postdoctoral Research Associate - Comparative Fungal Biology

Apply here: <https://careers.kew.org/vacancy/-postdoctoral-associate-comparative-fungal-biology-481299.html> The Royal Botanic Gardens, Kew (RBG Kew) is a leading plant science institute, UNESCO World Heritage Site, and major visitor attraction. Our mission is to understand and protect plants and fungi for the well-being of people and the future of all life on Earth. We are working to end the unprecedented extinction crisis and to help create a world where nature is protected, valued by all and managed sustainably.

We are seeking a highly motivated scientist to perform research on fungal phylogenomics to analyse, interpret, and publish genome data generated by the 'Discovering the Fungal Tree of Life' (DFToL) project (<https://www.kew.org/science/our-science/projects/fungal-tree-of-life>); and to explore the viability of our collections and their associated traits in fungal genomics research.

You will join Kew's science staff as a Postdoctoral Research Associate, conducting and publishing outstanding research and helping to develop funding streams to

further support your science within the Comparative Fungal Biology team, part of Trait Diversity and Function, one of five Priorities in the Science Directorate. This position will provide you with the opportunity and skills to gain international recognition.

You will be an enthusiastic early career scientist with a PhD in a relevant subject area (we are seeking candidates with bioinformatics skills and desirably fungal knowledge) and, ideally, some postdoctoral experience. You will have a proven aptitude for delivering excellent science publications and demonstrated potential to raise research income. You will be an outstanding and enthusiastic communicator who is ready to engage with students, peers and the general public.

The salary will be 35,000 per annum.

This role is based at Kew with the option of regular home working, subject to operational requirements.

Our fantastic benefits package includes opportunities for continuous learning, a generous annual leave entitlement, flexible working to help you maintain a healthy work-life balance, an Employee Assistance Programme and other wellbeing support such as cycle to work scheme and discounted gym membership. We also offer a competitive pension, an employee discount scheme and free entry into a wide range of national museums and galleries, as well access to our own beautiful gardens at Kew and Wakehurst.

Dr. Ester Gaya Senior Research Leader | Comparative Fungal Biology Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK Tel.:+44(0)208 332 5381 Email: e.gaya@kew.org

Ester Gaya <ester.gaya@gmail.com>

Senckenberg 3 Lichen Genomics html

<pre> Job announcement ref. #11-22010

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with more than 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (SBiK-F) explores the interactions between biodiversity, climate, and society.

The Senckenberg Biodiversity and Climate Research Centre invites applications for a

Postdoctoral Researcher (m/f/d) in Movement Ecology of Asiatic Wild Ass

(full-time position, 100%)

We are seeking a candidate (m/f/d) with a strong background in quantitative ecology to advance research in the movement ecology of Asiatic wild ass (*Equus hemionus*, Khulan in Mongolian). Possible topics include research related to animal movement behaviors, habitat selection, human disturbance, and related fields. We expect strong quantitative and conceptual skills, basic ecological knowledge, and an interest in understanding drivers of animal movements in relation to changes in land use and climate.

The research program is part of a scientific collaboration among SBIK-F, the Wildlife Conservation Society Mongolia (WCS Mongolia), and Inland Norway University of Institute of Applied Sciences (INN). You will have the opportunity to work on GPS tracking data of Khulan in relation to anthropogenic developments and climate change in the Mongolian Gobi ecosystem. You will collaborate with natural scientists and movement ecologists at SBIK-F and colleagues from WCS Mongolia and INN. Research questions will revolve around the effect of infrastructure on behavior and habitat selection and could also relate to activity patterns and navigation mechanisms in relation to key resources (e.g. water points). We expect you to be highly motivated to collaborate with researchers and conservation practitioners in Mongolia.

In addition, you will have the opportunity to develop your own research questions in collaboration with a large international and interdisciplinary research team, spanning expertise in movement ecology, community ecology, social ecology, and ecosystem functions at SBIK-F.

Tasks and Responsibilities

Develop models quantifying impacts of anthropogenic developments on movement and habitat selection of Khulan
 Develop your own research questions related to Khulan movement behavior
 Prepare training materials for students and researchers in Mongolia
 Travel to Mongolia
 Publish research results in international peer-reviewed journals
 Present research results at scientific conferences
 Your Profile

A PhD degree in Ecology, Geography, or a related field
 Excellent quantitative and statistical skills, excellent programming skills in R, and programming of large databases
 Experience with movement and spatial analyses
 Enthusiasm for collaborating across institutions and coordinating interdisciplinary and collaborative research projects

Salary and benefits are according to a full-time public service position in Germany (TV-H E13, 100%). The position is a one-year fixed-term post with a possible extension for one further year.

The Senckenberg Research Institutes support equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany.

You would like to apply?

Please send your application, mentioning the reference of this job offer (ref.#11-22010) until May 12th, 2022 by e-mail (attachment in a single pdf document) and include

a cover letter detailing research interests and experience
 detailed CV
 copy of your certification
 copies of two publications
 contact details of two potential academic referees
 To:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

This project takes place in the working group of Professor Thomas Müller.

For scientific enquiries please contact Dr. Nandintsetseg Dejid (nandintsetseg.dejid@senckenberg.de).

Mit freundlichen Grüßen / Yours sincerely

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung

(Rechtsfähiger Verein gemäß \S 22 BGB)

Senckenberganlage 25

60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG)

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales

- 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting)

- 1478 Gajcevic, Isabel

- 1564 di-Biase, Maria

- 1204 Reitinger, Jasmin

Fax: 0049 (0)69 / 7542-1445

Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Klement Tockner, Prof. Dr. Katrin Bohning-Gaese, Dr. Martin Mittelbach, Prof. Dr. Andreas Mulch, Prof. Dr. Karsten Wesche;

Präsidentin: Dr. h.c. Beate Heraeus;



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Senckenberg MolluscBioinformatics

We are recruiting a bioinformatician focussing on mollusc genomics in the lab group of Prof Dr Julia Sigwart based in the Senckenberg Research Institute and Museum, Frankfurt, Germany. This position will support a research programme investigating rare and “superweird” molluscs including target species with extraordinary adaptations and body forms. This is advertised as a postdoctoral position but a PhD is not strictly required - skills and experience are more important than qualification - please circulate widely.

Application deadline 11 MAY

To apply, please submit a CV, cover letter, and the anonymous application information form (details below) to recruiting@senckenberg.de

Job posting ref. #01-22014

For over 200 years the Senckenberg Gesellschaft für Naturforschung represents one of the most relevant institutions investigating nature and its diversity. Currently, scientists from more than 40 countries conduct research in the fields of biodiversity, earth system analysis and climate change in seven Senckenberg Institutes across Germany.

Following its mission to analyse and document biodiversity in earth system dynamics - to serve science and society, Senckenberg fosters curiosity-driven and application-oriented research. In Senckenberg at Frankfurt we seek to fill the position of a Bioinformatician

This position is funded by a five-year project designed to combine cutting edge technology for studying both

the anatomical and genomic basis for evolutionary novelties in molluscs, and test whether genomic novelties are more strongly associated with armour and shell morphology or rather physiological adaptations that allow the invasion of new niche spaces.

Your job would be to provide bioinformatics capacity especially in de novo genome assemblies of mollusc species.

Your tasks:

- Genome assembly and annotation of mollusc species that are sequenced via the LOEWE TBG and external partners using state-of-the-art sequencing technologies and compute infrastructure
- Support other members of the research group working on morphological features to identify specific research questions
- Perform independent research in collaboration with other members of the research group, the LOEWE-TBG, Senckenberg Ocean Species Alliance, and external collaborators on molluscan genomics
- Perform comparative analyses of resulting genomes including for phylogenomics

Your profile:

- Master degree or equivalent training and experience in bioinformatics / computational biology, genomics or a related area; a PhD degree in these fields is an advantage but not strictly required
- Experience with shell scripting and Unix tools
- Previous experience in genomics, genome assembly and/or annotation using non-model organisms, preferably molluscs
- Familiarity with measures of genome assembly data quality and completeness, troubleshooting, screening data for contamination
- Genuine curiosity and interest in nature, the oceans and their inhabitants, and especially molluscs

What can you expect?

- An interesting and challenging task in a dynamic and stimulating team of researchers, technicians and communicators
- Excellent benefits and work-life balance: Flexible working hours - dual career service - leave of absence due to family reasons - parent-child-office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt - leave of 30 days/ year

Senckenberg supports equal opportunity for men and women and places an emphasis on fostering career opportunities for women and under-represented groups. Qualified women and other under-represented groups are strongly encouraged to apply. Part time options are available. Equally qualified applicants with disabilities will be given preference.

Senckenberg is a globally connected institute. The working language within this project is English. Frankfurt is a vibrant, international, culturally diverse city and one

of the world's travel hubs. We welcome candidates from all nations and will provide support with your relocation process.

Location: Frankfurt am Main, Germany

Volume of employment: 100 % full-time position (40 weekly working hours)

Type of contract: Employment shall start as soon as possible and will be limited for a two-year contract

Remuneration: According to a German public service collective agreement TV-H EG 13

“julia.sigwart@senckenberg.de”
<julia.sigwart@senckenberg.de>

SwissOrnithInst GenomicConflictTEsSVs

Postdoc position: Escalation of TE-related genomic conflict under hybridization in birds

An SNSF-funded 2-3-year postdoc position on bird genomics is available in the research group of Reto Burri at the Swiss Ornithological Institute (<http://www.vogelwarte.ch>), Switzerland.

The Project The project is fully funded by the Swiss National Science Foundation (SNSF). It focuses on a songbird system characterized by pervasive hybridization to test key hypotheses on the role of escalating genomic conflicts between TEs and their repressors in reproductive isolation. To this end, the research leverages extensive linked-read genome resequencing data to test the hypotheses that (1) hybrids exhibit increased TE proliferation and thereby increased rates of chromosomal rearrangements (SVs) and (2) the TE-related genomic conflict constrains gene flow between species. The research builds on available state-of-the-art genomic resources.

The working environment The research group is interested in the molecular underpinnings of phenotypic adaptation and speciation in birds and the trajectories along which they evolve. To this end, we apply population genomic, phylogenomic, and comparative genomic tools on large-scale whole-genome resequencing data. The host institution, the Swiss Ornithological Institute (<http://www.vogelwarte.ch>), is a non-profit research institute in Switzerland. We perform research on birds to address basic scientific and applied/conservation questions, disseminate information on bird ecology and

conservation to the public, media, and authorities, and provide foundations for the effective conservation of birds. Together with our partners, we aim to ensure that nature benefits from the existing scientific knowledge.

Your specific tasks and qualifications The successful applicant holds a PhD degree and has experience in genomics and/or population genomics, ideally with a specialization in the inference and analyses of TEs and/or SVs and a solid background in population genomics, or genomics of adaptation/speciation. Your main tasks will be the inference and validation of TEs and SVs at population scale and the testing of hypotheses deriving from theories on genomic conflict and its role in speciation.

We offer - A dynamic, young, international research group working on bird population genomics - Collaborations with leading international researchers - A salary in accordance with the regulations of the Swiss National Science Foundation (<http://www.snf.ch>) at the salary scale of the Swiss Ornithological Institute (ca. 80'000.-CHF gross in the first year).

The position is open for 2-3 years. Preferred starting date is 1st September 2022. Please submit your application *in a single PDF*, including (i) a motivation letter detailing your research interests and fit to the position (max. 2 pages), (ii) your CV including publications, and (iii) contact details of 2-3 academic references. Please submit your application by email to Reto Burri (reto.burri@vogelwarte.ch). Applications will be reviewed from 1st June on until the position is filled. For more information about the project and the position, please contact Reto Burri (reto.burri@vogelwarte.ch).

Reto Burri <Reto.Burri@vogelwarte.ch>

Switzerland InsectBirdMovements

Post-doctoral researcher (80 - 100%) “Aerial insect and bird movements, 80 - 100%

Apply here: <https://my.jobalino.ch/de/jobpreview/2720>

Company profile The Swiss Ornithological Institute (<http://www.vogelwarte.ch/>) in Sempach is a non-profit foundation supported by the public and focuses on a wide range of research topics on wild birds within and beyond Switzerland. We aim to acquire the scientific basis for the understanding of biological systems and for the conservation of birds and their habitats. In the

bird migration department, we aim at understanding the temporal and spatial patterns of bird migration by quantifying mass migration across Europe using radar and tracing the routes of individual birds with the help of geolocators. To understand migratory bird movements, we also study the movements of other taxa such as bats and insects, to uncover cross-taxa interactions and the impacts these have on migratory birds.

Job description The MoveInEurope project is an international scientific collaboration aiming at quantifying the biomass flows and movement patterns of aerial insects in Europe, from regional to continental scales and over timescales from days to years, using radar data. We are particularly interested in identifying the atmospheric, climatic, and landscape/habitat drivers of migratory animal movements. MoveInEurope grew out of GloBAM (<https://globam.science/>), a BioDivERsa (<http://www.biodiversa.org/>) research project with partners in Switzerland, Belgium, Finland, The Netherlands, and the USA.

We are seeking to fill a postdoctoral researcher position within the MoveInEurope project to: (1) analyse the interactions between bird and insect abundances and movements, and (2) improve the taxonomic detail of insect identification from radar data.

Your tasks - Enhance the extraction of biological information (especially insects) from radar data through improvements in signal processing, feature extraction, and classification algorithms, and the collection of insect field/air reference data - Analyse data from >15 radars across Europe to quantify bird and insect abundances and movements over time, and in particular the links between the two taxa - Upscale estimates from vertical-looking radars using weather radar data

Your profile - PhD in ecology, biology, remote sensing, or related discipline - Background in radar aeroecology, migration ecology, or other relevant fields - Strong quantitative skills and proficiency in a programming language, preferably R - Excellent communication skills and interest in working in a collaborative project

We offer - An international, dynamic, and flexible research group working on animal migration - Collaboration with leading national and international researchers - Salary in accordance with the regulations of the Swiss Ornithological Institute (À± 6200 CHF gross per month in the first year). - The position is for 2 years with possibility of extension for an additional year, with a preferred starting date of 1 July 2022.

Contact text Application and contact We look forward to receiving your online application by 15 May 2022. Please send your application documents (motivation

letter detailing your research interests and fit to the position requirements - max 2 pages, your CV with publication list, and contact details of two academic references) in a single PDF file. Other applications will not be considered

Interviews will take place in the second half of May 2022. For more information about the position or the MoveInEurope project, please contact Birgen Haest (<mailto:Birgen.Haest@vogelwarte.ch>) and Silke Bauer (<mailto:Silke.Bauer@vogelwarte.ch>).

The Swiss Ornithological Institute is committed to increasing the representation of women in leadership roles and research and specifically encourages applications from qualified women.

Birgen Haest <Birgen.Haest@vogelwarte.ch>

TempleU EvolutionaryGenomics

Multi-year NIH-funded support is anticipated for a post-doctoral researcher in the Hey lab at Temple University. Experience in evolutionary or population genetic theory, particularly in mathematical modelling or statistical analysis of evolutionary genomic data, is desired. The successful candidate will become a member of both the Center for Computational Genetics and Genomics (CCGG) and the Institute for Genomic and Evolutionary Medicine (iGEM) at Temple University.

Project Description: The primary focus of the research will be on the development and application of improved analyses of selected and neutral substitutions, building on an approach first described in doi.org/10.1073/pnas.2023575118

The salary will follow current NIH postdoctoral guidelines, based on years of postdoctoral experience. Full benefits are included.

Applicants should submit the following in a single document as an attachment to hey@temple.edu: (1) a cover letter (include expected completion date of PhD, if appropriate), (2) a CV, and (3) contact information for three references.

Temple is an R1 university, located in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is the birthplace of America and home to many academic and research institutions.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community.

Jody Hey hey@temple.edu Director, Center for Computational Genetics and Genomics Professor, Department of Biology Temple University 1900 N. 12th Street Philadelphia, PA 19122

Jody Hey <hey@temple.edu>

UAruba TropicalSeascapeGenetics

The University of Aruba, in collaboration with KU Leuven (Belgium), and facilitated with funding from the European Development Fund (EDF), set up the SIS-STEM (Sustainable Island Solutions through Science, Technology, and Engineering (STEM)) program. This program includes a Bachelor program and research center in bio-environmental engineering, technology, engineering, informatics, and data sciences. We are looking for a motivated, and internationally oriented scholar with an excellent research record and a sound appreciation for research and outreach in a small island context for a 15-month postdoctoral fellowship on:

POSTDOCTORAL FELLOW IN TROPICAL SEASCAPE GENETICS (1 fte.)

The fellow is embedded in the SISSTEM program (University of Aruba) and the Division Ecology, Evolution and Biodiversity Conservation (KU Leuven). Marine science in the perspective of small islands offers excellent prospects for a career, especially during the United Nations Decade of Ocean Science for Sustainable Development 2021-2030.

Research assignment: The research profile focuses on advanced expertise in seascape genetics to investigate research questions at the interface of marine evolution and global change biology. More specifically the candidate will determine the ecological and evolutionary interdependency of populations by studying the genetic structure and connectivity of tropical corals in the environmental context of the Southern Caribbean Sea (Southern Antilles). You genotype four coral taxa with high throughput genetic tools and analyze connectivity patterns with an individual- and population-based statistical models. The study will result in advice on the conservation management of coral reefs fitting in a context of regional anthropogenic impact. The position is funded by the European Union. The candi-

date is expected to further develop the analysis of high-throughput microsatellite genotypes with biostatistical tools, and prepare high-quality scientific publications. You will be supported in your research by colleagues skilled in molecular tools and data analysis, and in the oceanographic and biological context of tropical research. Scientific, societal, and internal services are an integral part of the assignment.

The ideal candidate:

??? Is an excellent, internationally oriented researcher and strengthens a research program at the forefront of seascape genomics;

??? Publishes at the highest scientific level in top 25% journals of her/his research field;

??? Holds a Ph.D. in Marine Science, Oceanography, Molecular Ecology, or related disciplines.

??? Well acquainted with molecular ecology.

??? Skilled in academic teaching.

??? Holds adequate diving certification.

??? International research experience is an important advantage.

??? Has excellent verbal and written communication skills in English.

We offer full-time employment in an intellectually challenging environment, in an exciting EU-funded project for a one 15 months contract. The selected candidate will work in Aruba and Leuven and is embedded in the SISSTEM teaching and outreach program at the UA. The contract provides an attractive benefits package including APFA pension, additional health insurance, and a competitive wage.

Interested? Visit our website and submit through our career portal: <https://careers.portal.ua.aw> before Friday, April 15, 2022, your motivation letter, resume, a summary of your Ph.D. thesis, a short commentary on your 5 most significant publications, evidence of accomplished skills and competencies, and contact details of 3 reference persons with full addresses. Interviews will be organized in the second half of April 2022.

View an extensive version of this vacancy on our career portal: <https://careers.portal.ua.aw>. If you need further information regarding the position, contact prof. Eric Mijts (UA) via email eric.mijts@ua.aw. and/or prof. Filip Volckaert (KU Leuven) via email filip.volckaert@kuleuven.be. One (or more) job interviews, a medical exam, an assessment test, and a certificate of good conduct are in accordance with our rules of application and a standard part of our recruitment and selection procedure.

Filip Volckaert <filip.volckaert@kuleuven.be>

UBuffalo EcolEvolBio

Exciting opportunity for an Ecological and/or Evolutionary Biology Postdoctoral Associate in the Department of Biological Sciences, College of Arts and Sciences, University at Buffalo.

Job posting link: <https://www.ubjobs.buffalo.edu/-postings/33804> The Santos Laboratory (<https://arts-sciences.buffalo.edu/biological-sciences/faculty/-faculty-directory/scott-santos.html>), recently relocated to the University at Buffalo, utilizes a variety of molecular tools, computational approaches and field- and laboratory-based studies to examine the ecology, evolution, genetics, physiology, and symbiosis biology of a range of terrestrial and aquatic (both freshwater and marine) organisms, including host- and environmentally-associated microbiomes.

In the above context, three broad areas of current research are:

- Phylogeography and physiology of microbiomes and crustaceans from the anchialine ecosystem of the Pacific Basin
- Animal-microbial interactions via grazing or symbioses
- The genetic basis of coloration variation and longevity in crustaceans

The successful candidate will have a chance to work with existing, as well as generating novel, large-scale datasets including genomic (DNA/RNA) resources. The candidate will have the opportunity to collaborate with researchers from multiple institutions and government agencies on projects involving the above. The candidate would also be expected to work with Dr. Santos on developing research proposals to funding agencies such as the National Science Foundation (NSF) in the above areas. The Santos Lab has a history of having diverse personnel and a multidisciplinary research program and is interested in recruiting from different backgrounds to continue this tradition.

The candidate should have a Ph.D. preferably in ecological and/or evolutionary biology, population genetics, physiology, computational biology, bioinformatics, or microbiology. Experience in handling large datasets (e.g., high-throughput 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 1.5-page) cover letter outlining research interests and career goals (including personal perspectives in diversity, equity, and inclusion in the biological sciences). Applications will be accepted until the position is filled.

Outstanding Benefits Package Working at UB comes with benefits that exceed salary alone. There are personal rewards including comprehensive health and retirement plan options. We also focus on creating and sustaining a healthy mix of work, personal and academic pursuit - all in an effort to support your work-life effectiveness. Visit our benefits website to learn about our benefit packages.

About The University at Buffalo The University at Buffalo (UB) is one of America's leading public research universities and a flagship of the State University of New York system, recognized for our excellence and our impact. UB is a premier, research-intensive public university dedicated to academic excellence. Our research, creative activity and people positively impact the world. Like the city we call home, UB is distinguished by a culture of resilient optimism, resourceful thinking and pragmatic dreaming that enables us to reach others every day. Visit our website to learn more about the University at Buffalo.

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.

Minimum Qualifications: - PhD (or MD) preferably in ecological and/or evolutionary biology, population genetics, physiology, computational biology, bioinformatics, or microbiology conferred within the past five years.

Preferred Qualifications: - 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.

Interested applicants should submit: - a CV - names of three references - a brief (no more than 1.5-page) cover letter outlining research interests and career goals (including personal perspectives in diversity, equity, and inclusion in the biological sciences).

Please do not send application materials directly to the posting contact. Please use posting link (<https://www.ubjobs.buffalo.edu/postings/33804>) for applying to this opportunity.

Applications will be accepted until the position is filled.

Scott R. Santos Empire Innovation Professor

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UCalifornia SanFrancisco HumanEvolutionMachineLearning

Multiple Postdoctoral Positions in Computational Biology, Evolution, and Machine Learning

Multiple funded postdoctoral scholar positions are available in the lab of John A. (“Tony”) Capra at the University of California, San Francisco. The positions offer competitive salaries above the NIH scale, benefits, and support for moving expenses.

The Capra Lab develops integrative computational methods for interpreting genomes to answer fundamental questions about human disease and evolution. We have open positions in several areas: - Interpreting the genomes of archaic hominins and ancient humans

- Designing machine learning methods for electronic health records
- Developing novel methods for analyzing the genomes of individuals with undiagnosed disease
- Mapping the genetics of gene regulation in human brain network evolution

For more information about the group and our work, visit <http://www.capralab.org/>. The successful candidates will lead projects under one or more of the areas listed above. There is substantial room for the development and initiation of new projects. The scholars will benefit from the diverse and collaborative environment in the Capra Lab and UCSF. They will also obtain training and experience in teaching, mentoring, and project management.

The Capra Lab is located in the Bakar Computational Health Sciences Institute, the campus hub for computational method development and data integration. We also collaborate closely with the active UCSF Evolutionary Genomics community.

A record of successful publications and a PhD in bioinformatics, genetics, evolution, computer science, statistics, or a similar discipline is preferred. Programming and

analytical skills are essential for these positions. We welcome interested candidates from diverse backgrounds.

Interested applicants should send a CV and a cover letter outlining qualifications and research interests to Tony Capra <FIRSTNAME@capralab.org> with the phrase “postdoc application” in the subject line. Please provide contact information for three references.

Tony Capra <http://www.capralab.org/> Tony Capra <tony@capralab.org>

UCambridge EnvironmentalMicrobialGenomics

The Ecosystems and Global Change Group led by Prof Andrew Tanentzap at the University of Cambridge (www.ecosystemchange.com) is seeking a full-time Post-Doctoral Research Associate (PDRA). The PDRA will join a new project funded by the Canada-Inuit Nunangat-United Kingdom Arctic Research Programme (<https://www.ukri.org/what-we-offer/browse-our-areas-of-investment-and-support/canada-inuit-nunangat-uk-arctic-research-programme/>). The project seeks to develop a community-led wildlife health monitoring programme for Nunavik with a highly multidisciplinary team of 14+ Inuit, Canadian, and UK researchers, including anthropologists, epidemiologists, and veterinarians. The PDRA will interact with this larger team and receive additional supervision from Prof James Wood (www.vet.cam.ac.uk/staff/professor-james-wood-obe).

The primary goal of this post is to develop and validate novel techniques to detect wildlife diseases at a watershed-scale using eDNA/eRNA. The PDRA will be responsible for co-designing sampling approaches with Inuit partners and embedding in local communities to sample drainage waters across Nunavik. In the lab, they will use state-of-the-art genomics approaches to estimate the presence and abundance of known pathogens of concern. These estimates will be validated with targeted qPCR assays on tissue samples collected from a range of keystone Arctic species (e.g., caribou, ptarmigan, seal, beluga Arctic char) by local hunting and trapping associations. Using the sequencing data, the PDRA will also identify gene transfer events and emerging zoonosis risks.

A key objective of the project is to build long-term capacity in Inuit Nunangat research in accordance with the National Inuit Strategy on Research. The PDRA

will therefore develop online training materials in bioinformatics and deliver a short course at the end of the project on the analysis of genetic sequence data at the Nunavik Research Centre.

The post can start immediately, and funds are available for up to 36-months subject to satisfactory completion of a 6-month probationary period. Salary ranges from $\dot{ı}_{\frac{1}{2}}$ 33,309 to $\dot{ı}_{\frac{1}{2}}$ 40,927 per year.

The successful candidate must have a proven track record of publication in leading peer-reviewed journals, ideally demonstrating innovative approaches in the study of eDNA/eRNA. They will have a PhD in microbial genomics, bioinformatics or a related subject. A track record of engagement with community-led science, and some experience with developing training materials, is highly desirable.

Questions about the post should be directed to Prof Andrew Tanentzap (ajt65@cam.ac.uk).

Apply at <https://www.jobs.cam.ac.uk/job/34625/> by the 13 May 2022.

Andrew Tanentzap <ajt65@cam.ac.uk>

UCambridge EvolutionBrazilianInvasiveMoths

More information here: <https://www.jobs.cam.ac.uk/-job/34326/> A Research Associate post is available for 20-24 months in the Insect Evolution and Genomics Group directed by Chris Jiggins in the Department of Zoology at the University of Cambridge. Start date from 1st of June - 1st of October.

The position is funded by a Bilateral BBSRC-FAPESP award (BB/V001329/1) with collaborators Celso Omoto and Alberto Soares in Sao Paulo, Brazil; Tom Walsh at CSIRO in Australia; and Frank Chan from the Max Planck in Tuebingen.

The successful candidate will study ongoing pesticide resistance evolution of a highly damaging invasive moth in South America, *Helicoverpa armigera*, which has been found to hybridise with native *H. zea*.

They will lead the sampling and genomic analyses to study contemporary evolution of *Helicoverpa* pests in Brazil initially assessing the extent and prevalence of each species in new outbreaks, with a particular focus on the economically valuable Bt soybean. They will work in close collaboration with Brazilian colleagues at the

University of Sao Paulo to design a monitoring scheme for new outbreaks, collate information from farms, carry out genome sequencing on existing or new F2 screening crosses, and study the genetic basis of any novel insecticide resistance or host plant adaptations.

The successful candidate should have PhD in a relevant subject such as evolutionary biology, genetics, or biological sciences. They should have excellent communication skills in English and Portuguese (written and oral), good understanding of evolutionary biology, and strong quantitative skills. They should have keen interest in crosses, QTLs, and GWAS methods and experience with computer programming / scripting / data analysis (e.g. R, Python, unix shell). Please see the Further Particulars for other essential and desirable requirements.

Informal enquiries are welcomed and should be directed to: Professor Chris Jiggins Email: cj107@cam.ac.uk

Fixed-term: The funds for this post are available up until 31 May 2024.

“G. Montejo-Kovacevich” <mgm49@cam.ac.uk>

UCollege London ResAssoc StatisticalPhylogenetics

Research Associate in computational genomics in University College London, - Ref: 1883743

Research Associate in computational genomics, at Department of Genetics, Evolution & Environment, UCL Grade: 7 Hours: Full Time Salary: Grade 7 $\dot{ı}_{\frac{1}{2}}$ 36,770 - $\dot{ı}_{\frac{1}{2}}$ 44,388 per annum including London Allowance

Duties and Responsibilities The post holder will work in the group of Professor Ziheng Yang FRS to conduct research in the area of computational genomics. You will become a member of a research team that takes an integrative approach to speciation biology by combining computational science, field ecology, and genomic analysis. The project is a collaboration with Anne Yoder (Duke University, genomics) and Marina Blanco (Duke Lemur Center; behavioural field ecology).

The successful candidate will participate in the development of Bayesian inference methods and implementation of computer software for analysing genomic sequence data from closely related species under the multispecies coalescent model. They may be expected to design and implement computational algorithms, conduct computer simulation, analyse genome-scale datasets, and write

up results for publication in international peer-reviewed journals. For a sample of our recent work in this area, please see Flouri et al. 2020 *Mol Biol Evol* 37:1211-1223; Jiao & Yang 2021 *Syst Biol* 70:108-119; Jiao et al. 2021 *Nat Sci Rev* 8:nwab127; Zhu & Yang 2021 *Mol Biol Evol* 39:3993-4009.

The post is funded by the NERC for 23 months in the first instance. The post is available immediately.

Key Requirements We seek a research scientist with expertise in computer programming (C/C++), Bayesian inference (MCMC), or computational and speciation genomics.

A PhD (or working towards a PhD) in one of the following areas is essential: computational science (e.g., C programming for HPC), statistical inference (e.g., MCMC), and phylogenomics and population genomics. Individuals with a biology PhD are invited to apply if they can demonstrate strong computational/statistical skills. Ability to work in a multi-disciplinary collaborative environment is essential, as is fluency with Linux. A proven track record of effective research will be required.

Please note: Appointment at Grade 7 is dependent upon having been awarded a PhD; if this is not the case, initial appointment will be at Research Assistant Grade 6B (Salary £32,217 - £33,958 per annum, including London Allowance) with payment at Grade 7 being backdated to the date of final submission of the PhD thesis (including corrections).

Further Details A job description and person specification, can be accessed at the bottom of this page. Please ensure you read these carefully before applying for the post.

To apply for the vacancy please follow the link at the bottom.

If you would like to discuss the post please contact Professor Ziheng Yang FRS at z.yang@ucl.ac.uk.

If you have any queries regarding the application process please contact Biosciences staffing on biosciences.staffing@ucl.ac.uk quoting the vacancy reference number: 1883743. UCL Taking Action for Equality We will consider applications to work on a part-time, flexible and job share basis wherever possible. Closing Date: 8 May 2022 Latest time for the submission of applications: 23:59 Interview date: TBC

Our department holds an Athena SWAN Bronze award, in recognition of our commitment to advancing gender equality. This appointment is subject to UCL Terms and Conditions of Service for Research and Support Staff.

Please use these links to find out more about

UCL working life < <https://www.ucl.ac.uk/human-resources/working-ucl/jobs-ucl> > including the benefits we offer and UCL Terms and Conditions < http://www.ucl.ac.uk/hr/salary_scales/-Support_Research_tcs.php > related to this job.

“Yang, Ziheng” <z.yang@ucl.ac.uk> “Yang, Ziheng” <z.yang@ucl.ac.uk>

UConnecticut SticklebackEvolution

University of Connecticut Job: Postdoctoral Researcher studying evolution of gene co-expression networks in stickleback

A postdoctoral research position is available in Dr. Daniel Bolnick's research group (<https://bolnicklab.wordpress.com>), in the Department of Ecology and Evolution at the University of Connecticut. The position is available for up to four years, supported by a National Science Foundation Rules of Life: Emerging Networks grant. A consortium of researchers recently established 8 replicate whole-lake experimental evolution populations of threespine stickleback. The postdoc will apply network statistics methods to study changes in gene co-expression networks as the experimental populations evolve, and diverge. The postdoc may also pursue analyses that integrate the gene expression networks with host-parasite, predator-prey and host-microbiome networks. The project also entails developing and applying innovative analytical methods in network statistics, in collaboration with Dr. Tina Eliassi Rad (Northeastern University, <http://eliassi.org>) and Miaoyan Wang (Univ Wisconsin Madison, <https://pages.stat.wisc.edu/~miaoyan/index.html>). Additional project collaborators include Dr. Rowan Barrett, Dr. Kathryn Milligan-McClellan, and Dr. Jesse Weber. Opportunities exist to pursue side-projects along with the core project task.

Tasks: The postdoctoral researcher may contribute to some or all of the following activities: field work to collect samples, laboratory work to generate sequencing libraries for transcriptomics and genomics, bioinformatic processing of sequence reads, developing or adapting network statistics methods, applying existing network analysis tools to gene expression data, and publishing manuscripts arising from the work. It is not expected that the postdoc would have prior mastery of all these elements.

Duration: The position is currently funded for up to four years, with extensions subject to availability of

grant funds. The start date is flexible.

Qualifications: Applicants must have a PhD in evolutionary biology, genetics, computational biology, or statistics with an emphasis on network analysis. Previous research experience and publications should demonstrate a commitment to basic research, ethical conduct of research, computational skills, organizational ability, and publication productivity. Prior experience with generating or analyzing genomic or transcriptomic data is strongly preferred. Expertise in statistical analysis of network data is preferred.

Applications should electronically submit a single pdf file with:

- 1) a Coverletter outlining research achievements, skills, and goals as pertinent to the advertised project.
- 2) a copy of the applicant's CV,
- 3) copies of up to three publications or submitted manuscripts
- 4) A list of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates. Please notify the references that they may be contacted by Dr. Bolnick for recommendations.

An initial application should be emailed to Dr. Daniel Bolnick (daniel.bolnick@uconn.edu). Include the subject line "Network Evolution Postdoc: <YOUR NAME>". Applications will be reviewed beginning May 15 and will remain open until the position is filled.

For questions about this position, please email Dr. Bolnick (daniel.bolnick@uconn.edu). For information about the Bolnick Lab visit the lab website (<https://bolnicklab.wordpress.com>), lab photostream (<https://www.flickr.com/photos/98765823@N08/-albums>), and Dr. Bolnick's Google Scholar page (<https://scholar.google.com/citations?user=-3Dcfwxm0AAAAAJ&hl=3Den>).

The University of Connecticut is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Connecticut Disability Services Office. A statement of BolnickLab values can be found here: <https://bolnicklab.wordpress.com/2015/10/01/labvalues/>

Dr. Daniel I. Bolnick Editor-In-Chief, The American Naturalist Professor, Ecology and Evolutionary Biology & Institute for Systems Genomics

daniel.bolnick@uconn.edu

MAIL TO: Department of Ecology and Evolutionary Biology 75 N. Eagleville Road, Unit 3043 University of

Connecticut Storrs, CT 06269-3043, USA

Office Phone: 860-486-3156 Lab Phone: 860-486-3937
Cell Phone: 512-809-6217

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UDurham SnowPetrelPopGenomics

Postdoctoral Research Associate in Antarctic Molecular Ecology at the University of Durham, UK

(3 years)

Foraging ecology and population genomics of the snow petrel using ancient and modern DNA and metagenomic analysis of stomach oil deposits (up to thousands of years old) in the context of climate change. Skills in ancient DNA and genomics desirable.

Application Deadline: May 24th, 2022, 23:59 BST. For full details see: <https://antsie.webspace.durham.ac.uk/-2022/04/26/pdra-Antarctic-molecular-ecology/> For informal inquiries contact erin.mcclymont@dur.ac.uk and a.r.hoelzel@dur.ac.uk

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

UEastAnglia DrsophilaLifeHistory

Two positions open at the University of East Anglia.

CLOSING DATE: 5thApril

Title: I see / smell / touch / hear and therefore I am: sex differences in perception alter survival and reproduction.

Applications are invited for the posts of Senior Research Associate and Research Technician, on a new BBSRC-funded project (joint between UEA - PI T Chapman; Co-I Alex Maklakov - and the University of Leeds - Co-I Amanda Bretman) to investigate, using the fruitfly model system, the importance and contrasting roles of perceptual effects of the social and sexual environment on lifespan, ageing and reproduction in males versus females. We aim to test how these effects are linked to

sex-specific effects of nutrient sensing genes that themselves have well-documented effects on lifespan.

Post-doc post:

<https://myview.uea.ac.uk/webrecruitment/pages/-vacancy.jsf?vacancyRef=RA1950> Tech post:

<https://myview.uea.ac.uk/webrecruitment/pages/-vacancy.jsf?vacancyRef=TC799> Closing date: 5th April 2022

Prof Tracey Chapman | School of Biological Sciences

University of East Anglia, Norwich Research Park, Norwich, NR4 7TJ

Email: tracey.chapman@uea.ac.uk

Web: traceychapmanresearch.com

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

ULausanne PlantSexualSystems

Postdoc, University of Lausanne, Switzerland: Evolution of plant sexual systems

A postdoc position is open in John Pannell’s lab in the Department of Ecology and Evolution, University of Lausanne, to study the evolution of plant sexual systems, with a focus on evolutionary transitions between hermaphroditism and dioecy. The scope of the project can be partly tailored to the particular interests of the successful applicant. We are currently using experimental evolution to address questions concerning the quantitative genetics and genomic architecture of sexual-system transitions, including but not only sex chromosomes. The postdoc could potentially play a leading role in taking this study forward (it is now in its 11th year), with substantial latitude to use the genetic material generated so far to conduct further experiments and/or investigate the genomic architecture of responses to selection. The postdoc could also study aspects of sex-chromosome evolution in plants, working on one of three different study systems we have developed in the lab to understand links between sex chromosomes, sex allocation and sexual dimorphism.

The project could start from September 2022, but the starting date is flexible. Further details about the lab, including recent papers on which this project will build, can be found at: <https://www.unil.ch/dee/-pannell-group>, or on writing to john.pannell@unil.ch.

Research scope and skills sought The successful candidate for this position should have a strong interest and background in evolutionary biology and evolutionary genomics, including wet-lab skills and experience in the analysis of genomic data. He/she should also have proven ability to write up research results, as demonstrated in published or accepted papers, or in high-quality preprints, good communication and interpersonal skills, and an ability to work in a team. Although not a requirement (the language of the lab and the research environment of the department is English), some knowledge of French would be an asset. Ideally, the candidate will have received his/her PhD in the last couple of years.

Host Department and University The Department of Ecology and Evolution hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and is close to the Swiss and French Alps.

Applications Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications should be uploaded to the link below and should include (1) a cover letter detailing your research interests, experience and motivation for applying, (2) a CV, (3) an example of previous research work (one or more published articles or preprints, or thesis chapters, and (4) the names of two referees. All applications received by 15 May 2022 will receive full consideration.

Application link: <https://bit.ly/3xMZAog> University equality policy The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

John Pannell <john.pannell@unil.ch>

UNaples PlantEvolutionaryGenomics

Postdoctoral Position at the University of Naples Federico II, Italy

We are accepting applications for a two-years post doc-

torate fellow position in plant evolutionary genomics to identify genes and processes associated with evolutionary and functional switch from kidney shaped to dumb-bell stomata among related sedge (*Cyperus*) species.

Review of applications begins on mid-May 2022.

OVERVIEW:

We are looking for an enthusiastic candidate with an interest in plant biology alongside a strong background in next-generation sequencing and bioinformatic analyses. The candidate must have completed a Ph.D. degree in the last three years, preferably in the areas of plant genomics, gene expression, molecular evolutionary biology, phylogenetics, computational biology and must show a clear record of research in these areas. The work will focus on bioinformatics methods to analyse genomic and transcriptomic data and to estimate the tempo and mode of genes evolution from comparative genomic data. In addition, the candidate will collaborate with researchers at ETH Zurich.

HOW TO APPLY:

To apply, please submit in one PDF file: (i) one page cover letter including motivation and research interests, (ii) a CV, and (iii) contact information for two references electronically, to cozzolin@unina.it. Review of applications will continue until the position is filled. Job can start as early as July 2022.

*The selected candidate will be required to present official credentials from all his/her academic degrees.

If you have questions about the position, please email me.

Kind regards,

Prof. Salvatore Cozzolino Ph.D Dept. of Biology University of Naples Federico II Complesso Universitario di Monte S. Angelo Via Cinthia, 80126, Napoli, Italia Building 7, room 0D-27 Email: cozzolin@unina.it Phone: +39-081679186 (room); +39-081679185 (lab) <https://www.docenti.unina.it/salvatore.cozzolino> Questa email è stata esaminata alla ricerca di virus da AVG. <http://www.avg.com> salvatore cozzolino <cozzolin@unina.it> salvatore cozzolino <cozzolin@unina.it>

This project is funded by Predator Free 2050, to develop genomic datasets that allow an understanding of gene flow in Norway and Ship rat populations in Aotearoa. This project will be carried out as part of a broader PF 2050 project, investigating the application of genetic-based control methods to eradicate rat populations in Aotearoa.

We welcome applications from postdoctoral candidates who have experience in molecular biology, evolutionary and population genetics/genomics, and bioinformatics.

To be successful in this role you will be highly self-motivated and be able to work alongside a wide variety of people. In addition, you will have a strong commitment to research excellence with a track record of high research productivity based on international, peer-reviewed publications commensurate for career stage.

This role is based in the Department of Anatomy, at the University of Otago, and working in collaboration with researchers from Plant and Food Research. The Department makes major contributions to the undergraduate and postgraduate education of students in science, medicine, dentistry, pharmacy, physiotherapy, medical laboratory sciences, and physical education. Its research activities fall within four interdisciplinary programmes encompassing: biological anthropology; clinical anatomy; neuroscience; reproduction, genomics and development.

This is a full-time, fixed term position for two years (1 July 2022 - 30 June 2024).

Applications from Māori and Pacific candidates, and tangata Tiriti, are warmly encouraged.

Please address any questions to Catherine Collins (catherine.collins@otago.ac.nz)

For more information and to apply: <https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=3Den&job=3D2200760> Working at Otago - Your Career, University of Otago (s01) Click the link provided to see the complete job description. otago.taleo.net

catherine.collins@otago.ac.nz

UOtago PopulationGenomicsRats

We are seeking an outstanding Postdoctoral Fellow to carry out research for a new project (Population genomics in Norway and Ship rat populations in Aotearoa).

UPorto LittorinaAdaptation

The Evolutionary Genetics and Genomics research group at the Research Centre in Biodiversity and Genetic Resources CIBIO/InBIO, University of Porto, Portugal (EVOLGEN- <https://cibio.up.pt/en/groups/>

[evolutionary-genetics-and-genomics-evolgen/](#)) is recruiting a postdoc researcher to work in the project “ The role of chromosomal inversions in adaptation and reproductive isolation across the speciation continuum ” funded by the Portuguese Science Foundation (FCT), aiming to develop quality research in adaptation and speciation, specifically focused on the role of chromosomal rearrangements in diversification in marine snails of the genus *Littorina*.

Overview : We will generate whole-genome sequencing, including long reads and Hi-C, and SNP data to infer new chromosomal rearrangements/structural variants in Iberian populations of *L. saxatilis*, their frequencies and their evolutionary history using model-based demographic inference . We will also characterize genetically and phenotypically individuals collected across environmental transects encompassing hybrid zones between and within ecotypes, which will be complemented by mating experiments and correlations with environmental variables. The candidate is mainly expected to analyze (comparative and population) genomic s datasets, but also to participate in sampling, fieldwork, phenotyping and possibly (depending on the profile) lab work. The selected candidate will work directly with the Principal Investigator Rui Faria at CIBIO ([<https://scholar.google.com/citations?user=ubDybpQAAAAAJ&hl=en> | <https://scholar.google.com/citations?user=ubDybpQAAAAAJ&hl=en>] ; <https://rmigueldefaria.wixsite.com/farialab-1>) and the co-PI Professor Roger Butlin (University of Sheffield, UK: [<https://www.sheffield.ac.uk/biosciences/people/academic-staff/roger-butlin> | <https://www.sheffield.ac.uk/biosciences/people/academic-staff/roger-butlin>]), as well as with all the project team, including: Miguel Carneiro, Pedro Andrade and Fernando Lima (CIBIO); Kerstin Johannesson (University of Gothenburg, Sweden), Anja Westram (IST, Austria); Juan Galindo (University of Vigo, Spain); and Vitor Sousa (CE3C, University of Lisbon, Portugal); and the vibrant international research team working in *Littorina* (<https://littorina.group.shef.ac.uk/>).

The expected profile: Highly-motivated evolutionary genetic s specialist with strong bioinformatic skills, self-driven, responsible, excellent communication (orally and written) skills and high work ethic standards, enjoy team work, be fascinated by the relationships between organisms and their natural environment , and some molecular lab experience (Having completed the PhD is mandatory)

We offer: 2 years and 7 months contract for a full-time post with a monthly remuneration to be paid as set by article 23 (3) of RJEC, corresponding to level 33 of the Single Salary Table, approved by Order no. 1553-C/2008

of December 31st, i.e. 2153,94 Euros.

Workplace: BIOPOLIS/CIBIO - Research Center in Biodiversity and Genetic Resources, in Campus de Vairão, Rua Padre Armando Quintas n.º7, Vairão, Portugal and may involve travel in Portugal and abroad , namely in Spain, UK and Sweden, among others , for fieldwork, meetings, etc.. Biopolis is the largest Portuguese project in Environmental Biology, Ecosystems and Biodiversity and aims to transform [<http://cibio.up.pt/en/> | CIBIO] into an international superstructure linking scientific research with civil society and the business sector to address the emerging global challenges

Application : For additional information and formalization of applications please visit: [<https://www.cibio.pt/?p=2054> | <https://www.cibio.pt/?p=2054>] . The following documents must be submitted in a PDF format: i) Curriculum vitae , ii) Motivational Letter , iii) Qualifications Certificate ; iv) Name and contact of two references; v) Breve description of the most relevant research activities in the last 5 years (max. 1 page) ; and vi) and other relevant documentation . Applications close on 2022, the 15th of May.

Next Steps: We expect to contact you by email within one week after the closing date to let you know whether or not you have been shortlisted to participate in the next stage of the selection process.

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UPrimorska WildlifeMonitoring

The University of Primorska is the coordinating institution of the Horizon 2020 project Step change focusing on citizen science for wildlife monitoring. We are looking for a post doc with experience in camera traps and data analysis.

Your tasks: You should be able to implement a comprehensive approach to combine spatial and presence information with fragmentation of the landscape, time-frame, ecological characteristics of the area etc. You are also expected to be able to run and test models to validate collected data and infer past and future trends and you are expected to contribute to project management.

Good communication skills with stakeholders would be appreciated.

Your profile: - A relevant university education with a completed doctoral/PhD degree and a strong potential in research. - Relevant knowledge and willingness to work in ecological statistics. - Willingness to supervise graduation/master theses, and to promote young scientists. - Excellent spoken and written English is required. Slovene would be advantageous.

We offer: - The advertised position is for an initial period of 2 years - The position will be paid according to category of the Collective agreement for employees at Slovenian universities.

Application instructions: Interested applicants are requested to send the application in electronic form to stepchange@famnit.upr.si, and "Postdoc in wildlife management" in the object. Please attach in pdf format: - A cover letter explaining your interest in the position and how you fit the description - a CV - a list of publications highlighting the with five the most relevant ones.

Application deadline: May 08th, 2022

Best regards,

Elena Prof. dr. Elena Buzan, Vice-Dean

Faculty of Mathematics, Natural Sciences and Information Technologies University of Primorska Glagoljaska 8, SI-6000 Koper, Slovenia Phone: +386 5 6117570, Fax: +386 5 6117571 E-mail: elena.buzan@famnit.upr.si

Web:

<https://www.famnit.upr.si/sl/zaposleni-in-sodelavci/-elena.buzan/> Elena <elena.buzan@famnit.upr.si>

UPuertoRico 2 ButterflyEvolution html

<pre> University of Puerto Rico, Rio Piedras: Butterfly wing color pattern evolutionary and functional genomics

Two Postdocs positions in evolutionary and functional genomics.

The Papa's lab (<https://www.riccardopapalab.com>) is in San Juan, the capital of the beautiful island of Puerto Rico, which provides amazing research opportunities and lifestyle. The selected postdoc will explore the genetic and epigenetic source of variation for natural selection and adaptation to work upon. This research project will investigate what governs patterns diversity, what limits

it, and what promotes its potentials. To do so, methods of pure genetics, phylogenetics, epigenetics, single cell genomics, developmental cell biology, and functional genomics will be utilized. The final goal is to characterize the molecular architecture of single cells/scales of unique colors.

Two NSF-funded postdoctoral positions are available in the laboratory of Dr. Riccardo Papa in the Department of Biology of the University of Puerto Rico, Río Piedras Campus. These positions are looking to increase diversity in the research group and foster collaboration and knowledge transfer. The laboratory has a rich background in studying the natural history of *Heliconius* butterflies, with a genomic, evolutionary developmental focus. Our research is using high-end genomic approaches and functional assays to characterize the genetic and epigenetic architecture of color pattern development in butterflies. We are using whole genome resequencing, ATAC-seq, ChIP-seq and CRISPR to better understand the pathways involved in color pattern development and their evolution. We have enough data to test strong hypotheses in butterfly wing color pattern development using a single cell genomic approach. Our lab has state of the art genomic technology which includes, an Illumina Miseq, an Illumina NextSeq 2000, and a single cell 10X Chromium among many other equipment. We generate all the data locally and can perform CRISPR experiments using our butterfly rearing facility.

SPECIAL REQUISITES

The candidate must have completed a Ph.D. degree, preferably in the areas of genomics, population genetics, developmental biology and or computational biology. The position requires skills in the areas of genomics, development and computational biology, and a strong record of research in these areas. Being highly motivated will be necessary to collaborate with National and International research groups. The work will focus on bioinformatics methods to analyze large genomic and epigenomic data. Specifically, this includes generating single cell genomic data and building pipelines to assemble and analyze such dataset (epigenetic and expression) to determine cell fate and butterfly's wing color pattern development with a precision never available before. Candidates from Minority Serving Institutions (MSI) are strongly encouraged to apply for the position

HOW TO APPLY

To apply, please submit in one PDF file: (i) one page cover letter including motivation and research interests, (ii) a CV, and (iii) contact information for two references electronically, to riccardo.papa@upr.edu and rpapa.lab@gmail.com. Review of applications will start immediately and will continue until the position is filled.

Job can start as early as July 2022.

*The selected candidate will be required to present official credentials from all his/her academic degrees.

This job opportunity is financed with external funding and does not consider the expectation of a probation position.

Riccardo Papa Full Professor, Department of Biology Director of High Throughput Sequencing Facility University of Puerto Rico - Río Piedras Julio García Díaz (JGD) 213 Río Piedras, San Juan PR 00931

tell: 787-764-0000 ext 4827(office) or 7764(lab) fax: 787-764-3875 Lab WebPage (under construction): <http://www.wix.com/ricpapa/Papa-Riccardo-Lab> Topics 2013 (Genomic Frontiers in Modern biology): <http://biotopicsuprrp.weebly.com/index.html> Riccardo Papa <rpapa.lab@gmail.com>

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UTexas Austin MolecularEvolution

Postdoctoral Positions at the University of Texas at Austin

Postdoctoral positions in the areas of molecular evolutionary biology, population genetics, bioinformatics, microbial and viral diversity, and/or genomics are available in the research groups of Howard Ochman or Nancy Moran at the University of Texas.

Potential research topics include:

• Evolutionary Dynamics of Microbiomes

• Determinants of Genome Evolution in Bacteria and Viruses

• Molecular Mechanisms Underlying Host-Microbe Interactions

Applicants should be curious, and able to formulate their own ideas and research directions. Successful applicants will play a major role in defining their own research projects.

Salary, in the range of \$55,000 to \$60,000, will be commensurate with academic level and experience, and accompanied by funds for relocation.

Initial appointments would be for one year, with potential to extend to 2 or 3 years. UT Austin offers a stimulating academic and research environment, with outstanding colleagues and facilities in microbial sci-

ences, genomics and computation. Austin is a vibrant city with many options for recreation and cultural activities.

If interested, please send a C.V and brief statement of research interests and career goals to Kim Hammond (kim.hammond@utexas.edu).

Please include the names and contact information for two or three references familiar with your scientific work. Please direct any queries about projects, positions or timing to Howard Ochman (howard.ochman@austin.utexas.edu).

“Ochman, Howard” <howard.ochman@austin.utexas.edu>
“Ochman, Howard” <howard.ochman@austin.utexas.edu>

UZurich ExptEvolutionaryBiology

Postdoc in experimental evolutionary biology

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The fellow will study the evolution and evolvability of biomolecules either through experimental evolution or through the large-scale analysis of adaptive landscapes, using methods such as CRISPR-Cas genome editing. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. Recent experimental work in the lab ranges from the directed evolution of proteins to experimental evolution of microbes (e.g., Zheng et al., Science 2020; Karve and Wagner, Molecular Biology and Evolution 2022). Ongoing projects characterize adaptive landscapes of biomolecules via deep-scanning mutagenesis. The successful candidate will have flexibility in designing their own project, as long as it falls within the purview of the lab's general research area (see also <http://www.ieu.uzh.ch/wagner/>).

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will help develop. The successful candidate will have a strong background in microbiological techniques and molecular cloning. Applicants with experience in approaches such as deep-scanning mutagenesis, molecular barcoding, and CRISPR-Cas-based library design will be especially welcome. Experience with flow cytometry, as well as with computational analysis

of high-throughput DNA sequence data, and machine learning applied to biological data will be a plus, as will be a research history in evolutionary biology. The position offers a highly competitive salary of up to three years on annually renewable contracts.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs.wagner@ieu.uzh.ch: CV including publication list, academic transcripts, three academic references. In addition, we require a brief sketch of an experimental evolution project that you would like to pursue, and that is part of a brief statement of research interests not exceeding three pages. Please include the word "EXPPDOC22" in the subject line of your application. Applications will be considered until May 3, 2022, or until the position has been filled. The position is available from September 1, 2022.

Annette Schmid Administrative Assistant of Prof. A. Wagner/ HR University of Zurich Department of Evolutionary Biology and Environmental Studies Wagner lab, Y27-J52 Winterthurerstrasse 190 CH-8057 Zürich Switzerland Mail to: annette.schmid@ieu.uzh.ch

Monday (whole day), Home office: Tuesday - Thursday (morning)

IEU [wagnerjobs <jobs.wagner@ieu.uzh.ch>](mailto:wagnerjobs@jobs.wagner@ieu.uzh.ch)

WSL Switzerland EcolEvolDataScience

WSL.Switzerland.EcolEvolDataScience

The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is part of the ETH Domain. Approximately 600 people work on the sustainable use and protection of the environment and on the handling of natural hazards. The Research Unit Biodiversity and Conservation Biology studies the diversity of life in its various forms, from genetic diversity to the diversity of species and ecosystems as well as their interactions.

In the framework of the Swiss Forest Lab project RemHybridMon the Evolutionary Genetics Group (<https://sites.google.com/view/evolgenetgroup>) is look-

ing from July 1st, or by arrangement, for 12 months for a PostDoc in ecological/evolutionary data science (80-100% workload).

RemHybridMon is aimed at developing a cost-effective remote sensing tool to monitor the hybridization between closely related beech species (*Fagus* spp.) upon their introduction in the framework of assisted migration programs. Monitoring the rate of hybridization and the spread of adaptive genetic variants using field sampling and genetic evaluation is impractical and expensive. This project will use state-of-the art genomics and optical spectroscopy to develop a protocol based on machine learning to uncover the relationship between the two. Field data will be collected by our team at three sites during the summer of 2022. Although the position will be based at the WSL, the future postdoc will closely interact with Prof Dr Meredith Schuman and her research group in Spatial Genetics at the University of Zurich (<https://www.geo.uzh.ch/en/units/sg.html>) Desk space will be available at both institutions.

Ideal candidates hold a PhD degree in imaging spectroscopy, data science, and/or population genomics/bioinformatics. Experience with machine learning, fluency in python and in R are essential for this position. Fluency in English (oral and written) as well as experience in writing scientific publications is expected. The language of both groups is English.

Please send your complete application to Michi Bucher, Human Resources WSL, by uploading the requested documents through our webpage. <https://m.refline.ch/273855/1304/pub/1/index.html> Applications via email will not be considered. Dr Katalin Csillery, katalin.csillery@wsl.ch, will be happy to answer any questions. The WSL strives to increase the proportion of women in its employment, which is why qualified women are particularly called upon to apply for this position.

Katalin Csillery <kati.csillery@gmail.com> Katalin Csillery <kati.csillery@gmail.com>

WSL Switzerland ScientificOutreachCoordinator

Scientific & Outreach Coordinator for Biodiversity Research (60-80%)

We offer an interesting and versatile workplace in a diversified research environment. You will act both as

manager of activities of the WSL Biodiversity Center, as a support scientist for collaborative research and facilitator of outreach activities. You will provide logistical and management support for the main activities hosted by the Biodiversity Center. You will be responsible for networking across existing activities, groups, units and programs within WSL, nationally and internationally, and you will identify and support opportunities for interactions between WSL researchers and practitioners. You will work closely with the head and the steering committee of the WSL Biodiversity Center to foster research and outreach excellence and contribute to products and initiatives of the Center including support with data analyses and writing. You have a PhD in biology, ecology, environmental sciences, or in a related field and several years of experience working in a scientific environment. You have proven skills in networking, coordination and organizing teams of scientists and/or practitioners. Your communication skills are strong and you are fluent in English and at least in one national language of Switzerland (GE, FR, IT). You are experienced in biodiversity research and ideally skills in modelling and analysing biodiversity data (preferably R). Finally, you have experience in writing scientific articles and producing outreach publications and you do like to work in an international team.

Please send your complete application to Michele Bucher, Human Resources WSL, by uploading the requested documents through our webpage. We will start reviewing applications by mid of April and will continue until we find a suitable candidate. Applications via email will not be considered. Dr. Catherine Graham, leader of the Biodiversity Center +41 (0)44 739 23 61, catherine.graham(at)wsl.ch, will be happy to answer any questions or offer further information. The WSL strives to increase the proportion of women in its employment, which is why qualified women are particularly called upon to apply for this position.

<https://apply.refline.ch/273855/1300/pub/1/-index.html> deborah.leigh@wsl.ch

YaleU
Population Genomic *Aedes albopictus*

A position as a postdoctoral researcher/fellow in population and evolutionary genetics is available at the

Department of Ecology and Evolutionary Biology, Yale University, in Dr. Adalgisa (Gisella) Caccone research group.

Project description: This project is part of an NIH funded project in its 4th year to look at the evolutionary history of an invasive mosquito species, *Aedes albopictus*, the tiger mosquito, capable of vectoring several viral diseases.

We are using whole genome data and SNP-chip data to reconstruct the invasion history and reconstruct demographic dynamics in the invasive range. We are also carrying out a GWAS analyses to describe the genetic architecture of a trait, diapause, which has enabled this species to also invade temperate areas.

The Yale PI is Adalgisa Caccone (<https://caccone.yale.edu/>). The project is in collaboration with with the research groups of Peter Armbruster (Georgetown University) and Jacob Crawford (Verily LifeScience). The position is for one year for possibility of renewal for a second year depending on performance and funding.

Duties: The postdoctoral hire will be responsible for collecting and analyzing population genomic data, including SNP chip and whole genome data.

Qualifications required: For this position, the candidate must hold a PhD degree within evolutionary biology or another relevant field, with experience in population and landscape genomics and phylogeography. They need to be able to express themselves fluently in spoken and written English, work independently, thrive in a multicultural and collaborative environment, and willing to support the training of undergraduate and graduate students.

You are welcome to submit your application by April 30, 2022. Applications will be reviewed as they come. The tentative start of the position is July 2022. To apply please send a CV and a description of your interest and qualifications and how they fit with the job description to Adalgisa (Gisella) Caccone (adalgisa.caccone@yale.edu).

Adalgisa Caccone Senior Research Scientist ESC 140 Ecology and Evolutionary Biology Yale University 21 Sachem St. New Haven, CT 06520 Tel 203-432-5259 fax 203-432-7394

“Caccone, Adalgisa” <adalgisa.caccone@yale.edu>

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Cleveland PaleobotanyRevBayes Jun24

SSB is sponsoring a workshop on paleobotany and divergence time estimation at the 2022 Evolution Meeting in Cleveland, Ohio. Participants will learn about morphometric methods for fossil analysis and how to combine data from extinct and extant taxa to estimate divergence times in RevBayes. The workshop will take place on June 24th and grants (up to \$600 for travel and other costs) are available for graduate students who are US citizens through an NSF award. To apply, please fill out this form < https://docs.google.com/forms/d/e/1FAIpQLSfDppXsugVm2x8TjU5DMiUsp_1TTAjGHI_j1kVnVn1b1uWKvg/-viewform >; review of applications will begin April 15th. Feel free to contact Dr. Rocio Deanna (rociodeanna@gmail.com) with any questions about the workshop.

Dr. Rocio Deanna University of Colorado at Boulder (US) Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC, Argentina) < <https://rociodeanna.weebly.com> > < <https://rociodeanna.weebly.com> >

Rocio Deanna <rociodeanna@gmail.com> Rocio Deanna <rociodeanna@gmail.com>

Finland MathEcolEvolution Aug21-28

THE HELSINKI SUMMER SCHOOL ON MATHEMATICAL ECOLOGY AND EVOLUTION 2022

Application deadline extended to 10 May

We are glad to announce the 7th edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics, to be held between 21 and 28 August 2022 in Turku, Finland.

The core program consists of five series of lectures:

Josef Hofbauer (University of Vienna): Dynamical systems in mathematical ecology
 Gergely Rost (University of Szeged): The mathematics of infectious diseases
 Pieter Trapman (Stockholm University): Stochastic models of epidemics
 Jarno Vanhatalo (University of Helsinki): Linking ecological models to data through Bayesian statistics
 Christian Hilbe (Max Planck Institute for Evolutionary Biology): Dynamics of social behaviour

All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate

students of mathematics, but we also welcome students of biology with sufficient background in mathematics, advanced undergraduates, and postdocs.

For more information and details of the application procedure, please visit the school's webpage

<https://wiki.helsinki.fi/display/BioMath/->

[The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Evolution+2022](https://wiki.helsinki.fi/display/BioMath/-The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Evolution+2022)

With best regards, Eva Kisdi (eva.kisdi@helsinki.fi)

"Kisdi, Eva" <eva.kisdi@helsinki.fi>

Groningen AnthropoceneSummerSchool Jul3-8

Welcome to the Anthropocene! Summer School at the University of Groningen 3 - 8 July 2022 For whom: PhD, Master, and advanced Bachelor students Deadline for application: 1 May 2022

<https://www.rug.nl/education/summer-winter-schools/anthropocene/?lang=en> Topics covered: Paleontology: Shifts in subsistence and environmental impact Evolutionary biology: Are we friendly neighbors? Interspecies relationships Geology: Will Homo sapiens leave a geological mark? Ethics & Philosophy: How anthropocentric is the Anthropocene?

With contributions by Will Roebroeks (ULeiden), Katherine MacDonald (ULeiden), Liesbeth Bakker (NIOO/UWageningen), Barbara Gravendeel (Naturalis/UNijmegen), Erle Ellis (UMaryland), Will Steffen (Australian Natl U), Jan Zalasiewicz (ULeicester), Raymond Corbey (ULeiden). Organised by Daniella Vos (UGroningen), Kees Klein Goldewijk (UUtrecht), Martine Maan (UGroningen).

More information at: <https://www.rug.nl/education/summer-winter-schools/anthropocene/?lang=en> Contact: anthropoceneschool@rug.nl

m.e.maan@rug.nl

Online ConservationGenomics Jun27-30

Dear all,

we have the last seats available for the 2nd edition of the Conservation Genomics course in June (27th-30th).

This course will introduce attendees 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.

Course website: (<https://www.physalia-courses.org/courses-workshops/course62/>)

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>)

Online EukaryoticMetabarcoding Jul4-8

Dear all,

we have the last seats available for the 7th edition of the Eukaryotic Metabarcoding course.

Dates: online 4th-8th July

Course website: (<https://www.physalia-courses.org/courses-workshops/course4/>)

This workshop gives an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the workshop, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw

next-generation sequence data and (3) design their own metabarcoding projects, using bespoke primer sets and custom reference databases.

The syllabus has been planned for people which have some previous experience running simple commands in Unix and using the R environment (preferently RStudio) for performing basic plots and statistical procedures.

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 GenomeAssembly May16-19

The University of Connecticut’s Computational Biology Core is offering a workshop on genome assembly.

The workshop will cover basic concepts and walk through the code for several strategies on a high performance computing cluster. The goal is to familiarize attendees with the steps necessary to sequence, assemble, and evaluate a genome.

All code required to complete the full analysis will be provided in a public github repository, and session recordings will be available to all participants after the workshop.

The workshop will take place over 4 days for 3-3.5 hours each day.

Dates: May 16-19 2022 Time (ET): Day 1: 8:30am-12:00pm, Days 2-4 9.00am - 12.00pm Location: Online Cost: \$350/\$483USD for UConn affiliated/External attendees.

Workshop schedule: Day 1: Introduction to Linux/HPC Day 2: Introduction to k-mer analysis, high throughput sequencing, quality control of sequence data, contaminant detection Day 3: Genome assembly strategies and short-read assembly Day 4: Long-read and hybrid assembly, post-processing, assembly benchmarking

Registration:

To register, please follow this link: <https://forms.gle/-daCLSmFtDhJQ7ndQA> Other upcoming virtual workshops: RAD-seq - June 6-9 2022 Variant detection with WGS - July 25-28 Differential expression analysis with RNA-seq, reference genome based - August 22-25

Workshop FAQ:

Who should attend?

Anyone who wants to learn the fundamentals of genome assembly.

What are the prerequisites?

Prior bioinformatic experience is not required. We have dedicated the first day of the 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 \$350/\$483USD for UConn affiliated/External attendees.

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 Zoom.

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.

Do you offer scholarships or tuition waivers?

Yes. For each workshop we offer waivers to up to two attendees without other funding sources. Preference will be given to students from primarily undergraduate institutions, from countries classified by the World Bank as low or middle-income, and those from underrepresented groups. Applicants for waivers may submit a one paragraph justification to cbcsupport@uconn.edu.

Questions?

If you have any questions, please don’t hesitate to con-

tact us at cbcsupport@uconn.edu

“Reid, Noah” <noah.reid@uconn.edu>

Online IntroAncientMetagenomics Aug1-5

Dear colleagues,

The SPAAM Community is offering a new 5 day virtual summer school course sponsored by the Werner Siemens Foundation: *Introduction to Ancient Metagenomics*.

DATE AND SCHEDULE: Online from Monday 1st to Friday 5th of August from 09:00 to 17:00 (CEST, Leipzig time zone).

ORGANISERS: Dr. Christina Warinner (Harvard University, Max Planck Institute for Evolutionary Anthropology) and James Fellows Yates (Max Planck Institute for Evolutionary Anthropology, Leibniz Institute for Natural Product Research and Infection Biology Hans Kn- ll Institute).

INSTRUCTORS: Dr. Aida Andrades Valtue- a, Dr. Theseas C. Lamnidis, Dr. Arthur Kocher, Dr. Alex H- bner, Dr. Irina Velsko, Dr. Alexander Herbig, Megan Michels, Alina Hi- , Clemens Schmid, Maxime Borry (and more TBC)

COURSE OVERVIEW: Ancient metagenomics applies cutting-edge metagenomic methods to the degraded DNA content of archaeological and paleontological specimens. The rapidly growing field is currently uncovering a wealth of novel information for both human and natural history, from identifying the causes of devastating pandemics such as the Black Death, to revealing how past ecosystems changed in response to long-term climatic and anthropogenic change, to reconstructing the microbiomes of extinct human relatives. However, as the field grows, the techniques, methods, and workflows used to analyse such data are rapidly changing and improving.

In this *hands-on summer school (block praktikum)*- we will go through the main steps of ancient metagenomic bioinformatic workflows, familiarising students with the command line, demonstrating how to process next-generation-sequencing (NGS) data, and showing how to perform de novo metagenomic assembly. Focusing on host-associated ancient metagenomics, the course consists of a combination of lectures and hands-on exercises, allowing participants to become familiar with

the types of questions and data researchers work with. Round table discussions with experts at each stage of the workflow will be held to allow participants to get advice on their own projects and research.

By the end of the course, participants will have an understanding of how to effectively carry out the major bioinformatic components of an ancient metagenomic project in an open and transparent manner. Attendees will be eligible for ECTS points (awarded by the JSMC Graduate School, Friedrich-Schiller University, Germany) or a certificate of completion (Max Planck - Harvard Research Center, MHAAM).

SYLLABUS

Day 1

- * Lecture: Introduction to NGS data - * Practical 1: BareBonesBash 1 - * Practical 2: BareBonesBash 2 - * Round table: Introductions

Day 2

- * Lecture: Introduction to ancient DNA - * Practical 1: Bytesize git - * Practical 2: ancientMetagenomeDir - * Practical: nf-core/eager - * Round table: Project organisation

Day 3

- * Lecture: Introduction to metagenomics - * Practical 1: Introduction to R and the tidyverse - * Practical 2: Taxonomic profiling, OTU tables and visualisation - * Round table: Taxonomic classifiers

Day 4

- * Lecture Introduction to microbial genomics - * Practical 1: Genome mapping - * Practical 2: Genome assembly - * Roundtable: Databases

Day 5

- * Lecture Evolutionary biology - * Practical 1: Phylogenomics - * Practical 2: Functional genomics - * Round table: Workshop review

ELIGIBILITY: The course is aimed at masters students and early-stage PhD students, to a maximum of 25 participants. Course instruction will take place online.

APPLICATIONS: Applications are open from April 19 to June 1 2022. To apply, please visit our website: <https://spaam-community.github.io/wss-summer-school/> For questions or more information, contact James Fellows Yates (james.fellows_yates@eva.mpg.de) or Christina Warinner (christina_warinner@eva.mpg.de)

Best regards Christina and James

– James A. Fellows Yates

Microbiome Sciences Group, Dept. of Archaeogenetics

Max Planck Institute for Evolutionary Anthropology
 Dept. of Paleobiotechnology Leibniz Institute for Natural
 Product Research and Infection Biology Hans Kn- ll
 Institute

“James A. Fellows Yates”
 <james_fellows_yates@eva.mpg.de> “James A. Fellows
 Yates” <james_fellows_yates@eva.mpg.de>

Online IntroductionToSnakemake May3-4

Dear all,

we have the last few seats left for the Snakemake course
 with Dr. Johannes K_ister (University of Duisburg-
 Essen, GER).

Dates and time: 3-4 May (2-8 pm Berlin time zone)

This course will introduce the Snakemake workflow defi-
 nition language and describe how to use the execution
 environment to scale workflows to compute servers and
 clusters while adapting to hardware specific constraints.
 Further, it will be shown how Snakemake helps to create
 reproducible analyses that can be adapted to new data
 with little effort.

Course website: ([https://www.physalia-courses.org/-
 courses-workshops/course41/](https://www.physalia-courses.org/-courses-workshops/course41/))

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
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 low us on (<https://twitter.com/Physacourses>)

“info@physalia-courses.org” <info@physalia-
 courses.org> “info@physalia-courses.org”
 <info@physalia-courses.org>

Online IntroMultivariateEvolAnalysis May9-11

ONLINE COURSE - Introduction To Multivariate Anal-
 ysis In Ecology And Evolutionary Biology

[https://www.prstatistics.com/course/online-course-
 introduction-to-multivariate-analysis-in-ecology-
 and-evolutionary-biology-ima01-this-course-will-be-
 delivered-live/](https://www.prstatistics.com/course/online-course-introduction-to-multivariate-analysis-in-ecology-and-evolutionary-biology-ima01-this-course-will-be-delivered-live/) Please feel free to share!

ABOUT THIS COURSE

This community analytics course is designed for students
 who have recently started their projects or researchers
 who are starting using the R ecosystem. During this
 three-day course, we will cover the basic concepts of
 multivariate analysis and their implementation in R.
 This course is a complement to the PR Statistic offering
 allowing also beginners and non-programmers to dis-
 cover the statistical tools needed to analyze an ecological
 dataset in research, natural resource management or
 conservation context. This course is not geared toward
 any particular taxonomic group or ecological system.

We will cover diversity indices, distance measures and
 multivariate distance-based methods, clustering, classi-
 fication, and ordination techniques. We will focus on
 the concept of the methods and their implementation
 on R using different R packages. We will use real-world
 examples to implement analyses, such as describing pat-
 terns along gradients of environmental or anthropogenic
 disturbances, quantifying the effects of continuous and
 discrete predictors, data mining. The course will consist
 of lectures, work on R code scripts, and exercises for
 participants.

Please feel free to contact oliverhooker@prstatistics.com
 with any questions.

<https://www.prstatistics.com/live-courses/> [https://-
 www.prstatistics.com/recorded-courses/](https://www.prstatistics.com/recorded-courses/) Oliver Hooker
 PhD. PR statistics

Oliver Hooker <oliverhooker@prstatistics.com>

Online IntroToTidyverse Jul18-21

Dear all, we have the last seats available for the course “DATA ANALYSIS WITH THE TIDYVERSE” in July (18th-21st).

The course will be held online and it is a mixture of lectures and practical exercises. During the week, we'll cover dplyr, tidy data, tibbles, dates/times and string manipulation, Data Visualization using ggplot2 and functional programming with purr.

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

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 Macroevolutionary Analyses May2-6

Dear colleagues,

There are a few slots available for Transmitting Science online course Introduction to Macroevolutionary Analyses Using Phylogenies - 10th Edition.

Dates: May 2nd-6th, 2022 Monday to Friday, from 15:00 to 19:00 (Madrid time zone)

Instructor: Dr. Juan L. Cantalapiedra (Universidad de Alcalá, $\frac{1}{2}$, Spain)

COURSE OVERVIEW

Phylogenetic trees have changed the way we study and understand life on Earth. Taking phylogenetic information into account in our analyses is critical to account for the non-independence of biological data. Also, phylogenies allow us to get a deep-time perspective of the processes that have shaped the evolutionary history of groups, including diversification and trait evolution. This course will introduce participants to the use, mod-

ification and representation of phylogenetic trees. Also, we will focus on the use of phylogenetic information to reconstruct ancestral characters and biogeographic histories, using different phylogenetic comparative methods. This course will also tackle trait evolution modelling and the assessment of phylogenetic signal. Finally, we will learn about the shape of phylogenetic trees and its evolutionary causes, and how to estimate the rates of diversification throughout the history of groups. Participants are encouraged to bring their data sets to use in the practical classes. The course includes an optional first introductory day to basic R. Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees. Software: Mesquite, FigTree, R (ape, TreeSim, TreePar, Geiger, OUwie, BioGeoBEARS).

You can find more information at <https://www.transmittingscience.com/courses/-evolution/introduction-macroevolutionary-analyses-using-phylogenies/> or writing courses@transmittingscience.com

Best wishes

Sole

– Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban 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

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Online MappingTraitEvolution Jul4-8

Dear colleagues,

Transmitting Science is offering a new edition of the course Mapping Trait Evolution 5th edition. This course will be held live online (synchronous). Max 16 participants.

Dates: July 4th-8th, 2022, from 14:00 to 18:00 (Madrid time zone)

Instructor: Jeroen Smaers (Stony Brook University, USA)

COURSE OVERVIEW

The course provides a comprehensive overview of the state-of-the-art methods in mapping phenotypic trait evolution and will provide participants with a springboard to using these methods to answering their own research questions.

We focus on analyses that use a phylogenetic tree and observed trait information from tip taxa (extant and/or extinct) to describe how traits have changed along the branches of a phylogeny. The course covers methods that estimate and test patterns related to changes in mean, covariation, and rate. Applications for continuous and categorical, and univariate and multivariate research designs are discussed.

At the end of this course, participants will have developed an understanding of:

(1) Brownian motion and Ornstein-Uhlenbeck models

of evolution.

(2) How these models can be applied to estimate and test patterns of trait evolution.

(3) What the advantages and disadvantages are of different models/methods.

(4) How to recognize which model/method is most appropriate given a particular dataset and research question.

We provide several data sets that will be used to exemplify the application of these methods. We do, however, encourage participants to work with their own data so as to get direct experience with analysing precisely what they expect to analyse.

Methods from the following R packages will be discussed: ape, geiger, phytools, evomap, llou, bayou, surface, OUwie, mvMORPH, geomorph (this list may change as new packages become available).

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees, the methods we cover in this course assume that a phylogeny is known.

You can find more information here: <https://www.transmittingscience.com/courses/evolution/mapping-trait-evolution/> or writing courses@transmittingscience.com

Best wishes

Sole

- Soledad De Esteban-Trivigno, PhD Director
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<soledad.esteban@transmittingscience.com>

Online NanoporeDirectRNASequencing Jun24-26

Dear all,

registration is now open for the 2nd edition of the course "AN INTRODUCTION TO NANOPORE DIRECT RNA SEQUENCING".

Dates: 24-26 June

This course is structured over 3 days of theoretical and hands-on training and covers the majority of the concepts and challenges commonly faced when analysing

direct RNA-Seq data. It will start from common tasks such as data QC and gene expression quantification and then move on to more advanced topics such as transcriptome assembly, polyA-tail length measurements and RNA modifications detection.

Course website: (<https://www.physalia-courses.org/courses-workshops/course59c/>)

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 Palaeogenomics May17-21

Dear colleagues,

Transmitting Science is offering a new course: Introduction to Palaeogenomics - concepts, methods and applications of ancient human and non-human DNA data.

Date and schedule: Online live sessions from Monday 17th to Friday 21st of May from 16:00 to 21:00 (GMT+2, Madrid time zone).

Instructors: Dr. Marcela Sandoval Velsaco (University of Copenhagen, Denmark) and Dr. Jazmīn Ramos-Madriral (University of Copenhagen, Denmark).

COURSE OVERVIEW:

Ancient DNA (aDNA) research, defined as the retrieval and analysis of DNA sequences from various degraded biological materials, has been evolving as a research field for four decades. Through advances in DNA isolation and amplification techniques, sequencing technologies and data analysis pipelines, the field has revolutionized and transitioned to what we now know as palaeogenomics. DNA extracted from archaeological samples, and museum specimens has proven useful to study species and life on earth from the genomic perspective. It has made it possible to measure changes in genetic diversity through time, test hypotheses about the association of environmental phenomena and genetic changes in natural populations, and to resolve long-standing questions about the evolutionary relation-

ships between species.

In a combination of interactive lectures and hands-on practical sessions, this course will provide a theoretical overview of molecular biology laboratory techniques for the retrieval of aDNA from ancient samples from different species and an introduction to the bioinformatic pipelines for the analysis of palaeogenomic data. Students will be introduced to the standard bioinformatic methods often used in palaeogenomic projects for the analysis of aDNA data from human and non-human samples. We will also review the history and developments of the field to understand how it came to be what it is today, and consider and discuss the practical problems of ancient DNA recovery, the theoretical problems associated with the interpretation of palaeogenomic data, and the ethical implications embedded in this type of research.

At the end of the course, students will have gained a general understanding of common key methods and tools used in palaeogenomics projects: from the basics in the field to the interpretation of the results, as well as ethical and responsibility aspects and implications of aDNA research.

More information and registration: <https://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-palaeogenomics-concepts-methods-and-applications-of-ancient-dna-data/> With best regards

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban 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

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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>

Online Phylogenetic Analysis Using R Jul18-22

Dear colleagues,

Registration is open for the course “Phylogenetic Analysis Using R” - 9th Edition. This course will be held live online (synchronous). Max 16 participants.

DATES: July 18th-22nd, 2022 from 13:00 to 18:30 (Madrid Time Zone)

INSTRUCTORS:

Dr. Emmanuel Paradis (Institut de Recherche pour le Développement, France) and Dr. Klaus Schliep (Graz University of Technology, Austria)

COURSE OVERVIEW

This course is for biologists dealing with the analysis of multiple molecular sequences at several levels: Populations, species, clades, communities. These biologists address questions relative to the evolutionary relationships among these sequences, as well as the evolutionary forces structuring biodiversity at different scales.

The objectives of the course are: (i) to know how to choose a strategy of molecular data analysis at the inter- or intraspecific levels, (ii) to be able to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics.

The software used for this course will be centered on the R language for statistics. This will include the use of specialized packages particularly ape, phangorn, and adegenet.

You can find more information at <https://www.transmittingscience.com/courses/evolution/-phylogenetic-analysis-using-r/> or writing to courses@transmittingscience.com

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter [@SoleDeEsteban](https://twitter.com/SoleDeEsteban) 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.

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Online Population Genetics Using R

PR STATISTICS RECORDED COURSES

Moving our courses online due to the COVID pandemic has allowed us to archive all our previous courses and offer them in a recorded format.

<https://www.prstatistics.com/recorded-courses/> This is ideal for;

People with busy schedules who can't take long periods off work to attend workshops.

Allows attendees to work at their own pace with email support.

Suitable for people from all timezones.

The recordings are taken from our Live Online Courses which ensures all materials and software packages are constantly up-to-date.

You can now complete our past course;

Fundamentals Of Population Genetics Using R (FOPG01R) <https://www.prstatistics.com/course/-fundamentals-of-population-genetics-using-r-fopg01r/>

Please email oliverhooker@prstatistics.com with any questions on enquiries or you can book directly using the link above Please feel free to share anywhere you see fit.

Oliver

Oliver Hooker PhD. PR statistics

Oliver Hooker <oliverhooker@prstatistics.com>

Online Spatial Data Analysis Apr 25-28

The methods taught are used frequently in Population Genetics and Landscape genetics so relevant to evolutionary data. Lesson 8 for example is purely focused on the Mantel test and problems you may encounter applying it to Pop-Gen / Landscape-Gen data.

ONLINE COURSE -Advances In Spatial Analysis Of Multivariate Ecological Data: Theory And Practice (MVSP05) This course is pre-recorded with live help

<https://www.prstatistics.com/course/advances-in-spatial-analysis-of-multivariate-ecological-data-theory-and-practice-mvsp05/> Instructor- Prof. Pierre Legendre

25th - 28th April 2022

Please feel free to share!

ABOUT THIS COURSE

The course will describe recent methods (concepts and R tools) that can be used to analyse spatial patterns in community ecology. The umbrella concept of the course is beta diversity, which is the spatial variation of communities. Researchers in spatial ecology, population genetics and landscape genetics will find these methods useful as they are applicable to all types of communities (bacteria, plants, animals) sampled along transects, regular grids or irregularly distributed sites. The new methods, collectively referred to as spatial eigen-function analysis, are grounded into techniques commonly used by community ecologists, which will be described first: simple ordination (PCA, CA, PCoA), multivariate regression and canonical analysis, permutation tests. The choice of dissimilarities that are appropriate for community composition data will also be discussed. The focal question is to determine how much of the community variation (beta diversity) is due to environmental sorting and to community-based processes, including neutral processes. Recently developed methods to partition beta diversity in different ways will be presented. Extensions will be made to temporal and space-time data.

Monday 25th

Lesson 1: Ordination in reduced space Section 1.0. Ordination in reduced space: An introduction Section 1.1. Principal component analysis (PCA) Section 1.2. Correspondence analysis (CA) Section 1.3. Principal coordinate analysis (PCoA) Section 1.4. Metric ordination methods in ecology (included with 1.3)

Practical 1

Tuesday 26th

Lesson 2: Dissimilarities and transformations

Lesson 3: Tests of statistical significance

Lesson 4: Linear regression Section 4.1 Multiple linear regression Section 4.2 Partial regression and variation partitioning

Practical 2

Wednesday 27th

Lesson 5: Canonical analysis

Lesson 6: Beta diversity Section 6.1. Partitioning beta diversity Section 6.2. Replacement and richness difference Section 6.3. Temporal beta diversity

Practical 3

Thursday 28th

Lesson 7: Spatial modelling Section 7.1. Origin of spatial structures in ecology Section 7.2. Spatial eigenfunction modelling Section 7.3. Space-time interaction

Lesson 8: Mantel test in spatial analysis

Practical 4

We have already scheduled our FREE course seminars for this course .

<https://www.prstatistics.com/course/advances-in-spatial-analysis-of-multivariate-ecological-data-theory-and-practice-mvsp05s/> if you would like access to the recording please email oliverhooker@prstatistics.com

<https://www.prstatistics.com/free-seminars/> Please feel free to contact oliverhooker@prstatistics.com with any questions.

Thanks,

Oliver

Oliver Hooker PhD. PR statistics

Oliver Hooker <oliverhooker@prstatistics.com>

StAgustine Florida AdaptiveEvolution Jul24-27

Detecting adaptive evolutionary events in genomes of polar species at the Whitney Laboratory for Marine Bioscience, St. Augustine, Florida July 24-27, 2022 National Science Foundation awards #1935635 and #1935672 A two-day workshop will be held at the Whitney Laboratory for Marine Bioscience (University of Florida) during July 24 - 27, 2022. Participants should plan to arrive on the afternoon of July 24th and depart in the afternoon of July 27th. The workshop organizers, Dr. Scott Santagata and Dr. Joseph Ryan, will lead participants through a series of computational exercises having the following goals.

§Construct orthologous gene assignments (OrthoFinder), prune paralogous genes (PhyloPYPPruner), align orthol-

ogous gene (MAFFT), and multi-gene phylogenetic relationships (IQ-TREE).

§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.

§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 Cottages 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, 2022) 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. D) Sars-CoV-2 Vaccination Status. 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>

Subject:Workshop:Online NatHist Alaska May24-26

SEAK2022 Workshop May 24-26 - 2ndannouncement

We are pleased to announce SEAK2022 - a virtual Workshop May 24-26 focusing on the natural history of SE Alaska, and neighboring regions along the British Columbia coast. We are seeking presentations on climate change, ice sheet dynamics, volcanic geohazards, Ice Age refugia, biodiversity, and biogeographic history.

Please visit the workshop website for more information and updates:

<http://www.glyfac.buffalo.edu/Faculty/briner/-SEAK2022/> Note that the deadline for a talk suggestion has been extended to April 29!

Deadline for abstract submission is May 6. Registration is free.

Registration: To indicate interest and suggest a talk, click here and fill out the Google form (please also fill out the form if you have already emailed us with your interest)

(<https://docs.google.com/forms/d/e/1FAIpQLSfgKvMr8vSJghrJoaZQCxGXfAfaGqtEJ-ev6MxVMh9CgET-Yg/viewform>)

If you have any questions about registration, please email jbriner@buffalo.edu.

The program will be dictated by those interested in participating. We envision having one day focused on identifying gaps in knowledge about the geologic history, with a focus on past glaciation and volcanism in the Quaternary. We envision another day focused on identifying gaps in knowledge of biodiversity patterns and biogeographic history through the last glaciation and across the Holocene. We plan to make time for breakout discussions that will lead to a workshop report that identifies key gaps in knowledge, and how to fill them.

Best wishes from the organizers,

Jason Briner

Charlotte Lindqvist

University at Buffalo

Charlotte Lindqvist <cl243@buffalo.edu>

Switzerland ArtificialSelection Aug22-25

Workshop on “The evolutionary consequences of unintended artificial selection on population fitness” in the Swiss Alps on Aug 22-25, 2022

In a remote but well-equipped hotel (<https://www.faleralp.ch/>) in the Jungfrau-Aletsch-Bietschhorn UNESCO World Heritage.

Faculty participating: - Fanie Pelletier (University of Sherbrooke, Canada) - Anna Kuparinen (University of Jyväskylä, Finland) - Andrea Pilastro (University of Padua, Italy) - Philine Feulner (EAWAG-ETHZ, Switzerland) - Marty Kardos (Northwest Fisheries Science Center NOAA, USA) - J. Andrew de Woody (Purdue University, USA) - Claus Wedekind (University of Lausanne, Switzerland)

The workshop is open to PhD students, postgraduate students, postdocs and academics from all universities worldwide, but the number of participants is limited to 30.

Abstract: Wild populations are shaped by natural selection, sexual selection, and (mostly unintended) artificial selection. The latter include, for example, a decline of the mean breeding value for horn size in response to trophy hunting, or reduced individual growth rates in response to size-selective fishing. Previous research in this context has concentrated on the evolutionary responses in the specific traits that are under selection. The effects of unintended artificial selection on population fitness are still largely unclear. Artificially changed selection regimes can increase the genetic load of natural populations, either by directly selecting against individuals of high breeding value for fitness (e.g. if fast growth is an indicator of low genetic load), or by relaxing natural and sexual selection and hence reducing purifying selection (e.g. in supportive breeding programs). We will discuss the problem in the context of current environmental changes and the potential of rapid evolution.

Application is now open. Participants are expected to present and discuss their work in the light of the topic of the workshop. Please send a title and abstract before May 15th, 2022.

Further information: https://www.cuso.ch/activity/?p=1128&uid*11 Claus Wedekind Department of Ecology and Evolution, Biophore, University of Lausanne,

1015 Lausanne, Switzerland. Tel. +41 21 692 42 50, Fax +41 21 692 42 65 <https://www.unil.ch/dee/wedekind-group> Claus Wedekind <claus.wedekind@unil.ch> Claus Wedekind <claus.wedekind@unil.ch>

UGroningen Anthropocene Jul3-8

Welcome to the Anthropocene! Summer School at the University of Groningen 3 - 8 July 2022 For whom: PhD, Master, and advanced Bachelor students Extended deadline for application: 15 May 2022, 23:59 CET

<https://www.rug.nl/education/summer-winter-schools/anthropocene/?lang=en> Topics covered: Paleontology: Shifts in subsistence and environmental impact Evolutionary biology: Are we friendly neighbors? Interspecies relationships Geology: Will Homo sapiens leave a geological mark? Ethics & Philosophy: How anthropocentric is the Anthropocene?

With contributions by Will Roebroeks (ULeiden), Katherine MacDonald (ULeiden), Liesbeth Bakker (NIOO/UWageningen), Barbara Gravendeel (Naturalis/UNijmegen), Erle Ellis (UMaryland), Will Steffen (Australian Natl U), Jan Zalasiewicz (ULeicester), Raymond Corbey (ULeiden). Organised by Daniella Vos (UGroningen), Kees Klein Goldewijk (UUtrecht), Martine Maan (UGroningen).

Martine E. Maan Associate Professor and Rosalind Franklin Fellow Groningen Institute for Evolutionary Life Sciences (GELIFES) University of Groningen PO Box 11103 9700 CC Groningen The Netherlands +31 (0)50 363 2196

Visiting address: Nijenborgh 7 9747 AG Groningen The Netherlands building 5171, room 01.42

<http://www.rug.nl/staff/m.e.maan> "m.e.maan@rug.nl" <m.e.maan@rug.nl>

Vairao Portugal Domestic Animal Archaeogenomics May 23-27

REGISTRATION DEADLINE EXTENDED TO APRIL 25

THE ARCHAEOGENOMICS OF DOMESTIC ANIMALS

*May 23-27, 2022 | BIOPOLIS-CIBIO-InBIO | Vairão, Portugal *

Diachronic genetic studies are required in order to infer the origins and evolutionary trajectories of domestic animals. Data spanning long time scales from zooarchaeological specimens allow the investigation of genomic variation within populations over time. Analysis of ancient DNA opens a direct window into the past for reconstruction of the genetic history of animal populations.

The objective of this course is to provide an overview of the most recent Archaeogenomics findings on the origin and evolution of domestic animals. It will also cover some of the recommended bioinformatics tools and methods for the study of ancient DNA genomics data. There will be hands-on sessions, including bioinformatics on how to filter, infer damage patterns and authenticate next-generation-sequencing data obtained from archaeological specimens, as well as on population genomics. One invited speaker in Archaeogenomics will also contribute to the course.

At the end of the course students should understand the importance of including genomic data concerning past populations to make evolutionary inferences, as well as get familiar with the challenges and peculiarities of ancient DNA analysis.

IMPORTANT DATES Registration deadline: April 25, 2022 Notification of acceptance: April 18, 2022 Full details, including the course programme and instructors, application form, selection criteria and requirements, can be found here: <https://www.biodiv.pt/en/events/the-archaeogenomics-of-domestic-animals/> This course is aimed at Ph.D. students, postdocs and other researchers in the fields of evolutionary biology, zooarchaeology and archaeology with a specific interest in Archaeogenomics.

Catarina Ginja, PhD Researcher, Team Leader ARCHGEN < <https://cibio.up.pt/en/groups/-archaeogenetics-archgen/> > CiênciA ID: 8511-380F-548D < <https://www.cienciavita.pt/portal/8511-380F-548D> > ORCID ID: 0000-0003-2278-7089 < <https://orcid.org/my-orcid> >

1. CIBIO, Centro de Investigaçãõ em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal

2. BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661

Vairi, 1/2o, Portugal

ARCHAIC project: Archaeogenetics of Iberian Cattle
< <http://archaic.campus.ciencias.ulisboa.pt/> >

Catarina Ginja <catarinaginja@gmail.com> Catarina
Ginja <catarinaginja@gmail.com>

Venice EvoDevoCharacters

Aug22-26

Dear all,

EXTENDED DEADLINE: we will still be accepting applications until APRIL 30!

*** Venice Summer School 2022 - The character concept in metabolic, physiological, and developmental evolution *** Aug 22 - Aug 26, 2022, Centro Culturale Don Orione Artigianelli, Venice, IT

Organisers: Johannes Jaeger, Complexity Science Hub (CSH), Vienna, AT, jaeger@csh.ac.at James DiFrisco, KU Leuven, BE, james.difrisco@kuleuven.be

Teaching Panel:

Graham Budd, University of Uppsala, SE

James DiFrisco, KU Leuven, BE Scott Gilbert, Swarthmore College, USA Thomas Hansen, University of Oslo, NO

Johannes Jaeger, Complexity Science Hub (CSH) Vienna, AT

Antónia Monteiro, National University of Singapore, SG Edwige Moyroud, Sainsbury Laboratory, Cambridge, UK Laura Nuño de la Rosa, Universidad Complutense de Madrid, ES

Mihaela Pavlicev, University of Vienna, AT Nicole Repina, Friedrich Miescher Institut, Basel, CH

Günter Wagner, Yale University, USA

Course description:

The concept of “characters” lies at the heart of many central issues in evolutionary biology. Characters distinguish taxa, cause fitness differences, and generally are the fundamental units of comparison for studies of phenotypic evolution. Historically, the concept of characters originated in morphology and comparative anatomy, where it was intimately connected to the issue of homology. At the same time, characters in evolutionary genetics have been understood as the effective

dimensions along which a population is evolving. Both the more historical and functional conceptions of biological characters presuppose that phenotypes are modular enough that it makes sense to compare or model parts of organisms directly rather than whole organisms. Today, the notion of characters or traits is increasingly used to describe dynamic lower-level phenomena such as metabolic, physiological, and developmental processes. This raises a number of challenging but interesting conceptual issues. How can we define characters or traits when the object under study is a process? Is it possible to modularize regulatory mechanisms into quasi-independent characters? What light can contemporary systems biology shed on the partitioning of the phenotype into characters? We do not yet have answers to these important questions. We have gathered a select group of empirical investigators and theoreticians from the fields of biochemistry, physiology, developmental biology, and evolutionary biology together with mathematical modelers, and philosophers of biology to discuss how characters can be defined, identified, and characterized in the age of integrative systems biology. Is it still useful to talk about characters? And if so, what should the concept incorporate to guide research in the right direction? Evolutionary biology lies at the very heart of biology. Therefore, this topic is relevant far beyond its boundaries. Properly tackling it requires the kind of transdisciplinary exchange of ideas and approaches we are planning to implement in this course. The summer school is mainly aimed at early-stage (PhD or postdoc) empirical and theoretical researchers with a general background and/or interest in developmental and/or evolutionary biology. More senior investigators are welcome to apply as well. Exceptions can be made for motivated masters students. Participants of previous Venice Summer Schools in Evo-Devo are expressly encouraged to reapply as this course has an entirely different topic than previous editions. The course will equip participants with the conceptual tools to engage in a productive discussion of the notion of “characters,” and to relate this notion to their own research questions and explanations.

*** Detailed programme, further information, and registration at:

<https://meetings.embo.org/event/21-evolution-venice>
Applicants are required to submit an academic CV, and a motivation letter. Optionally, also add an abstract if you would like to present your own work as an elevator pitch on the first day of the course.

*** EXTENDED APPLICATION DEADLINE: Apr 30, 2022. Applicants will be notified whether they have been accepted (or not) by May 15, 2022. The payment deadline for successful applicants is Jun 30, 2022.

Follow @VeniceEvoDevo on Twitter for updates.

On behalf of all the organisers, Yogi Jaeger

Dr. Johannes Jaeger Freelance Researcher, Philosopher

& Educator Associate Faculty, Complexity Science Hub (CSH), Vienna

Johannes Jaeger <yoginho@gmail.com>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.