E v o l D i r

July 1, 2021

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

Foreword

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

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

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

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Conferences

Madison Wisconsin MidwestPopGenetics Aug20-21

Dear colleagues,

I am excited to announce tentative plans for an in-person edition of the Midwest Population Genetics Meeting, planned for August 20 and 21 in Madison, Wisconsin (USA). Whereas large conferences have understandably been postponed this year, I believe that our smaller conference can be conducted safely at this stage of the pandemic, and we can be nimble in changing plans if needed.

This will be the 7th incarnation of this regional meeting, which has occurred annually since 2014 with the exception of last year. The meeting will include talks (mostly from graduate students and postdocs), posters, and opportunities for informal interaction. The meeting is typically held from roughly 1pm on a Friday through 5pm on a Saturday, but this year's exact schedule remains to be determined. Conference policies and planning will prioritize a range of COVID-19 safety measures, including mask-wearing, social distancing, outdoor-ventilated conference space, and outdoor food breaks. We also expect that all participants would be vaccinated by the time of the meeting.

The purposes of this message are to: (1) Serve as a "Save the Date" notice as you consider your summer plans, and (2) Invite you to sign up to receive updates, such as announcing when conference application opens. This

is important because I anticipate that demand for this meeting may be greater than usual, in light of the lack of in-person conferences during 2020 and 2021. And yet, space and social distancing will necessitate a limited number of attendees at this meeting. Therefore, it is likely that we will need to implement an application system, and to prioritize attendance based on career stage, diversity and focus of research topics, and COVID safety.

If you think you may be interested in attending this meeting, then I strongly encourage you to sign up for the following e-mail group, so that you will have opportunity to apply while space remains. You must either: (A) Visit the link below and click the "Join group" or "Ask to join group" button: https://groups.google.com/a/g-groups.wisc.edu/g/mwpg2021 OR (B) Send an e-mail to: mwpg2021+subscribe@g-groups.wisc.edu When you then get an automatic e-mail from the group, DO NOT click the link it contains, but instead just reply to that e-mail with a blank message.

Please also consider forwarding this message to colleagues at your institution or elsewhere in our region who may be interested in this meeting.

Best regards, John Pool Associate Professor of Genetics University of Wisconsin - Madison

John E Pool <jpool@wisc.edu>

Wisconsin - Madison

John E Pool <jpool@wisc.edu>

Madison Wisconsin MidwestPopGenetics Deadline June15

Dear colleagues,

The outlook for an in-person Midwest Population Genetics Meeting (MWPG) in Madison this August continues to look favorable. However, because we anticipate both elevated demand for this meeting and ongoing limits on the density of indoor gatherings, we are implementing an application system for this meeting. Applications are now being accepted through June 15 via the link at the bottom of this message.

MWPG 2021 is scheduled to take place at the University of Wisconsin - Madison on Friday/Saturday August 20/21, with exact schedule including start and end times of the meeting to be announced. We have reserved the "Lake Mendota Room" at Dejope Hall for this event. The large size (4700 sq ft) and outdoor ventilation of this space will contribute to our safety precautions. There will also be a mask requirement, food breaks will be held outdoors, and we expect that all participants will have been vaccinated against COVID-19 before this event.

A consistent priority for MWPG has been to offer grad students and postdocs a venue to present their research. There will be a limited number of talk slots available in our schedule (it may not be possible to grant all talk requests). There will also be dedicated time in the schedule for posters. There should also be a Friday evening barbecue or similar interactive event.

There is no registration fee for this event. Some food is likely to be provided. Attendees will be responsible for their own transportation and lodging costs. A block of rooms has been reserved at the on-campus Union Hotel.

In spite of the likely limits on our conference attendance, we really do encourage everyone who is interested to apply (who knows - we may yet have room for everyone). Applications are due by June 15th (end of day), and we will aim to confirm our invited list of meeting attendees by July 2nd. No deadline reminder messages are anticipated, so please apply based on this notice. Application (which includes abstract submission if presenting) consists of the following online form: https://forms.gle/-5WKx2QVD3qarhtvX6 We hope that you can join us by the lake this August for a great meeting.

John Pool Associate Professor of Genetics University of

Online 2ndAsiaEvo CallForAbstracts Jun20

Dear all:

The 2nd AsiaEvo conference is now calling for abstract for a total of 20+ symposia. There are great invited speakers and awards for selected contributed talks from Ph.D.s and postdocs.

More details please check https://-evolgen.biol.se.tmu.ac.jp/asiaevo2/symposia.html
 Regards

Qi Zhou, PhD Professor Life Sciences Institute Zhejiang University http://qizhoulab.net/ Qi Zhou <zhouqi1982@zju.edu.cn>

Online CIGENE May19

Dear EvolDir members,

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

Date: 19.05.2021

Presenter: Mark Ravinet

Title: The evolution of human commensalism in Passer sparrows.

Abstract: From early civilization to the development of modern cities, human activity has shaped the evolution of other species. Some taxa are able to survive, adapt and even thrive in an anthropogenic niche. Human commensal species are a special case, having evolved a dependency on human resources without our direct influence. Intriguingly, human commensal relationships have arisen multiple times across many different species and even in parallel within the same genus. What factors drive the evolution of human commensalism? Is it a case of being in the right place at the right time? Or are there particular (pre)adaptations, traits and genes that mean some species are better able to exploit human resources than others? To explore these questions, I will

focus on the repeated evolution of human commensalism in a single genus - Passer sparrows. I will show that we are able to use genomic data to reconstruct when and where human commensalism arose in each species. In particular,

I will demonstrate that major human cultural transitions, i.e. the development of agriculture, have led to range expansions in these widespread and well-known birds. Finally, I will show that by combining phenotypic and genomic data, we are able to investigate the genetic basis for key traits involved in adapting to a human commensal life history.

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

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

on how our understanding of health and the evolution of senescence has been altered with the development of indicators and biomarkers of senescence such as epigenetic clocks and telomeres. These biomarkers have shed light on the relative impact of social, environmental, genetic and trans-generational effects on senescence. A synthesis of advances in the evolutionary theory of senescence, the occurrence and life-history consequences of senescence, and the underlying genetic and non-genetic mechanisms driving variation in individual senescence will significantly further the field. This knowledge is vital to understanding why senescence has evolved and how variance is maintained.

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

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

Abstract submission: through the ESEB website https://www.eseb2021.cz/en/satellite-symposia-2021 Registration: free of charge, through the ESEB website https://www.eseb2021.cz/en/satellite-symposia-2021 "H.L. Dugdale" <h.l.dugdale@rug.nl>

Online ESEB2021 BiomarkersEvolOfSenescence Jul6-7

Abstract submission and registration deadline extended until Friday June 4th

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

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

As individuals reach older ages their bodies deteriorate - a process known as senescence. Individuals within the same species can differ greatly in the age they start to senesce, and the rate at which they senesce. However, why individuals senesce so differently remains unresolved and is one of the biggest unanswered questions in evolutionary biology. Understanding the drivers of senescence has important ramifications for veterinary medicine, conservation, health and society, as it could help individuals to live longer, healthier lives. This symposium will seek to address this knowledge gap by bringing together researchers with expertise in senescence from theoretical, laboratory and field settings. In particular it will focus

Online ESEB SexChromosomeEvolution Aug30-Sep1

Online ESEB symposium: Sex Chromosome Evolution, 30 Aug.-01 Sep. 2021

Subject main text:

Abstract submissions are invited for 15 min talks and 5 min speed-talk at the online ESEB 2021 satellite symposium:

"The remarkable diversity in the rate and mechanisms of sex chromosome evolution"

30 Aug.-01 Sep.2021: 13:00-18:00 GMT

Registration deadline: 30 June 2021

No registration fee, but registration is mandatory for all participants at: https://www.eseb2021.cz/en/satellite-symposia-2021 Possibility to participate in the homonymous special issue on the Journal of Evolutionary Biology More informationabout thissymposium can be found at:https://www.eseb2021.cz/en/the-

remarkable-diversity-in-the-rate-and-mechanisms-of-sex-chromosome-evolution   Sex chromosomes are assumed to evolve from a pair of homologous autosomes, where the emergence of a sex-determining locus and recombination suppression triggered gradual structural changes such as accumulation of sexual antagonistic alleles, recombination arrest, accumulation of repeats, loss of functional genes and heterochromatinization. This model represents the classical paradigm for decades, implying a roughly linear process of sex chromosome degeneration from homomorphism to heteromorphism. Recently, comparative genomics have revealed an incredible diversity on the morphology, structure, age and stage of sex chromosomes in non-model species, questioning the role of previously assumed evolutionary drivers and other aspects of sex chromosome differentiation. It remains unclear why lineages differ so substantially in the degree of differentiation and the long-term stability of sex chromosomes. The current advances on genetic and genomic methodologies allows us to explore long lasting enigmas on the evolution of sex chromosomes across the tree of life, such as the role of sexual antagonism, chromosomal rearrangement, mechanisms of dosage compensation and differentiation rates. Therefore, in the current meeting, we welcome all studies exploring the evolution of sex chromosomes and sex determination with either theoretical or empirical approaches. The list of invited speakers is available below. In parallel to the online meeting, we invite all attendants to participate in the homonymous special issue on the Journal of Evolutionary Biology, with a review manuscript or original investigation. The submission deadline for the special issue is 31 December 2021.

List of invited speakers:

https://www.eseb2021.cz/en/list-of-invited-speakers-1
Dr. Astrid Bohne, Zoological Research Museum Alexander Koenig, Germany

Dr. Stu Nielsen, Florida Museum of Natural History, USA

Dr. Paris Veltsos, University of Kansas, USA

Asst.Prof. Alexander Suh, University of East Anglia, UK

Prof. Qi Zhou, Zhejiang University, China

Asst.Prof. Tony Gamble, Marquette University, USA

Assoc. Prof. Melissa Wilson Sayres, Arizona State University, USA

Assoc. Prof. James R. Walters, The University of Kansas, USA

Prof. Ben Evans, McMaster University, Canada

Prof. Catherine Peichel, University of Bern, Switzerland

Prof. Doris Bachtrog, UC Berkeley, USA

Prof. John Pannell, University of Lausanne, Switzerland

Prof. Judith Mank, University of British Columbia, Canada

Prof. Lukas Kratochvil, Charles University, Czech Republic

Prof. Nicole Valenzuela, Iowa State University, USA

Prof. Stephen Wright, University of Toronto, Canada

Prof. Tatiana Giraud, University of Paris Saclay, France

Distinguished Prof. Arthur Georges, University of Canberra, Australia

ABSTRACT SUBMISSION

https://www.eseb2021.cz/en/satellite-symposia-2021
REGISTRATION

FREE of charge, need registration to participate through the ESEB website: https://www.eseb2021.cz/-en/satellite-symposia-2021 ABSTRACT SUBMISSION DEADLINE:

30 June 2021

We look forward to meeting many of you at the online symposium in the summer!

Organizers:

Wen-Juan Ma (wenjuanma84@gmail.com,University of Kansas, USA) Michail Rovatsos (mirovatsos@gmail.com,Charles University, Czech Republic)

Dr. Wen-Juan Ma

NIH Senior Postdoctoral Research Associate

4055 Haworth Hall Department of Molecular Bioscience The University of Kansas 1200 Sunnyside Avenue Lawrence, Kansas 66045 USA

My website: http://www.wenjuanma.com/ Twitter: @WenJuanMa84

Wen-Juan Ma <wenjuanma84@gmail.com>

Online ESEB TandemRepeats Jun29

We are organizing a virtual ESEB Satellite Meeting on 'Tandem Repeats: methods and their role in molecular evolution' on June29 afternoon. This is a unique opportunity to meet researchers from all around the world

working on this topic. We definitely encourage you to give a talk and discuss your work with the community, as well! The new deadline to register freeof chargeis June 10th.

To register:https://www.eseb2021.cz/en/-satellite-symposia-2021 For information:https://-tandemrepeats.wordpress.com Keynote speakers:

Melissa Gymrek, UCSD, California Miguel Andrade, Johannes Gutenberg University, Mainz

Organisers: Tugce Bilgin, Columbia University, New York Maria Anisimova, ZHAW, Zurich

—

Dr. Tugce Bilgin Sonay

Lecturer in Discipline

Department of Ecology, Evolution, and Environmental Biology

Columbia University

Yoga Instructor Head of Evolutionary Genomics Winterschool

tugcebilgin.net

Tugce Bilgin Sonay <tb2879@columbia.edu>

Online EvolutionEcol May19

Dear EvolDir,

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

—

Wed 19 May

Dr. Alejandro Gonzalez Voyer

(Instituto de Ecologia, Universidad Nacional Autonoma de Mexico (UNAM), Mexico)

Brain size in a changing world and its relation to life history

—

When: 5PM BST/ 9AM PDT

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

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars

How to join: our Slack 'Evolution and Ecology Seminars' here: bit.ly/EvoEco2

Please follow our Twitter feed and join the Slack group for details of future upcoming talks.

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

Many thanks,

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

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

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

Online EvolutionEcology Apr28

Dear EvolDir,

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

—

Wed 19 May

Dr. Alejandro GonzÂ'lez Voyer

(Instituto de EcologÂÂa, Universidad Nacional AutÂÂnoma de México (UNAM), Mexico)

Brain evolution - title tbc

—

When: 5PM BST/ 9AM PDT

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

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

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

Online EvolutionEcology May26

Dear EvolDir,

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

—

Wed 26 May

Dr. Brandon Ogbunu

(Department of Ecology & Evolutionary Biology, Yale University, USA)

"Environment by everything Interactions: from protein evolution to the ecology of infectious disease"

—

When: 5PM BST/ 9AM PDT

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

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars

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Aaron Vogan Dr. Sarah Worsley

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

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

Online Galaxy Jun28-Jul10

2021 Galaxy Community Conference (GCC2021) 28 June through 10 July Virtual, in both European Central Time, and US Eastern Time

https://www.vibconferences.be/events/gcc2021-virtual-edition https://gcc2021.sched.com/ https://-galaxyproject.org/news/2021-04-gcc-reg/ ——

DEADLINES 7 May: Abstracts due 7 May: Galaxy Community Fund Fellowship applications due. 1 June: Early registration ends

ABOUT GCC2021 The 2021 Galaxy Community Conference will take place in a virtual format from 28 June to 10 July and bring together clinicians, researchers and students working in data science. The event features * A week of online training (28 June - 2 July), * three days of conference (6-8 July) and * a 2 day CollaborationFest (9-10 July).

The combination of very low registration, plus content in multiple time zones (see below for details on both) make this event the most affordable and accessible GCC ever. If you are working in data intensive science (life sciences and beyond), GCC2021 is an ideal conference to share your work, learn from others, and find new collaborators. We look forward to meeting you there!

ABOUT GALAXY Galaxy is an open data integration and analysis platform used and supported by a global community of researchers, bioinformaticians, developers, infrastructure providers, and trainers, all doing and supporting data intensive research Galaxy was originally developed to support life science research, but is now used in multiple fields including computational chemistry and molecular modelling, climate modeling, social science, and natural language processing. GCC is the community's annual gathering. See https://galaxyproject.org for more.

TRAINING Training will run for 5 days, from 28 June through 2 July. This will be an online event, spanning

all time zones. All training sessions are pre-recorded, so you can work through them at your own pace, and manage your own time. A large community of GTN trainers will be available 24/7 online support to answer all your questions on Slack. Training features 3 tracks: 1. Galaxy for Scientists 2. Galaxy for Developers 3. Galaxy for Administrators (enrollment is limited)

See https://galaxyproject.org/events/gcc2021/-training/ for what is in each track

MEETING The conference includes a 3 day meeting, 8-10 July, and features accepted talks, Q&A, poster/demos, sponsors, birds-of-a-feather sessions, and lots of social interaction and networking. Talks will be pre-recorded, but EVERYTHING else, including Q&A will be live. ALL MATERIAL WILL BE PRESENTED TWICE EACH DAY, once in the original Central European time zone, and then again 9 hours later in the Americas.

ABSTRACTS Talks and poster/demo presentations will be selected from abstract submissions. Talks can be either full (15-20 minutes) or lightning (5-7 minutes). We welcome submissions that use, implement or extend the Galaxy platform and ecosystem, including integrating and analyzing datasets in any research area, enhancing reproducibility in computational analyses, and fostering collaboration in scientific workflow development. Abstract submissions are due 7 May.

REGISTRATION Registration rates are very affordable, with deep discounts for researchers and students, and especially for researchers and students in developing economies. Early registration rates for students in developing economies start at Â3.25 for Training Week and Â6.00 for the meeting (plus VAT). See https://-galaxyproject.org/news/2021-04-gcc-reg/ for details.

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

Online GenomeEvolution May19-21

Dear EvolDir,

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

Studies of genome evolution are generally based on two approaches, phylogenetic methodology that relies on inter-species variation, and population genetics methodology that relies on intra-species variation. The two approaches, thus, focus on two different time-scales, and different models and methods have emerged in both disciplines. Different model assumptions have led to a separation of the two disciplines, and informa- tion content extracted by each of the two approaches is rarely combined. However, motivated by the recent increase in genome sequence data, efforts in method development have been made to counteract the distinc- tion between phylogenetic and population genetics methodology.

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

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

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

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

http://katalog.uu.se/profile/?id=N8-1504 När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy Carina Farah Mugal <carina.mugal@ebc.uu.se>

keep an eye out for an email announcement)

Plenary speakers:

Michael Eisen - University of California, Berkeley. Title: TBA

Hannah Fraser - University of Melbourne. Title: "Meta-research from ecological and interdisciplinary perspectives"

Michael Jennions - Australian National University. Title: "A Drunkard's Walk: from negative results to reverse P-hacking"

Julia Stewart Lowndes - National Center for Ecological Analysis and Synthesis. Title: "Openscapes: Towards more open, reproducible, inclusive practices for research teams and communities"

Richard McElreath - Max Planck Institute for Evolutionary Anthropology. Title: "Science is Like a Chicken Coop"

Malvika Sharan - Alan Turing Institute. Title: "The Turing Way Guide to Reproducible, Ethical and Collaborative Research"

We want to facilitate lively exchanges of ideas, and so the following three event types will be the heart of the conference:

Unconferences: Facilitated discussions of ideas for how to make ecology, evolutionary biology, and related disciplines more open, reliable, and transparent. Facilitation involves moderating the conversation with ideas and examples, but there are no formal presentations.

Hackathons: Group projects with well-defined goals (papers, techniques, software, protocols, organizations, etc.).

Workshops: Facilitators will teach tools for implementing open, reliable, and transparent practices.

We strongly encourage you to propose one of the above types of Facilitated Sessions at www.sortee.org/events . We also invite you to propose a Short Presentation to share your experience with issues of openness, reliability, and transparency in scientific research that are relevant to people working in fields related to ecology and evolutionary biology. For example, you could reflect on failures in your own work and what they taught you, present tools or methods that can help others make their research more open, reliable, and transparent, present plans for an upcoming project, or present research that integrates open science practices in an inspiring way.

We strongly encourage proposals for all contribution types from people at a wide range of career stages and from members of underrepresented groups.

Online InsectPlantRelationships Jul25-30

Dear All,

De deadline for submitting abstracts for the 17th edition of the Symposium on Insect Plant relationships is approaching quickly (31 May 2021). We still have room for oral contributions. The online symposium deals with all relevant topics on Insect Plant Interaction ranging from Ecology, Evolution, Genomics, Metabolomics, weed control with insects to plant pollinator interactions. Each topic is introduced by a world leading expert in the field. On the website, you will find a preliminary schedule indicating time (Central European summertime (UTC +2)) and themes. Note that we restricted the number of presentations on a day and included several breaks to optimize the potential to interact with peers. For more details, registration and submission of abstracts see the website: https://www.universiteitleiden.nl/sip2021 Don't miss this opportunity to be an active member of the community of researchers on plant-insect interactions.

Best regards,

Peter Klinkhamer and Klaas Vrieling

Deadline for submissions : 31 May 2021 Deadline for registration: 30 June 2021

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

Online SORTEE Jul12-14

Content submissions for the inaugural conference of the Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology (SORTEE.org/events) < https://www.sortee.org/events/ > close on June 1st. This is a hard deadline!

Conference location & dates: Virtually, world-wide. The conference will run continuously from 12 July 0700 UTC to 14 July 0700 UTC, in order to cover all timezones (with Europe/Africa and the Americas spanning July 12-13, and Asia/Pacific spanning July 13-14).

Registration price: FREE (registration will open soon,

For facilitated sessions (Workshops, Unconferences, and Hackathons), we welcome proposals from small teams (as well as individuals). We encourage teams to include diverse perspectives, for instance with facilitators from different countries and balanced in terms of gender and career stage. Facilitation by early career researchers (students or early career postdocs) is warmly encouraged.

We encourage people with any questions about accessibility in the submission process or the events themselves to contact us via sorteeconf2021@gmail.com. Similarly, please feel free to contact us if you would like guidance as you prepare your proposals and submissions.

For a look at the questions you will be asked when you submit your proposal(s), please click here: https://docs.google.com/document/d/-1h_aZ5zyVTBIf3bsqy6foj1SH7VlQnDXHtqjBZhrR4G0/-edit?usp=sharing   Tim   Parker <parkerth@whitman.edu>

UMalaga BiodiversityNatureConservation Sep16-19

Dear all,

The Center of Scientific Collections of the AlmerÂÂa University (CECOUAL), in collaboration with Botanical Garden of University "Marta Abreu'Â± de lasVillas, Cuba, is glad to announce the 5th Symposium on Biodiversity and Nature Conservation: Dissemination and transfer of knowledge among all social sectors.

The fifth annual Symposium will take place on September 16-19th, 2021 at the University of Malaga, Spain.

This will become a great venue for a diversity of researchers, managers, conservationists, environmental journalists, and the general public, so we hope to attract a diverse group.

Information about our meeting:

Our goal is to better integrate all society sectors focused on conservation. We plan to continue annual workshops in every corner of Spain. This will be our 5th annual meeting and we have been attracting scientists from all over the country and overseas.

Registrations are now open.

Abstract and early bird registration is due on June 1st,

2020.

Symposium has a limited capacity of students.

Link to meeting information: https://-congresoconserbio.com http://www.facebook.com/-conserbio/ For further information, please feel free to contact us: infoconserbio@gmail.com

The organizing director

Dr Marga L Rivas

Scientific researcher

University of Almeria, Spain

marga lopez rivas <margaflor13@hotmail.com>

Virtual Evolution Jun21-25 DeadlineExtended

Deadline extended - there are still a few openings left, so you can still submit a scheduled, faux-live talk title and keywords until Monday, 5/3 at midnight EDT.

Submissions for on-demand talk titles (available throughout the conference) will remain open until 5/15/2021.

Recording of talk videos begins May 1 and ends June 1, 2021.

Registration will remain open until the end of the conference (6/25/2021). Registration rates are listed below.

The Evolution conference is the joint annual meeting of the American Society of Naturalists < http://-/www.amnat.org/ >, the Society for the Study of Evolution < http://www.evolutionsociety.org/ >, and the Society of Systematic Biologists < https://-www.systbio.org/ >. The meeting is the premier opportunity for sharing research on evolutionary biology each year.—For 2021, our conference will be virtual with live-streamed plenaries, scheduled faux-live concurrent sessions, on-demand talks, and topical networking events. For more information: https://-www.evolutionmeetings.org/ * The conference will be held over five days, June 21 - 25. o The conference will run up to eight hours each day starting at 2:00 PM GMT (10:00 AM Eastern Daylight Time) for convenient participation of attendees from a wide range of time zones. * Registration and talk submission will open in March. * *Registration rates: Society members/ $10.00 /$50.00/ $125.00 Non-members— /$50.00 /$100.00/$175.00 *(for students [grad + undergrad]—/postdocs / professionals, respectively)*. * * Registration for society members

from countries classified as low-income, lower-middle-income or upper-middle-income economies are *free* —(send requests for the free registration to this address: TBA).

* Each day—will be highlighted by a live-streamed plenary talk. On Friday, the 25th, we will live stream award symposia and talks.

* All talk submissions—will be accepted (each attendee is limited to one presentation, but can be a coauthor on more than one). Due to scheduling limitations, only the first 1,000 submissions—will be included in the 'faux-live' (recorded talks are played in sequence at a specific time) concurrent sessions (and available on-demand after the session). The remainder of submissions will be made available on-demand (available to view anytime) throughout the conference. All contributed talks will be recorded.

* Talks scheduled in faux-live concurrent sessions will be limited to 10 minutes. On-demand talks will be offered instead of posters and will be limited to—6 minutes. Talk recordings can be made through an online app on our—web interface, or can be uploaded.

* We will have numerous opportunities for networking/discussion. o After each concurrent session the speakers and attendees will participate in discussion/networking Zoom sessions focused on the same topic. o Networking lounges will be available in the conference lobby. o An open Zoom room will be available in the lobby to mingle and meet with other attendees throughout the conference. Breakout rooms will be available for group conversations. o A dedicated Slack workspace will be available for attendees to create topical channels, find other attendees with similar interests, arrange group meetings, and advertise conference-related activities. o You will be able to sign up to participate in faculty-student networking groups for coffee, lunch, or happy hour meetings

For more information: https://www.evolutionmeetings.org/ Mitch Cruzan (He/Him) Professor of Biology Portland State University PO Box 751 Portland, OR 97207 USA Web:https://cruzanlab.weebly.com/ Evolutionary Biology - A Plant Perspective

/Mitchell B. Cruzan// Available through all good bookshops, or direct from Oxford University Press < https://global.oup.com/academic/product/evolutionary-biology-9780190882679?cc=us&lang=en&# >/

Mitchell Cruzan <cruzan@pdx.edu>

GradStudentPositions

EstonianU AdaptationFish

PhD position on multifaceted mechanisms of humic adaptation in fish. Genotype and environment interactions in Eurasian perch: analysis of morphological, physiological and behavioural traits.

We are looking for an enthusiastic PhD student for studying morphological, physiological and behavioural mechanisms of adaptation to dark and acidic environment in Eurasian perch. The successful PhD candidate will be part of an active international team working with ecology, genomics and molecular ecology of aquatic organisms at the Estonian University of Life Sciences.

Understanding the process of adaptation is one of the most active fields of research in evolutionary biology but despite enormous interest and a growing number of analysis tools, it is still a daunting task to obtain a comprehensive picture of the mechanisms of local adaptation at different levels of biological complexity. Humic lakes typically exhibit low pH (3.5-4.5), reduced oxygen (O2) concentrations, strong O2 and temperature stratification, reduced light penetration and a shift towards longer wavelengths. One of the very few fish species that is able to thrive in both dark and clear water habitats is Eurasian perch (Perca fluviatilis). It is therefore expected that perch populations inhabiting humic lakes would have evolved specific adaptations at multiple levels of biological organization that allow to succeed in poor light, low pH and oxygen saturation conditions. The proposed research represents a concerted effort to advance our knowledge about genetic and environmental components responsible for adaptation to humic environment by combining experimental crossing, common garden experiments and field studies with analysis of wide range of morphological, physiological and behavioural traits.

More specifically, the PhD project aims at: 1. Characterizing the genotype-environment interactions in morphological, physiological and behavioural traits (incl. the distribution, type and number of neuromasts, eye size, pigmentation, transcript abundances, boldness and feeding efficiency). 2. Characterizing the genotype-environment interactions of egg survival and sperm properties in relation to low pH, humic substances and ion pump blockers. 3. Characterizing the genetic architecture and functional consequences of variation in lateral line morphology.

Qualifications required: To be eligible for a PhD-student position the applicant must hold a master's degree (or equivalent) in Evolutionary Biology, Ecology, Physiology, Population Genetics, Bioinformatics or a related field. Candidates must be able to express themselves in spoken as well as written English.

Qualifications desired: We are looking for a highly motivated candidate with experience in evolutionary biology, ecology, physiology, genomics, or other closely related fields of research. It is desirable that candidates are familiar with one or more programming languages (such as Python, Perl, or R) and statistics.

Application: The preliminary application should include 1) a letter of intent describing yourself, your research interests and motivation of why you want to do a PhD, and why you are suitable for the position, 2) your complete CV, including a short description of your education, 3) a copy of your master thesis if available and your course grades, 4) the names and contact information to at least two reference persons (e-mail address and phone no.). The application should be written in English and sent to: anti.vasemagi@slu.se and riho.gross@emu.ee. Please submit your preliminary application at the latest by 18st of June 2021.

Deadline for submitting of formal application (upon approval of preliminary application by supervisors): 1st of July 2021 List of documents to be submitted: 1. Completed application form at https://estonia.dreamapply.com/en_GB/ 2. Doctoral thesis project - recognized by the supervisor at Estonian University of Life Sciences 3. Academic curriculum vitae (CV) 4. Copy of the passport page stating the applicant Âs personal particulars 5. An official copy of the diploma and diploma supplement (transcript of records/ mark sheet) of the preceding study levels* in the original language. Official documents must be provided from the institution awarding the degree or certified with an Apostille. 6. Official translation of the diplomas and diploma supplements into English 7. One of the following language certificates: - A recent TOEFL Certificate: only internet-based test scores are accepted, with the minimum score being 61. The result must be sent directly to the University by the Educational Testing Service. TOEFL designated institution code for the Estonian University of Life Sciences is 7708. - A recent IELTS Certificate: minimum score: 5.0; - A recent First Certificate in English of the University of Cambridge; - A recent PTE (academic): minimum score 51).

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Genoscope France SeascapeGenomics

Investigating the role of oceanic circulation in plankton communities structure and functioning

Director of Studies: Daniele Iudicone

Department of Integrative Marine Biology

Seat: Naples, Italy

Project Summary

An enduring challenge in ecology is to comprehend how marine phytoplankton has developed and maintains its large diversity, characterised by a complex web of interactions, while living in a largely unstructured environment. As local assemblies are controlled by ocean circulation and resource delivery, understanding the relation between the species distribution and oceanographic patterns becomes crucial. A fundamental step to understand and predict the status and functioning of pelagic ecosystems is to abandon the terrestrial concept of landscape and, instead, consider the highly dynamic seascape, i.e., to fully contemplate that the substrate is a fluid, where resources and organisms are moved around by currents. Processes in the seascape cannot be easily disentangled and many knowledge gaps still exist about the role of its key components. We are also missing an understanding of connectivity to be operationally used for sustainable ES management and policy development. Finally, climate change is impacting the seascapes in many, often subtle ways, with impacts on biodiversity and on its services. Specifically, the understanding of the oceanic biogeography remains limited; e.g., the level of endemicity of planktonic species, a key question in ecology, remains unconstrained. This has important implications for the response to changes that depends on acclimation capacities but also on the degree of isolation and evolvability of the species, in turn related to the ecosystem connectivity. Here we will thus bring together complex systems, genomics and oceanography to explore how the physical connectivity between oceanic regions determines the local community structures (i.e., the coexistence of many species), supports stable biogeographies and stretches species distributions beyond their optimal conditions, thus impacting on the ecosystem stability. The project plan will exploit the genomic revolution in ecology, due to the direct access to genomic information on real ecosystems. The planned activities will combine the analysis of the recent data on the oceanic metagenomic functional diversity with a hierarchy of conceptual models describing circulation and plankton dynamics with increased complexity. As main intellectual merit, our interdisciplinary team will promote an innovative approach to the understanding of the system via the validation of long standing hypotheses. In addition, the study of the impact of dispersal will allow to bridge terrestrial and marine ecology, with broad impact on marine ecology and, especially, on climate change ecology. Finally, the identification of the degree of locality of species and their equilibrium with oceanic dispersal will create new avenues for theoretical and applied research.

Contact : daniele.iudicone(at)szn.it

Olivier Jaillon. Tel. 01.60.87.25.30 CEA - Genoscope. 2 rue Gaston Crémieux. 91057 Evry Cedex. France

Olivier Jaillon <ojaillon@genoscope.cns.fr>

Helsinki PhylogeneticsMacroevolution

Three-year PhD position in comparative phylogenetics at the Finnish Museum of Natural History

The University of Helsinki (https://www.helsinki.fi/-en) is an international scientific community of 40,000 students and researchers. It is one of the key multi-disciplinary research universities in Europe and ranks among the top 100 international universities in the world. The Finnish Museum of Natural History (https:/-/www.luomus.fi/en), which is part of the University of Helsinki, is a leading unit of systematic and evolutionary biology in Finland and a host to a vibrant community of researchers.

Applications are invited for the three-year PhD position at the Finnish Museum of Natural History.

We are looking for a highly motivated candidate to join the research groups of Drs. Sergei Tarasov & Pedro Cardoso and a broad network of collaborators. The successful candidate will work on a project, funded through the three-year research grant program of the University of Helsinki. She/he will aim at (i) developing a new phylogenetic method for reconstructing ancestral species ranges, and (ii) assessing the range evolution in the context of ecological and multidimensional phenotypic data. The successful candidate will work in tight collaboration

with the Lab's ongoing project on evolution of Malagasy dung beetles. The appointee will be encouraged to commit short visits to our collaborators abroad and will participate in the supervision of undergraduate students. This interdisciplinary project is an exciting opportunity to conduct research on statistical modeling, evolution and biosystematics.

Requirements: Applicants should have an MSc degree (or equivalent) in biology, computer science, statistics, bioinformatics or a related field. The successful candidate should have a strong background/interest in phylogenetics, computer science or computational biology and motivation to develop and apply new phylogenetic methods. Good written and oral communication skills in English are required. The following skills are considered advantageous but are not required: - Programming in R - Good understanding of statistics and stochastic processes - Research experience and publications Applicants are expected to acquire the doctoral student status in the Doctoral Programme in Wildlife Biology at the University of Helsinki during the standard 6-month probationary period (https://www.helsinki.fi/en/research/-doctoral-education/the-application-p...).

You will work together with the project's Principal Investigator and the collaborators. You will be responsible for the theoretical and applied research, data analysis, writing research articles and participation in academic conferences.

The starting date is July-October 2021. This is a full-time position, available for 3 years. We offer a competitive salary of 2500Â/month (before taxes).

The University of Helsinki offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services office (https://www.helsinki.fi/en/-university/working-at-the-university) assists employees from abroad with their transition to work and live in Finland.

Please leave your application in our recruitment system by proceeding to the official add website: https:/-/www2.helsinki.fi/en/open-positions/three-year-phd-position-in-comparative-phylogenetics?fbclid=-IwAR0zQ_eaElBRWXRA4DR0vIzjSJxUkrCw-TOo4tNRUkjGv5PGZpcyEuj_i_w   The applications should include the following:

- Cover letter describing motivation and research interests (max. 1 page) - CV with publication list - Contact details of two potential referees

Applications will be given full consideration if submitted by May 23rd, 2021, 23:59 (EET). Applications received after this date might be considered, if the position is not filled.

For more information about the position, please contact Sergei Tarasov or Pedro Cardoso.

Email ST: sergei.tarasov@helsinki.fi Email PC: pedro.cardoso@helsinki.fi

Labs Websites: https://www.tarasovlab.com http://-biodiversityresearch.org Sergei Tarasov, Ph.D. Curator of Coleoptera (beetles) Finnish Museum of Natural History (LUOMUS) P.O. Box 17 (Pohjoinen Rautatiekatu 13) FI-00014 University of Helsinki Phone: +358 294128853 Email: sergei.tarasov@helsinki.fi Website: https://www.tarasovlab.com sergei.tarasov@helsinki.fi

IGB Berlin EvolEcolArcticDaphnia

The Leibniz Institute of Freshwater Ecology and Inland Fisheries in Berlin, Germany is inviting applications for a PhD position (f/m/d) starting in November 2021 with a duration of 36 months. We seek to recruit a highly motivated and excellent doctoral student with an interest in evolutionary physiology / transcriptomics. The PhD project centres on the adaptation of Arctic Daphnia to environmental change with a strong focus on experimental work, including physiological assays and life history experiments. Daphnia will be hatched from lake sediment of the past 200 years, a time frame during which warming and related environmental fluctuation have been particularly rapid and severe in the Arctic. Applying the powerful experimental approach of "resurrection ecology", clonal lineages hatched from eggs of several time periods will be established in the laboratory to represent historic and modern Daphnia populations. Clonal lineages of different age will be experimentally exposed to environments reflecting historic and modern conditions in a controlled reciprocal transplant design. By integrating phenotype and gene expression data, this study will test to what extent phenotypic responses are reflected in the functional genome. The successful candidate will join an interdisciplinary team to integrate the fields of paleolimnology, genomics, transcriptomics and ecophysiology, with partners in the UK and Germany. The workplace is IGB in Berlin, associated with The Berlin Center for Genomics in Biodiversity Research (BeGenDiv). At least one field expedition to collect lake sediment cores in southwest Greenland near Kangerlussuaq is planned.

Your tasks - Isolation and resurrection of Arctic Daphnia (includes 1 - 2 field expeditions to Greenland) - Set-up and maintenance of Daphnia and algal cultures - Set-up and performance of experiments - RNA isolation, and bioinformatic analysis of RNAseq data - Publication of results in scientific journals and presentation at conferences - Completion of a doctoral dissertation

Your profile Essential: - MSc or equivalent in Molecular or Evolutionary Biology, Ecology or related field - Demonstrated experience in experimental or molecular work - Ability to perform intense lab work - Computational and data analysis/statistics skills - Collaborative teamworker - Good communication skills in verbal and written English Preferred: - Bioinformatic skills are desirable but not essential

Our offer We offer an exciting position in a multidisciplinary project. We foster your career development by providing qualification and training opportunities. We actively support the reconciliation of work and family life. Applicants are treated equally regardless of gender. Qualified women are particularly encouraged to apply. Severely disabled applicants with equal qualification and aptitude will be given preferential consideration.

This is a full-time position with 3 years duration and a tentative start date of 01.11.2021 (or shortly thereafter). Salary is paid according to the German salary scheme for the public sector for doctoral research (65% TVoD). The working language at IGB is English.

Are you interested? We look forward to receiving your application (letter of motivation indicating research interests and experience, CV, Bachelor and Master certificates, publication list, and two letters of recommendation) by 15.07.2021. Please state the job reference number 18/2021 and apply exclusively via our recruitment platform at www.igb-berlin.de/en/jobs .Enquiries can be directed to Dr. Dagmar Frisch at dghfrisch@gmail.com.

"Research for the future of our freshwaters" is the mission of the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB). The IGB is Germany's largest and one of the leading international research centres for freshwaters. We seek to understand the fundamental processes governing freshwaters and their communities. Our research findings help to tackle global environmental changes and to develop measures for sustainable water management. The IGB is a diverse and inspiring place to work and conduct research. We promote individual development at every career level and stand for lively exchange and cooperation. With more than 350 employees and guests from all over the world, we conduct research at five locations in Berlin and at Lake Stechlin (Brandenburg). IGB closely collaborates with numerous national and international universities and other partners in science and society and is a member of the Leibniz Association, which connects 96 independent public research institutes in Germany. www.igb-berlin.de Dagmar Frisch <dghfrisch@gmail.com>

JagiellonianU Krakow EvolutionaryBiology

We are seeking a motivated PhD student for the project: Biological Clocks in the Wild: the effects of artificial light at night on circadian rhythms of a migratory bird at the Institute of Environmental Sciences, Jagiellonian University (Poland)

What do we study: It is well established that biological rhythms are fundamental drivers of biochemistry, cell biology, physiology and behaviour. The regularity of behaviours is governed by endogenous clocks, which are adjusted and synchronised with environmental cues, primarily light. Rapidly expanding anthropopressure largely disrupts these cues. Yet, it is surprising how little we know about the effects of disorders in the functioning of the internal time-keepers in free-ranging animals. This project will aim at understanding the effects of disturbance in environmental cues, i.e. light exposure, on circadian clock of a wild migratory bird: collared flycatcher (Ficedula albicollis). We will employ an experimental setup introducing artificial light at night in nestboxes during breeding season, at different stages of development and quantify its effects on circadian clock, physiology and behaviour. As a result we will try to build a comprehensive understanding of shifts in circadian rhythms and their consequences in a natural population.

Job description: The PhD candidate will actively participate in fieldwork, collecting phenotypic, biological and environmental data, sample preparation and lab work. S/he will be interacting with the PI and other team members, collaborators in Poland and worldwide, and attend relevant workshops and conferences. It is expected that the candidate will learn a large ecological skill set that will allow him/her to infer the evolutionary ecology of disturbed photoperiods in wild flycatchers. Specifically, the tasks will involve:

* active participation in fieldwork across three breeding seasons (ca. 2-3 months each year) on the Swedish island of Gotland, * assessing the influence of artificial light at night on immune response of birds, * planning and performing PHA immune assays in the field, * analysing

gene expression of specific immune genes, * conducting statistical analyses, * presenting the work at local and international conferences and preparing publications in close collaboration with an international team.

Salary: A National Science Centre stipend is available for 36 months (3000 PLN, a tax-free addition to a doctoral stipend provided by the Doctoral School for the period of 48 months).

Requirements: 1) Formal conditions:

* MSc degree in a relevant field of life sciences: biology, ecology, molecular biology or similar achieved by the time of enrolment;

* admission to the PhD program in Biology at the Doctoral School of Exact and Natural Sciences at Jagiellonian University, effective on 1.10.2021 (programs in English, the topic IES-6: https://-/science.phd.uj.edu.pl/en_GB/rekrutacja/rekrutacja-2021/2022/phd-programme-in-biology or programs in Polish https://wb.uj.edu.pl/ksztalcenie/szkola- doktorska/biologia/rekrutacja).

2) Specific merit requirements for the project include:

* strong English language command, communication, organizational and collaboration skills; * experience with molecular laboratory analyses and/or field work (preferably with birds); * previous experience in statistical analysis of biological data is considered advantageous; * bird ringing/handling experience and ethical permits to work with animals and driving license are a plus.

Informal enquiries: email to the principal investigator Joanna Sudyka (joanna.sudyka@uj.edu.pl) or the project manager Wioleta Ole Â¶(wioleta.oles@uj.edu.pl).

The formal application should be sent by 8.06.2021 to to Wioleta Ole Â¶(wioleta.oles@uj.edu.pl) with the term "PhD position" as email subject line (please note that this is also the deadline for application to the Doctoral School in the irk.uj.edu.pl system) and include:

1) CV (maximum 2 pages) including information on relevant academic achievements, publications, conferences, awards, relevant experience and training and contact information for two referees;

2) cover letter (maximum 1 page), explaining how the applicant's background and research interests make him/her a suitable candidate for the position;

3) copy of the MSc diploma;

4) signed copy of a formal statement concerning the processing of personal data, available here: https://-cawp.uj.edu.pl/en_GB/wynagrodzenia/stypendia (Wzor o Âo przetwarzaniu danych osobowych)

The documents must be submitted in English or Polish. Diplomas issued

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JagiellonianU Poland InsectMicrobiomes

Ph.D. Student position: The patterns of the insect community and microbiome change during the Anthropocene

Several funded positions are open across Ph.D. Programs at Jagiellonian University in Kraków, Poland, including within the English-language Ph.D. Program in Biology: https://wb.uj.edu.pl/ksztalcenie/szkola-doktorska/phd-programme-in-biology . The Symbiosis Evolution Group (https://symbio.eko.uj.edu.pl/) at JU's Institute of Environmental Sciences, a collaborative, multi-lingual group that uses high-throughput sequencing and bioinformatics to study diversity and evolution of insects and their associated microorganisms, seeks a motivated Ph.D. Candidate. Specifically, we will support a student interested in applying for admission to the Ph.D. Program in Biology and, if successful, joining our group in researching the patterns of insect diversity and symbiosis, and how they change during the ongoing climate and ecological crisis.

We know that insect communities are changing rapidly and declining in response to anthropogenic pressures. We also know that insects frequently associate with microbes, forming different types of symbiotic associations that often play critical roles in insect biology. However, our understanding of the microbiome abundance and diversity patterns across insects, factors that drive these patterns, and the role of the microbiome in insect response and adaptation to the ecological challenges of the Anthropocene remain limited. The proposed project will use high-throughput sequencing and bioinformatic approaches to address how insect diversity and their microbiomes change across space and time, especially across gradients relevant to anthropogenic change. The Student will develop their research questions using extensive collections of diverse insects from Sweden, Poland, Madagascar, or Greenland. Depending on skills and

interests, they will have an opportunity to participate in international fieldwork, work with insect collections, conduct laboratory experiments, molecular work (automated DNA extraction, next-generation sequencing library preparation), analyses of microbiome diversity data, comparative genomics, and advanced microscopy. The available samples, expertise, research funding, and collaborations offer great potential for motivated students to explore their own ideas and evolutionary questions related to insect diversity and symbiosis, as well as to acquire cutting-edge research skills.

The successful applicant will have an M.Sc. degree in a relevant field by September 2021; a demonstrated interest in Evolution, Entomology, Microbiology, and/or Genomics; experience with, or a keen interest in learning, Bioinformatics, and Computational Biology; and strong English language, communication, and organizational skills. Previous experience with insect diversity, ecology, evolution and/or symbioses, molecular biology, microbiome surveys, phylogenomics and/or comparative genomics, and willingness to travel is advantageous.

The student will be supported by a four-year tax-free stipend from the Ph.D. Program in Biology at Jagiellonian University, with opportunities for additional research grant funding. The official start date of the Ph.D. Program is on 1st October 2021.

The application deadline for the Ph.D. Program through the University system is 8th June 2021, but the applicant will need to be selected from among the interested candidates beforehand. Therefore, the interested applicants are asked to send a letter explaining their experience and interest in the project, a CV, and the details of two references to Monika Prus (monika.prus@uj.edu.pl), as soon as possible. For informal inquiries, please contact Dr. Piotr ukasik (p.lukasik@uj.edu.pl).

Make sure also to check other proposed projects within the Ph.D. Program in Biology, and contact their PIs if interested!

dr hab. Piotr ukasik Zespó$Â^3$ Ewolucji Symbioz / Symbiosis Evolution Research Group Instytut Nauk o Ârodowisku / Institute of Environmental Sciences Uniwersytet Jagielloṅski / Jagiellonian University ul. Gronostajowa 7 30-387 Kraków Poland

Phone: +48 12 664 5195, +48 798 104 743 Email: p.lukasik@uj.edu.pl www: symbio.eko.uj.edu.pl

Piotr ukasik <p.lukasik@uj.edu.pl>

Jena Germany
SexChromosomeEvolution

PhD student position on Neo-sex chromosome Evolution in Grasshoppers

The Institute of Ecology and Evolution at the Faculty of Biological Sciences, Friedrich-Schiller-University Jena, offers a PhD student position, starting 01/09/2021 (with flexibility).

Background In species with heteromorphic sex chromosomes, the sex-limited chromosome (e.g. the Y in XY systems) has undergone recombination suppression, heterochromatinization, degeneration and gene loss, which means that the expression levels of X-linked genes in males will be half that of females. The solution is that the X chromosome would be selected for dosage compensation, a process countering the decay and silencing of genes on the Y chromosomes. However, it is unclear why some sex chromosomes have undergone complete dosage compensation while other have not.

Project The project seeks to understand the evolution of dosage compensation using the grasshopper Vandiemenella viatica species complex as a model system. Multiple chromosomal fusions between the ancestral X and autosomes (neo-X) in different races/species allow independent comparisons to investigate the timing and patterns of dosage compensation. The project will utilize independent chromosomal-level assemblies, DNA- and RNA-seq data and cytogenetics to explore the mechanisms underlying the maintenance of gene dosage across X0 and neo-XY sex chromosomes. Thereby the project will explicitly test several key hypotheses for evolution of dosage compensation and shed light on temporal sequence of molecular evolution by the formation of neo-sex chromosomes.

Roesearch environment The project is conducted in collaboration with Prof. Dr. Holger Schielzeth (involved in structured doctoral programs) offering a multitude of collaborative opportunities that give a perfect setting for the project. Jena offers a lively and collaborative research environment with a large faculty of Biological Sciences and several research institutes devoted to the life sciences.

Candidate requirements and work duties We are looking for a candidate with a Master?s degree in evolutionary biology, bioinformatics, genetics, or other relevant

discipline and documented skills in computational analyses. Proficiency in written and spoken English is essential, experience with DNA and RNA extractions is beneficial and willingness to work hands-on with lab stocks of grasshoppers is required. Experience with scientific writing will be a plus. Working duties will include chromosome-level assemblies using short- and long-sequencing reads and Hi-C data, genome annotation, transcriptome assemblies and gene expression analysis. The work duties can also include teaching and other departmental duties (no more than 20%).

How to apply The position is for 36 month and payment will be based on the tariff contracts for the public service (65% up to E13). The Friedrich-Schiller University Jena is an equal opportunity employer and strives to employ both genders equally, as well as to employ more individuals with disabilities. Therefore, we encourage all applicants, independent of their nationality, gender or disability, to apply for this position. Please send your application as a single pdf in English including a letter of motivation, summarizing your experience and future vision, CV of no more than 4 pages, list of publications, relevant certificates (degree certificates, etc.) and the names of two referees by 10/06/2021 to

Dr. Octavio M. Palacios-Gimenez Friedrich Schiller University Jena Institute of Ecology and Evolution Dornburger Stra?e 159, 07743 Jena E-Mail: octavio.palacios@uni-jena.de

Octavio M. Palacios-Gimenez, Ph.D. Friedrich Schiller University Jena Institute of Ecology and Evolution Population Ecology Group Dornburger Str. 159 07743 Jena, Germany E-mail: octavio.palacios@uni-jena.de website: https://www.popecol.uni-jena.de/palacios-gimenez https://octaviopalacios.wixsite.com/mysite Octavio Manuel Palacios Gimenez <octavio.palacios@uni-jena.de>

LaTremblade France MytilusGenetics

Hello,

Here is an offer for a PhD position in the Laboratory of Genetics and Pathology of Marine Molluscs (LGPMM), in La Tremblade, France.

https://ifremer-en.jobs.net/en-GB/job/phd-genetics-of-mortality-outbreaks-in-mytilus-sp-m-f/J3S3VX6WYYDDQ6SQ454   For all re-

quests, please contact Lionel DEGREMONT: Lionel.Degremont@ifremer.fr

Thanks

– (La réception de cet e-mail en dehors des horaires de bureau ne nécessite pas de réponse immédiate)

Germain Chevignon (PhD)

Laboratoire de Genetique et Pathologie des Mollusques Marins (LGPMM)

Station de La Tremblade - Avenue de Mus de Loup Ronce les Bains - 17390 La Tremblade

Tel. : 33 5 46 76 26 46 Email : Germain.Chevignon@ifremer.fr

https://annuaire.ifremer.fr/cv/27112/   https://-/gchevignon.weebly.com/   Germain Chevignon <germain.chevignon@ifremer.fr>

LMU Munich 2 AvianBehaviourEvolution

Ecology and evolution of social impact and responsiveness in a wild sparrow population

Two PhD-positions in Behavioral Ecology at LMU Munich. Application deadline: 15.06.2021

**

Project description

Social interactions characterize all wild populations and affect evolution whenever heritable traits are plastic in response to heritable traits of conspecifics. The evolution of "social responsiveness" to and "social impact" on other's phenotypes has attracted theoretical attention, but progress requires addressing key outstanding questions: Do wild populations contain individual variation in degrees of social impact and responsiveness? Does selection act on this variation, and which processes maintain it? These key challenges will be addressed in a research programme to understand social evolution. The overarching aim is to combine the strengths of cutting-edge behavioural ecology and quantitative genetics theory to uniquely study the interplay between social interactions and social selection in the wild. We will focus on social foraging strategies in house sparrows on Norwegian islands that use either private information and actively find food ("producers") or social information to exploit food patches found by others ("scroungers"). Game theory predicts socially responsive shifts towards

scrounging when others produce, and /vice versa/. Using innovative high-throughput behavioural screening of entire populations, we aim to assay >600 birds for their producer-scrounger social impact and responsiveness in >4,000 assays and determine genomic relatedness, survival, and reproductive fitness for all individuals. We will address the following key objectives:

*PhD-project 1*will establish whether individuals are repeatable in (i) average level of producing-scrounging ("personality"), (ii) level of adjustment in producing-scrounging to phenotypes expressed by partners ("social responsiveness") and (iii) producing-scrounging elicited in partners ("social impact"). We will quantify covariances between these traits', describe (social) environmental sources of variation within and among individuals, and test for covariances with various key behavioural (aggression, exploratory tendency) and morphology traits (body size and shape) predicted by adaptive theory.

*PhD-project 2 *will quantify how natural selection acts on producing-scrounging reaction norms and study whether selection pressures covary with key socioecological conditions; and thus determine the pathways (components of fitness) by which selection acts on this variation in the social phenotype in this well-studied system. This will make it possible to start exploring the potential evolutionary consequences of selection on social impact and responsiveness in the wild, thereby providing crucial new insights into the evolution of social behaviour and the role of social interactions in ecological and evolutionary processes.

Research and Project group

The PhD-students will be embedded in the Behavioural Ecology Group of the Ludwig Maximilian's University of Munich, located in Martinsried. The group works broadly on two topics: individual behaviour and life-history (Prof. NJ Dingemanse) and pre- and post-copulatory sexual selection (Dr. C Tuni). Our group consists of five PhD-students and two postdocs, offering a dynamic social environment. The PhD-projects are part of a collaboration with the Centre for Biodiversity Dynamics at NTNU (Trondheim). International collaborators: Profs. B-E Saether, H Jensen, T-H Ringsby, J Wright (NTNU), Prof. A. Wilson (Exeter) and Prof. J. Morrand-Ferron (Ottowa). PhD-students have the opportunity to apply for admission to the International Research School for Organismal Biology of the Max Planck Institute for Ornithology, which offers high-quality teaching programs for PhD-students and ample opportunity for networking and collaboration.

*Requirements *

The two successful candidates should have background training in evolutionary biology and behavioural ecology. We are looking for candidates that have experience with fieldwork, bird handling, and are able to work independently. Coding skills are required for programming electronics equipment (sophisticated PIT-tag readers) and performing complex statistical analyses (e.g. multivariate animal models to estimate IGEs). Social skills and ability to flourish in a team are important for winter fieldwork in Norway and various collaborative aspects. Successful candidates speak fluent English. Successful candidates also speak fluent Norwegian, Swedish or Danish to enable effective communication with farmers and landowners onsite.

Project duration and starting date

Successful candidates will be offered a three-year PhD-position funded by a grant of the German Science Foundation to Prof. NJ Dingemanse. Starting date is 01.09.2021.

Application package

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Lyon PopGenPhyl

We are advertising a PhD position at the interface of phylogenetics and population genetics, under the supervision of Laurent Guéguen, University of Lyon 1, France, and Carina F. Mugal, Uppsala University, Sweden. The PhD position is funded by a three-year grant from the BATantiVIr project, French Research Agency (ANR).

The selected candidate will work at the Laboratory of Biometry and Evolutionary Biology (LBBE), located in Lyon, France. The candidate will also visit the Department of Ecology and Genetics (IEG), located in Uppsala, Sweden, as part of the PhD project. Both institutions offer highly stimulating and international scientific environments. At the LBBE, the PhD student will interact with the molecular evolution team, and be part of the BATantiVIr project, involving also the "Centre International de Recherche en Infectiologie", ENS Lyon. At the EBC, the PhD student will interact with the evolutionary biology program, part of the "Department of Ecology and Genetics (IEG)", Uppsala University.

Interested students are encouraged to get in touch by email to Laurent Guéguen, Laurent.Gueguen@univ-lyon1.fr, and/or Carina F. Mugal, carina.mugal@ebc.uu.se.

Context:

The BATantiVIr project aims at studying the evolutionary history of adaptation of immune genes in bats (Chiroptera).

Bats are one of the most diverse and widespread mammalian order. They host many viruses, including high-profile zoonoses (rabies, Nipah, Ebola & Marburg filoviruses, SARS coronavirus) and viruses close to primate pathogens (poxvirus, Hepatitis B Virus). During bat evolution, lineage-specific adaptation may have occurred as a response to pathogen selective pressure, differentially shaping the innate immune repertoire in bat species. However, most of the evolutionary history and mechanism of bat antiviral immunity is still unknown.

The estimation of selection on genes frequently relies on phylogenetic methods. However, since immune genes in bats are highly polymorphic, it is crucial to incorporate polymorphism in those phylogenetic analyses.

The study of polymorphism lies at the core of population genetics theory, which focuses at the time-scale of a single species and does not explicitly extend to the inter-species scale. On the other hand, in classical phylogenetic analysis, the presence of polymorphism is ignored, and substitutions are assumed to occur instantaneously. The latter assumption biases the inference of natural selection. Typically, polymorphic sites are considered as substitutions, which results in an overestimation of the presence of positive selection.

Project:

The aim of the PhD project is to fill the gap between classical phylogenetics and population genetics, and provide a multi-scale approach for the estimation of natural selection that incorporates intra- and inter-specific data.

This work will be based on the theoretical work of Carina F. Mugal, which provides analytical solutions for the influence of polymorphism dynamics on the estimation of selection in classical phylogenetic approaches. The novel approach will implement the theory in order to compute the transition probabilities between polymorphic states and substitutions among species. For this purpose, the work also relies on models of speciation dynamics (starting with the simplest models of speciation, so-called isolation-without-migration models).

The novel approach will be implemented in Bio++ libraries, which are a set of C++ libraries dedicated to bioinformatics, phylogenetics, and molecular evolution.

Finally, building on these developments, the student will investigate the evolutionary dynamics of bat genes that lie at the core of the BATantiVIr project.

Requirements:

The ideal candidate has a good knowledge of molecular evolution, and a solid bases in mathematical modelling. She/he is familiar with bioinformatics, population genetics and phylogenetic concepts. Last, she/he is autonomous in C++ programming.

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

http://katalog.uu.se/profile/?id=N8-1504 När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy Carina Farah Mugal <carina.mugal@ebc.uu.se>

Lyon WaterStriderEvoDevo

Three-year PhD fellowship

Developmental phenotypic plasticity in water striders

Where: The Khila lab at the Institute of Functional Genomics, ÃÂcole Normale Supérieure de Lyon, UMR CNRS 5242, Lyon, France http://igfl.ens-lyon.fr/ http://igfl.ens-lyon.fr/equipes/a.-khila-developmental-genomics-and-evolution Starting date: October 1st, 2021 or slightly after Deadline for applications: June 30th, 2021 (Only short-listed candidates will be notified). Project title: Molecular origin of extreme growth variation with focus on DNA methylation

Background: Growth variation under environmental influence is widespread in nature, yet our understanding of the underlying molecular mechanisms remains limited. This process, known as developmental phenotypic plasticity, provides an invaluable opportunity to understand the genotype-phenotype relationship and the impact of the environment on this relationship.

Hypothesis: Variation in nutritional input causes extreme growth variation through changes in DNA methylation states and transcriptional regulation. This hy-

pothesis is supported by preliminary data.

Model system: We test this hypothesis in the water strider Microvelia longipes (Image). The males have longer legs than females, but also extreme variation in hind-leg length between males (Image). Our recent work showed that males use their hind legs as weapons during contests, and that long-legged males have significantly higher chance to dominate egg-laying sites and access females (Toubiana and Khila, Proc B. 2019). We recently identified the gene BMP11 as a primary regulator of scaling relationships between the body and the hind-legs in a male-specific manner (Toubiana et al. PLoS Biology, 2021). We also built the resources required for this project, including a high-quality genome and transcriptomes (Toubiana, Armisen et al. BMC Biology 2021), isogenic lines and lab populations (easy to keep), DNA methylation datasets, as well as various developmental genetics tools (Toubiana et al. PLoS Biology, 2021).

Project: The successful PhD candidate will collaborate with a team of postdocs and lab technicians studying how variation in nutritional input causes extreme growth variation through changes in epigenetic states and transcriptional regulation. The objectives are: - Build the genome-wide methylome of this species (using Bisulfite sequencing and isogenic lines) - Determine the fraction of DNA methylation sites that responds to nutritional treatment - Determine the genes whose expression profiles correlate with changes in nutritional treatment and changes in DNA methylation states. - Functionally test (by RNAi or Crispr-Cas) a small selection of the loci identified above.

Mandatory requirement: Master's degree (or equivalent). - Concepts: Epigenetics, genetic variation, nutritional manipulation, developmental genetics

Expertise we seek: - DNA methylation analyses, Bioinformatics, Statistics, Programming in R Skills: - Good English (written and spoken), motivation, creativity, curiosity, good work ethics, team-work, and good interpersonal relationship with colleagues. - Knowledge in evolutionary biology, epigenetics or development is a plus.

How to apply: By email to abderrahman.khila@ens-lyon.fr with a motivation letter explaining why you are interested by this position and how you think you are qualified, your CV and names and e-mail addresses of two or three referees who can write letters of reference on your behalf.

Institute of Functional Genomics Ecole Normale Supérieure de Lyon Université Claude Bernard, Lyon 46 Allée d'Italie 69007 Lyon, France office: +33 (0)4 26 73 13 36 Cell: +33 (0)6 25 67 15 44

http://igfl.ens-lyon.fr/   Abderrahman   Khila <abderrahman.khila@ens-lyon.fr>

MfN Berlin EvolutionaryGenomics

The Museum fuer Naturkunde Berlin is looking for a

RESEARCH ASSISTANT (PhD student) (f/m/d) in the field of EVOLUTIONARY GENOMICS

The position is externally funded for 36 months at the salary level E13 TV-L for 70% of the weekly working time

Application deadline: May 30th, 2021

The MUSEUM FUER NATURKUNDE BERLIN (MfN) is an excellent and integrated research museum of the Leibniz Association with an international reputation and globally connected research infrastructure. MfN is active in three closely interlinked fields: collection-based research, collection development, and research-based public and educational outreach. Over the next ten years, the Museum für Naturkunde Berlin will build up a science campus for nature and society in the centre of Berlin as science hub, together with the Humboldt Universität zu Berlin. New laboratories and workplaces for cutting-edge research will be established. One of the world's most comprehensive natural history collections with over 30 million objects will be housed in state of the art buildings as well as fully digitized. The implementation of the so-called Zukunftsplan (future plan), funded with a total of 660 million euros from the Federal Government and the State of Berlin, strongly relies on interdisciplinary national and international partners. Become part of our team.

PROJECT DESCRIPTION: The project 'Beyond Species' - newly funded within the Leibniz Collaborative Excellence - predicts biodiversity change by integrating genetic diversity into ecological niche models. Important generic variation might be hidden, and potentially lost, when focusing on the species level only. We will go beyond the species level by surveying intraspecific genetic diversity for the community of insect-predatory bats in Western and Central Asia in order to identify genetically distinct populations. The research focus of this position will be on the identification of evolutionary significant units (ESUs) and on the reconstruction of their evolutionary histories with genome-wide data sets. This will allow to evaluate the impact of geographic separa-

tion and genetic introgression after secondary contact of populations on the genetic diversity and local adaption.

RESPONSIBILITIES - High-throughput DNA-sequencing - Phylogenomic and population genomic analysis of genome-wide data sets - Participation in field work in the Caucasus and Central Asia - Publication of scientific results in peer-reviewed journals - Presentation of research results at international conferences

The project associated with this position will fulfill the requirements of accomplishing a doctoral degree.

REQUIREMENTS - Master's (or comparable) degree in Biology, Geography or Bioinformatics - Scientific background in evolutionary biology and genetics - Basic bioinformatic skills in handling genomic data sets are desirable - Very good English language skills (written and spoken) - Ability to work in a team, reliability and self-sufficiency

SPECIAL NOTES In support of equal rights applications from qualified women are particularly welcome. Handicapped individuals will be given preference in cases of identical qualifications.

We look forward to receiving your application with the usual documents (cover letter, curriculum vitae, certificates) by 30.5.2021, preferably via our online application portal.

For information on the research project, please contact frieder.mayer@mfn.berlin, for the application procedure recruting@mfn.berlin.

Link job advertisement: https://-jobs.museumfuernaturkunde.berlin/jobposting/-ced98695d3f0ddbaa858d4b590bae4cb8f58f99b "Mayer, Frieder" <Frieder.Mayer@mfn.berlin>

Naturalis Leiden IslandEvolution

2 PhD positions on trait evolution on islands

We are glad to announce two complementary PhD positions in The Netherlands. Project led by Frederic Lens (Naturalis Biodiversity Center) and Rampal Etienne (University of Groningen). With PhD co-supervisor Luis Valente (Naturalis Biodiversity Center).

The two PhD projects will focus on identifying traits that may have promoted diversification on islands. One PhD candidate will be based in Groningen and will develop a new, trait-dependent diversification model that will be specifically tailored for island lineages (PhD1).

The other PhD candidate (PhD2) will be based at Naturalis (Leiden) and will produce new empirical data from island plants (building molecular phylogenies using hybridisation sequencing as well as plant trait datasets) that will be used to test the new model. Both candidates are expected to closely collaborate with each other and with the local partners in the project. Excursions to the Canary Islands are foreseen to collect plant specimens.

PhD project 1: https://www.rug.nl/about-ug/-work-with-us/job-opportunities/?details=00347-02S0008B5P PhD project 2: https://www.naturalis.nl/-en/over-ons/phd-island-diversification-enw-klein Deadline of applications: May 26th Expected PhD interviews: May 31st Expected start date: October 1st

luislvalente@gmail.com

NordU Norway BrownAlgaeGenomics

A three-year PhD fellowship is available at the Faculty of Biosciences and Aquaculture (FBA), Nord University (Bodø, Norway), connected to the new research division 'Algal and microbial biotechnology'. The project will be lead by Dr. Alexander Jueterbock, in collaboration with Dr. Mark Cock from the Station Biologique de Roscoff in France, and with FBA genomics and ecology researchers Dr. Chris Hulatt, Professor Galice Hoarau, and Dr. Lars Martin Jakt.

For details see this link: https://www=2Ejobbnorge=-2Eno//en/available-jobs/job/206001/phd-fellowship-3-years-in-computational-exploitation-of-brown-algal-genomes Macroalgae are the foundation of diverse coastal ecosystems and are considered a promising target for a new sustainable aquaculture industry. While scientific advances in synthetic biology have a wide application potential to aid macroalgae restoration and farming, the necessary molecular knowledge is yet missing for this group of non-model organisms. This PhD project will apply bioinformatics analyses to exploit a novel resource of >70 brown algal genomes/transcriptomes in order to characterize the presence, variation, uniqueness, and evolution of genomic elements that are relevant to bio-engineering applications in brown macroalgae, including epigenetic factors, and transposable elements.

Aims:

1) Identify regulatory regions (e.g. CpG islands), and

enzymes (e.g. methyl- transferases) involved in DNA methylation and histone modifications, as well as potential miRNA target sites, characterize their specificities, and draw their evolutionary path in the brown macroalgae.

2) Characterize transposable elements and reconstruct their evolutionary activity in the sequenced brown algal genomes. This will facilitate the understanding of genome evolution in brown algae and provide information on how these can be harnessed to engineer gene expression (e.g. via relaxing silencing mechanisms), or gene function (e.g. via targeted mutational insertion).

3) Bio-engineering trials using a reverse-genetics approach with CRISPR- Cas9 in Ectocarpus.

The position will be available from 1st of January 2022.

Qualification requirements Essential:

MSc degree (to be completed before the start of the position) or equivalent in a relevant discipline such as genetics, epigenetics, computational biology, genome biology/evolution, molecular biology, or bioinformatics Grade average of B or better both for the programme in total and the master's thesis Fluency in written and spoken English Drylab skills in molecular biology (e.g. DNA extraction, PCR) Strong computational skills (using R or Python, Linux bash, bioinformatics analyses at the genome/transcriptome level) Demonstration of strong interest in and drive to work on the topic Ability to work independently and in teams High motivation and adherence to time lines Desirable:

Background in Phycology Experience in Machine Learning Experience in Genome annotation and data mining Papers published in peer-reviewed journals or presented at international conferences Knowledge of a Scandinavian language is beneficial for the position

Eligibility:

People of all nationalities, ethnicities and gender are eligible to apply. The faculty is international with English as a common working language. Applicants who already have a PhD in life sciences are not eligible.

The successful candidate will join the PhD program at Nord University and is expected to complete the study within the period.

Further information about the position can be obtained by contacting :

Dr. Alexander Jueterbock, email: alexander.juterbock@nord.no www.marinetics.org "Alexander-Jueterbock@web.de" <Alexander-Jueterbock@web.de>

Princeton EvolutionaryBiology

The Department of Ecology and Evolutionary Biology at Princeton Universityâ€is offering a special virtual preview weekend - the EEB Scholars Program - thisâ€upcomingâ€October 8th-15th â€for students considering graduate school. The goalâ€of this weekend is to invite competitive prospective graduate applicants toâ€campus in order to showcase the department, demystify the graduateâ€application process, and highlight participants' research experience.

Weâ€especially encourage students from underrepresented minority groups andâ€those inhabiting other axes of underrepresentation in STEM to apply.

To learn more about the program and the application process, please consider attending one of the two informational webinars we will be holding on June 1st and 15th. These will be 30-minutes each with a 15-minute presentation followed by a Q&A opportunity.

June 1st @ 11 AM, EST. To attend, register here < https://forms.office.com/Pages/ResponsePage.aspx?id=-FgH2LzF0XUK1rwd9d5G9pJZG14jvNndEtdb6ac1DMTBUN0dBMlNH >, or June 15th @ 3 PM, EST. To attend, register here < https://forms.office.com/r/CY4uk3zdkr >.

Please see https://eeb.princeton.edu/graduate/eeb-scholars-program forâ€more information and to apply. The application deadline isâ€July 1, 2021 at midnight, EST. The EEBâ€Scholars Program is open to all prospective graduate students, includingâ€rising juniors and seniors, as well as international applicants. Weâ€particularly encourage students from developing nations to apply. Please direct any questions toâ€EEB.Scholars@princeton.edu.â€

Yours kindly,

Beth Leman Program Administrator Department of Ecology and Evolutionary Biology (EEB) Bl5@princeton.edu 609-258-2798 (o) 973-610-1428 (m)

bl5@princeton.edu

SoutheasternLouisianaU FishEvolution

Southeastern Louisiana University, Hammond, Louisiana

MS position focusing on transcriptomics of cyprinodontiform fishes

The Piller lab at Southeastern Louisiana University is seeking a student interested in pursuing a MS degree in Biological Sciences. The focal project will examine transcriptomic variation and differential gene expression across a group of cyprinodontiform fishes with different life-histories. Prospective applicants should have research interests in evolutionary biology, genetics, and fish biology. In addition, applicants with previous experience with molecular techniques (i.e. PCR, RNA-Seq, qPCR, etc) and bioinformatics are preferred, but not required.

Financial support (tuition and stipend) will be provided through a recently funded project. A Research Assistantship will be available, starting Fall 2021, with up to three years of funding. Research in the Piller lab focuses on fish diversity using both molecular and morphological approaches. More information about the lab can be obtained at www.kylepiller.com. Information about Southeastern Louisiana's Biology graduate program is provided here: http://www.southeastern.edu/-acad_research/depts/biol/grad_degree/index.html Interested applicants should contact Dr. Kyle Piller (kyle.piller@selu.edu) for more information. Please include the subject line "MS Application" in your email.

Kyle R. Piller, PhD Edward G. Schlieder Foundation Professor of Environmental Studies and Sustainability, Curator of Vertebrates, and Graduate Coordinator Southeastern Louisiana University, Dept. of Biological Sciences Hammond, LA 70402 Kyle.Piller@selu.edu 985-549-2191 www.kylepiller.com Kyle Piller <kyle.piller@selu.edu>

TrentU EcolGenomics

MSc and PhD in Ecological Genomics, Trent University

The team: Aaron Shafer (Trent University) and Joe Northrup (OMNRF) based out of Peterborough, Ontario are seeking graduate students (PhD and MSc) for a management focused methylation study on large mammals.

Successful applicants will leverage a newly developed methylation array to build species-specific clocks and develop bio-markers linked to age and disease status. Field work is a possibility. Applicants must meet the requirements of the Environmental and Life Sciences Graduate Program at TrentU and international students are welcomed to apply. Please see: https://www.trentu.ca/els/ How to apply: Send cover letter (in email), CV, and contacts for two references to aaronshafer@trentu.ca.

Anticipated start date is flexible (Sept 2021, Jan 2022, May 2022).

shaferab@gmail.com

UCopenhagen WeedEvolEcol

PhDstudentship in weed evolutionary ecology

Department of Plant and Environmental Sciences,Faculty of Science, University of Copenhagen, Denmark.

Description of the scientific environment

The Department of Plant and Environmental Sciences conducts fundamental research and has a strong focus on applying basic science to solve real world challenges, primarily within the plant, soil and environmental sciences. Research and teaching cover natural resources, agriculture, biotechnology and synthetic biology from the molecular to landscape scales.

The weed ecology and evolution group investigates the eco-evolutionary processes that dictate the adaptation and persistence of weedy and invasive plants in agroecosystems. We have a gene to landscape focus using approaches from population and evolutionary genetics, evolutionary biology, plant ecology, modelling and epidemiology and crop science. Our basic research recognises that weedy plants are excellent models for studying rapid plant adaptation. We apply these insights to develop sustainable weed management strategies using eco-evolutionary principles.

Project description

Weedy plants can cause more crop yield loss than insect

pests and pathogens combined. We still do not fully understand why some plants evolve tobecome successful weeds, but the ability to rapidly adapt in managed agricultural habitats is clearly important.Alopecurus myosuroides(blackgrass) is one of Europe's most troublesome weeds, including in Denmark. This PhD addresses two important questions; (i) why has blackgrass become a major weed problem in the last 30-40 years in Europe and (ii) why is the species present as a non-weedy bystander in other global agroecosystems?

To address these questions, you will have access to a global collection of weedy and non-weedy blackgrass populations and to a recently completed reference genome. You will conduct classical plant evolutionaryecological (common garden and reciprocal transplant) field experiments to measure phenotypic variation in traits that determine competitiveness and weediness in blackgrass, comparing these traits in global weedy and non-weedy populations. You will sample plant tissue, extract high-quality DNA, and outsource genome sequencing services that enable plant genotyping-by-sequencing (GBS). These sequencing data will be analysed using open-source population genetics software to explore patterns of genetic differentiation within and amongst global blackgrass populations and to infer patterns of relatedness, evolution, and dispersal.

As a PhD student in the weed ecology and evolution group, you will carry out exciting research to answer questions about the evolution of one of the world's most economically damaging plants.You will receive training in plant ecology and evolution, plant molecular biology, and statistical population genetics. You will work closely with postdoctoral scientists in the group (weed ecology, evolution, and genetics) and collaborate with the International Weed Genomics Consortium (https://www.weedgenomics.org) of which University of Copenhagen is a research partner.

Principal supervisoris Professor Paul Neve, Department of Plant and Environmental Sciences,pbneve@plen.du.dk, Phone: +45 29611199.

Further details of the application and selection procedurecan be found athttps://jobportal.ku.dk/phd/?show=154036 PhD fellow in Weed Evolutionary Ecology

jobportal.ku.dk

Paul Neve <pbneve@plen.ku.dk>

UGhent EvolutionBehaviour

Dear All,

Please find the link for an advertisement for a PhD position at the University of Ghent, starting September or October 2021 (https://www.ugent.be/en/work/scientific/phd-student-55for more information). Application deadline is June 4, 2021.

A PhD position in animal experimental psychology is available for 2+2 years, co-funded by an ERC (European Research Council) consolidator grant and a Methusalem grant (Flemish government). The research will be led by Prof. Frederick Verbruggen (Department of Experimental Psychology) at Ghent University, in close collaboration with Prof. Luc Lens (Department of Biology) and Prof. An Martel (Department of Pathology, Bacteriology and Poultry Diseases at the Faculty of Veterinary Medicine).

The successful applicant will join the 'Cognition, Behavior and Ecology' lab (CoBE@UGent) to work on a project that focuses on response inhibition, and more specifically, the learning and development of inhibitory control in different environments ('Âeco-devo'Â), using Japanese quails as a model species.

Response inhibition refers to the ability to suppress or cancel actions that are premature, unduly risky, inappropriate, or no longer required. Response inhibition is a key component of 'executive functioning', and is essential for navigating everyday life. In humans, its derailment is also considered integral to numerous neurological and psychiatric disorders, and more generally, to a wide range of behavioral and health problems.

We are looking for a highly-motivated candidate with:

- An appropriate degree (preferably a research master) in psychology, biology, or a related discipline. The degree requirements must be fulfilled at the start of the job appointment

- Evidence of excellent research, communication, and cooperative skills

- Good English writing and communication skills are mandatory. Knowledge of Dutch is not required.

- Prior research experience (e.g., involvement in data collection)

- Good data analysis skills; knowledge of R is desired.

- A (FELASA) certificate for animal work or prior experience with working with animals is a plus.

To apply, please send a motivation letter, CV, transcripts of BSc and MSc courses and grades, copies of educational certificates (if applicable), and letters or contact information of two referees as a single pdf to Frederick Verbruggen (frederick.verbruggen@ugent.be).

For further information on the project or details about the position, please also contact Frederick Verbruggen (frederick.verbruggen@ugent.be). You can also find extra information about the lab by visiting our website-cobe.ugent.be

Closing date: June 4 2021. Interviews are expected to take place in the fourth week of June 2021.

Dr. Alizée Vernouillet Postdoctoral Researcher COBE Lab Universiteit Gent https://alizeevernouillet.com Alizée Vernouillet <alizee.vernouillet@gmail.com>

UGothenburg HostPathogenEvol

Fully Funded PhD Position in Host Pathogen Evolution and Sustainable Pest Control

Webpage for advertisement, including link for applying, is here: https://web103.reachmee.com/-ext/I005/1035/job?site=7&lang=UK&validator=-9b89bead79bb7258ad55c8d75228e5b7&job_id=-20544 Advertisement in Swedish is here: https://web103.reachmee.com/ext/I005/-1035/main?site=6&lang=SE&validator=-3038fcf1516ea1184a6da70a891f87da&rmpage=-job&rmjob=20406 *** PhD Student in Natural Science, specialising in Biology Ref PAR 2021/661 The University of Gothenburg tackles society's challenges with diverse knowledge. 53 500 students and 6 500 employees make the university a large and inspiring place to work and study. Strong research and attractive study programmes attract scientists and students from around the world. With new knowledge and new perspectives, the University contributes to a better future.

At the Department of Biological and Environmental Sciences (BioEnv) we have teaching and research activities that stretch from the alpine ecosystem, through forests, cultivated land and streams, all the way into the marine environment. In these environments we study different levels of biological organisation from genes, individuals and populations to communities and ecosystems. We

work within ecology, evolution, physiology, systematics, and combinations of these fields to understand the impact of natural and anthropogenic changes of the environment.

The department is placed at three different localities: in Gothenburg Botanical garden, at Medicinarberget in Gothenburg and Kristineberg Marine Research Station. The current position is placed at Medicinarberget.

*** Project description - Can biopesticides provide evolutionarily sustainable pest control?

Pathogens provide some of the strongest selection pressures in nature, driving continual dynamic coevolutionary interactions with hosts. Because pathogens tend to show specificity in their ability to infect hosts, genetic variation for resistance to pathogens is typically high: any one host is unlikely to be able to resist all extant genotypes of pathogen circulating in a population. Host-pathogen coevolution is therefore key to fundamental questions about how selection shapes diversity, but it may also provide a tantalising solution to the long-standing problem of pesticide resistance evolution.

Insect pests consume 10-20% of globally produced food during growth or in storage, and therefore represent a substantial threat to global food security. Conventional pest control using synthetic pesticides can be problematic because it often conflicts with other sustainable development goals by damaging nontarget organisms and disrupting natural food webs. Moreover, in spite of intensive research and development, insects continue to evolve resistance to synthetic pesticides with predictable regularity, eluding even the most ingenious attempts to circumvent evolution. Populations of some pests, such as the cotton boll moth (Helicoverpa armigera), have evolved resistance to nearly all synthetic pesticides, and can quickly cause significant economic losses, while simultaneously prompting the overuse of ineffective chemicals by farmers who are desperate to control the damage.

Recently, we have proposed an innovative and evolutionarily sustainable approach to pest control that harnesses rather than resists the enormous evolutionary potential of pest populations. It relies on the observation that the performance of pest genotypes towards genetically complex challenges (e.g., the infective ability of pathogens and the similarly complex defences of host plants) depends strongly on environmental context. This suggests that we can preserve genetic diversity for susceptibility to biological agents by ensuring that pests experience different challenges (both in terms of fungal pathogens and host plants) at a landscape scale. However, while we have demonstrated this proof of concept, the long-term response of pest genetic architecture to constant

or variable biopesticides remains unclear.

This PhD project can play a tremendous role in addressing one of the most wicked problems confronting sustainable development: the trade-off between abolishing hunger and preserving healthy environments. It will help clarify pressing but as yet unanswered questions about the long-term sustainability of evolutionarily sustainable pest control, while simultaneously shedding light on fundamental questions concerning host-pathogen evolution. The successful candidate will use a combination of quantitative genetic and laboratory evolution experiments to explore

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UGothenburg Tjarno EvolGenomicsRegulation

PhD student position in Marine Sciences specializing in Evolutionary Genomics Application deadline: May 28th, 2021

Type of employment: Fixed-term employment, 4 years Extent: 100 % Location: Tjärnö Marine Laboratory, Department of Marine Sciences, University of Gothenburg First day of employment: as soon as possible Reference number: PAR 2021/626

The Department of Marine Sciences, the Faculty of Science, University of Gothenburg, was recently launched (July 1, 2015) with the purpose to achieve the vision of "A University with marine research, teaching and cooperation of the highest international class". The department has about 110 employees - researchers, teachers, PhD students, technicians and administrators. The department carries out teaching and research in the various marine specializations, biology, oceanography, chemistry, marine geology, conservation of underwater cultural heritage, and environmental science. Research is conducted both within specialized individual projects as well as within larger interdisciplinary programs. The Department is situated in Gothenburg and at the University's research stations at Tjärnö and Kristineberg. This position will be based at the Tjärnö Marine Laboratory, 170 km from Gothenburg (https://www.gu.se/en/tjarno). More information on the Department can

be found at www.marine.gu.se . Project description The marine snail, Littorina saxatilis, has ecotypes that have evolved repeatedly in Sweden, United Kingdom and Spain, where a high-predation environment leads to a thick-shelled form and a high wave-action environment leads to a thin-shelled form. This PhD will be part of the Swedish Research Council Project: Ecological systems biology: disentangling the molecular mechanisms of ecological speciation. The goal of this project is to identify the genetic mechanisms responsible for these parallel phenotypes, specifically the shell phenotypes. We will examine the genetics of shell formation between ecotypes and assess the relative contribution of genetic vs plastic effects on gene expression in the mantle tissue. We will examine the regulatory architecture using gene expression, eQTLs, and open chromatin sequencing (ATACseq). We will synthesize these results along with other data available from members of the Littorina Research Group https://littorina.group.shef.ac.uk, including large-scale phenotyping, examination of hybrids, and whole-genome re-sequencing of L. saxatilis and related species.

Job assignments The main task is to conduct a PhD thesis, under supervision, following the basic project plan described above. This includes development of the PhD student's practical experience, analytical skills, and theoretical knowledge, particularly in molecular techniques and bioinformatics. As member of the project team, it is expected that the PhD student communicates and actively collaborates within the group. The PhD student will present results at conferences, seminars and project meetings. The PhD student is expected to publish their results in international peer-reviewed journals and write a final summarizing thesis in English, which is defended during a public dissertation. A Swedish Ph.D. thesis should be completed within 4 years full-time work including course work (60 ECTS), e.g. pedagogic and other soft-skill courses as well as courses to develop technical skills and knowledge related to the PhD topic (please see below).

Qualification/merits We seek a motivated person for PhD studies in marine biology with a deep interest in evolutionary genomics.

The applicant must hold a Master's degree or equivalent in evolutionary biology, genetics, molecular biology, cell biology or related field. The candidate should have good knowledge and practical experience of molecular laboratory work (i.e. DNA and RNA extraction and sequencing library preparation), and bioinformatic/computational skills for the analysis of RNA and DNA (familiar with R and unix command line software). Previous research experience is an added merit, including, conference attendance, grant funding and scientific

publications. These should be documented in the CV with a brief description of the applicant's role in the work.

The applicant should possess the ability to work independently and take responsibility for his/her own learning and research, as well as to collaborate as part of the research team. Excellent oral and written communication skills in English are necessary as communication within the group will be in English and the overall working environment is international.

In addition to the formal qualification requirements, great emphasis will be placed on personal qualities and suitability for the position.

Please apply online:

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UGroningen TheoIslandBiogeography

At the University of Groningen, The Netherlands, there is a PhD position available in Theoretical Island Biogeography in the group of Prof. Rampal Etienne. The position aims at incorporating trait evolution in island biogeography models. More information can be found here: https://www.rug.nl/about-ug/work-with-us/job-opportunities/?details=00347-02S0008B5P . "Rampal S. Etienne" <r.s.etienne@rug.nl>

UGuelph SoilBiodiversity

Ph.D. student sought to study soil biodiversity using bioinformatics tools & state-of-the-art environmental DNA technology

POSITION DESCRIPTION: We are seeking a strong and independent graduate student to study soil biodiversity and its response to varied restoration practices using state-of-the-art environmental DNA technology

and bioinformatic tools for data analyses. The candidate will be involved in developing novel molecular approaches to study soil biodiversity across multiple taxonomic levels including both prokaryotes and eukaryotes. The research will include opportunities to study species interactions (e.g. plant root microbiome) and the efficacy of varied soil amendments that could help accelerate ecological succession across soil disturbance gradients. The research will take place in the boreal forest of Northern Ontario and relates to mining operations taking place there. The selected candidate will gain experience in bioinformatics, molecular biology, spatial ecology, environmental chemistry, and environmental restoration. The candidate will be part of a collaborative research team that seeks to study biodiversity moderation at the landscape scale. The applicants should hold a M.Sc. degree in one of the following fields: Bioinformatics, Biology, Biotechnology, Molecular Biology, Soil Science, or in any other program that is relevant to the proposed research activities. The principal laboratory is located at the University of Guelph's Biodiversity Institute in Guelph (ON, Canada). The candidate will also interact with colleagues from Kirkland Lake Gold Corp, the University of Saskatchewan, and multiple faculty members from Guelph. The project will begin in September 2021.

PROGRAM CHOICE: This project includes both analytical and biological research components. Depending upon the applicants' background and primary research interests, the selected student could enroll through either the PhD program in Integrative Biology or the PhD program in Bioinformatics, University of Guelph.

HOW TO APPLY: All interested candidates need to send a letter of interest, a CV, a copy of University transcripts, a writing example (such as a publication, MSc thesis chapter, or other project), and the names and email addresses of three referees to: rhanner@uoguelph.ca & sadamowi@uoguelph.ca. If available, and particularly for applicants interested in the PhD in Bioinformatics program, we also encourage applicants to send a code example from your work or your GitHub link. Preference will be given to citizens and permanent residents of Canada. Review of applications will commence on May 10, 2021, and selected applicants will be invited for an interview via videoconferencing. After a discussion and mutual agreement about moving forward, the applicant will also need to apply formally to the appropriate PhD graduate program at the University of Guelph.

The University of Guelph is committed to equity in its policies, practices, and programs, supports diversity in its teaching, learning and work environments, and ensures that applications from members of under-

represented groups are seriously considered under its employment equity policy. All qualified individuals who would contribute to the further diversification of our University community are encouraged to apply.

FOR FURTHER INFORMATION: Please see the following links for further information about the University of Guelph, the relevant PhD programs, and stipend information.

https://www.uoguelph.ca/ https://www.uoguelph.ca/-ib/graduate_home https://www.uoguelph.ca/-bioinformatics/programs https://www.uoguelph.ca/-cbs/cbs-research/student-stipend-information Sarah Adamowicz <sadamowi@uoguelph.ca>

ULethbridge Canada AvianEvolution

Our lab is currently seeking applications for a funded MSc or PhD position focused on the evolution of brain and behaviour in birds (http://scholar.ulethbridge.ca/-iwaniuk) beginning in January 2022.

A range of student projects are available focused on sensory systems (vision, hearing, and/or somatosensation) and students are welcome to develop their own thesis projects focused on avian anatomy and evolution. All students in our lab gain valuable skills in dissections, histology, microscopy, and statistical analyses. Depending on the specific project, students can also gain experience in bioacoustics, micro-CT scanning, morphometrics, field techniques, and behavioural analysis. Opportunities for national and/or international travel to museums and collaborators may also apply.

Our lab houses one of the largest comparative brain collections in the world with over 190 species represented. Dedicated lab facilities include: microtomes, dissection microscopes, fluorescent microscope, high-resolution digital slide scanner, and state-of-the-art software for image analysis. As part of the Department of Neuroscience, we also have ample wet lab space, access to additional imaging techniques, and animal housing. Field research is supported by an array of field equipment, dedicated 4x4 field vehicle, and a lab trailer for preparing samples.

The position is fully funded and the University of Lethbridge offers scholarships that cover tuition based on grades and research experience. Additional information on scholarships and deadlines can be found at: https://-www.uleth.ca/graduate-studies/ . Applicants must have a background in biology or neuroscience, some hands-on research experience (of any kind) and a valid driver's license. Fieldwork experience is not necessary. International applicants are encouraged, but please note that due to the pandemic, all applicants residing outside of Canada will be subject to federal and provincial regulations regarding COVID19 testing and quarantine requirement.

To apply, send the following to andrew.iwaniuk@uleth.ca:

1) a cover letter outlining your interest in the lab

2) your c.v.

3) unofficial copies of academic transcripts

4) names and contact details of at least 2 references

Andrew N. Iwaniuk Associate Professor Canada Research Chair in Comparative Neuroanatomy Canadian Centre for Behavioural Neuroscience University of Lethbridge Lethbridge AB T1K 3M4 Canada office: +1 403 332 5288 http://scholar.ulethbridge.ca/iwaniuk/home Bird-brain (bÅ≫rd brān)1. a person regarded as silly or stupid.

"andrew.iwaniuk@uleth.ca"
<andrew.iwaniuk@uleth.ca>

UManitoba MicrobialEvolutionaryGenetics

Dear colleagues,

I am looking for an MSc student to join my group at the University of Manitoba (Winnipeg, Canada) to work on the distribution of neutral and beneficial mutations in the diploid human fungal pathogen Candida albicans. The project will involve a combination of laboratory work (experimental evolution, mutation accumulation) and bioinformatics. A candidate with an undergraduate degree in microbiology, genetics, or evolutionary biology could be appropriate. Prior computational training is preferred but not required, though a strong desire to learn to code is critical.

Start date: September 2021 (Canadian students only), January 2022 or May 2022 (any nationality)

Stipend: $17 500 CAD/year, 2 years

Additional information about the lab can be found here: https://microstatslab.ca Potential applicants should contact me for more information

(Aleeza.Gerstein@umanitoba.ca)

Please forward to any students you think may be interested!

Thank you kindly, Aleeza

Aleeza Gerstein, PhD. Assistant Professor Departments of Microbiology & Statistics University of Manitoba

Office: 364 Machray Hall Lab: 412 Buller Building Web: https://microstatslab.ca Aleeza Gerstein <Aleeza.Gerstein@umanitoba.ca>

UMassachusetts Lowell RotiferEvolution

Two PhD positions in Applied Biology to study the sexual evolution of rotifers

Two PhD student positions with full financial support as RA and TA-ships are available in Fall 2021/Spring 2022 in the Hochberg Lab, Department of Biological Sciences, University of Massachusetts Lowell (UML), USA.

I am looking for highly motivated students who are interested in studying the biology and evolution of microscopic animals called rotifers. Our team (Dr. Elizabeth Walsh and Dr. Jon Mohl, U. Texas El Paso; Dr. Robert Wallace, Ripon College, WI) is investigating the evolution of sexuality and life cycle dynamics in the largest lineage of rotifers, Monogononta. Each team member is directing different forms of research (molecular, taxonomic, morphological) to achieve a comprehensive understanding of rotifer biodiversity, systematics, and reproductive evolution in this lineage. Students will have opportunities to interact with all four team members through site visits, training, and conferences.

The role of the Hochberg lab in this research will be to describe the diversity of reproductive morphologies among rotifers and use this information to answer pertinent questions including: 1) Are maternal care and internal brooding ancestral or derived? 2) Are egg-shell characteristics (structure, mechanics, chemistry) correlated with life history strategies? 3) Have male genital and sperm diversity been driven by sexual selection? 4) Has male dwarfism evolved more than once? These questions and a host of others will be answered using advanced microscopical techniques including AFM, CLSM, SEM, TEM, and FIB-SEM. Most research will be conducted at UML, but some may take place at the

U. Massachusetts Medical School, which houses state-of-the art facilities. Students will have opportunities to present their research at national conferences and publish their research in respected zoological journals.

Minimum Requirements & Desirable Qualifications (preferred but not required)

B.S or M.S. in Biology or related fields

Experience with microscopy (electron and/or fluorescence) is preferable, but not necessary Experience with invertebrates, preferably microscopic species

Driver's license and transportation

Successful applicants will enroll in the PhD in Applied Biology program (Developmental and Evolutionary Biology tract), which is a minimum 4-year commitment. TA and RA assistantships are available for each academic year (including summers).

Please contact me (rick_hochberg@uml.edu) with any questions. If you are interested in applying, please send me the following information as single pdf file: (1) CV, (2) unofficial transcripts if available, (3) a cover letter outlining research interest and experience, and (4) contact information for 2-3 references. Please write "PhD applicant" in the Subject line.

Dr. Rick Hochberg Associate Professor of Biology University of Massachusetts Lowell OneUniversity Avenue, Lowell MA 01854, USA Office: 01.978.934.2885 http://www.hochbergbiodiversitylab.com "Hochberg, Rick" <Rick_Hochberg@uml.edu>

UNewHampshire ForestInsectEvolution

The Garnas lab (http://mypages.unh.edu/garnaslab) seeks a highly motivated PhD student to address basic and applied questions related to beech bark disease in eastern North America. A successful project will focus on eco-evolutionary feedbacks of relevance to the scale insects and multiple fungi associated with this disease, including those mediated via host tree response. Other elements of the project will be of the student's own design. Student stipend will be available for up to 5 years including a 3-year research assistantship; some service as teaching assistant may be required.

To apply for the PhD position you must have a Masters degree in a related field or equivalent experience, or provide sufficient motivation for acceptance directly from

an undergraduate program. Applicants must have a strong interest in field ecology and evolutionary biology, and in applying molecular and/or histological tools in natural (non-model) systems.

For an example of current work on this topic from our lab, please see: https://www.frontiersin.org/articles/-10.3389/ffgc.2021.673099 (available soon; biorxiv preprint here: https://www.biorxiv.org/content/-10.1101/2021.02.24.432696v1).

The University of New Hampshire and the Department of Natural Resources and the Environment are home to a vibrant community of productive researchers with a strong commitment to student success. Located in the town of Durham, UNH is a beautiful campus surrounded by forest and natural landscapes. Only 30 minutes from the ocean and 90 minutes to the White Mountains, outdoor and other recreational activities abound, including right on campus.

Interested applicants, please send (as a single pdf file) to jeff.garnas@unh.edu: - a CV - a brief statement of your motivation for pursuing a PhD in the field of ecology and evolution, including a summary of your specific research interests and any relevant experience - contact information for three references

The position is open until filled. Ideal start date is August 2021. Apologies for the late notice and for any cross-posting.

Jeff Garnas Associate Professor, Forest Ecosystem Health Natural Resources and the Environment University of New Hampshire 162 James Hall 603-862-2094 jeff.garnas@unh.edu http://mypages.unh.edu/garnaslab "Garnas, Jeff" <jeff.garnas@unh.edu>

UNottingham UK EvolutionGenomicsSnails

We are advertising a funded PhD in the evolutionary genomics of left-right asymmetry in Hawaiian snails, involving Mark Ravinet at the University of Nottingham and colleagues at the Bishop Museum in Hawaii. Exact balance of project, whether genetics, evolution, genomics, bioinformatics, field work will depend upon student. Bioinformatics training is available. Field work is certainly possible (virus permitting). Unfortunately, only "home" UK students are eligible.

The PhD is funded for 4 years through the 'Bioscience for Health' stream of the University of Not-

tingham BBSRC doctoral training programme (https://-/www.nottingham.ac.uk/bbdtp/index.aspx). In the first year, successful candidates undertake two rotation projects, then choose one for their PhD. Apply by May 26th: https://www.nottingham.ac.uk/bbdtp/-apply/how-to-apply.aspx . There is also a twitter advert here: https://twitter.com/angus_davison/status/-1390205252104867846 - but as most students are not on twitter, directed emails are more likely to reach the right person 'V please forward to anyone you think appropriate.

Note 1: Exemplar projects ONLY are provided on DTP web page. You won'Ât find details of this project, but it is funded, providing that we can find an appropriate student. https://www.nottingham.ac.uk/bbdtp/-our-research-areas/bioscience-for-health-exemplar-projects.aspx Note 2: This same project was advertised last year but withdrawn at short notice due to Covid. It is happening this year instead.

Finally, just to say that if any students are interested, then I would strongly recommend getting in touch with me first

Best wishes, Angus Davison

– Left-right asymmetry in Hawaiian 'Â¥Looking-glass'Â snails

About the Project

While most animal bodies are bilaterally symmetric on the outside, the internal organs usually show a consistent left-right (LR) asymmetry. Defining this LR asymmetry is a critical part of early development, such that left/right positional errors are an important class of human birth defect, and in later life numerous diseases affect apparently symmetric organs in an asymmetric fashion. Yet, in trying to understand how this LR asymmetry is established, it is straightforward to conceive how the LR axis is defined relative to front/back and top/bottom, but more difficult to comprehend how left and right are consistently orientated in the same direction. In the classic view, the solution is that LR asymmetry is signalled by a chiral structure, the fabled "F-molecule", which is directionally orientated relative to the other axes.

To date, a wealth of studies have revealed the genes that promote the propagation of asymmetric signals, but the earliest LR symmetry-breaking events are not clear. In seeking to understand if there is a common pathway, an emerging consensus is that LR asymmetry in diverse organisms originates from the cytoskeletal dynamics that underlie the asymmetric behaviour of individual cells Nonetheless, a central problem remains 'V how and why are left and right consistently orientated

in the same direction? The main approach to understanding this invariance has been to use rare mutants or manipulations in model animals (vertebrates, nematode/fly), to create individuals that are partly or wholly orientated in the opposite direction. This methodology has been fruitful, of course, but unfortunately, scientists have largely ignored the only animal group 'V snails 'V in which ordinary development can produce individuals that are LR orientated in different directions. Studies of LR asymmetry ("chirality") in snails may be key to understanding how and why are left and right consistently orientated in the same direction in nearly all other animals. In this project, we propose to use association mapping and long read genome sequencing to identify the gene that underpins natural variation in the LR asymmetry of Hawaiian snails of the genus Lymnaea or Auricullela. This knowledge will then be used to understand how molecular chirality defines the LR asymmetry of cells, organs and bodies, with implications for understanding human health and development. The project will involve a range of evolutionary genomic methods, including DNA sequencing / bioinformatics, and may also require field or lab work in Hawaii.

Representative publications:

Davison, A., Thomas, P. & Jeremy the Snail citizen scientists 2020. Internet 'Â¥shellebrity'Â reflects on origin of rare mirror-image snails. Biology Letters

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UppsalaU HostSymbiont EvolutionaryGenomics

A 4-year Ph.D. positions to work on evolution of Host-Symbiont interactions is available in the lab of Lisa Klasson at the Molecular Evolution programme, Uppsala University.

General description: The overall aim of the project is to use large-scale DNA and RNA sequencing to study how symbiotic interactions between bacteria and animal hosts affect both partners' genetic material and evolution. For the most part, we will analyze data from the endosymbiotic bacterium Wolbachia and different Drosophila species.

Duties: The Ph.D. student shall primarily focus on postgraduate studies, but other duties related to teaching and administrative work may be involved, up to a maximum of 20 % of the time. Information about doctoral education, eligibility requirements and admission rules can be found at the faculty website, http://www.teknat.uu.se/utbildning/utbildning-pa-forskarniva/.

Requirements: The applicant must have a master's degree in bioinformatics, evolutionary biology, molecular biology, or within another subject which the employer considers to be equivalent. Previous experience of working with next-generation-sequencing data and bioinformatic analyses is an asset. Familiarity with Linux and a scripting language such as Python, R or Perl is desirable. The applicant must have a good ability to work independently as well as in a group. Excellent written and oral knowledge of English is required, as the work takes place in an international environment.

Read more and apply at https://www.uu.se/en/about-uu/join-us/details/?positionId=404234 Lisa Klasson <lisa.klasson@icm.uu.se>

USherbrooke PDF 2PhD EvolutionaryBiology

PhD or Post-doc : Demography of tree swallows: explaining the contemporary decline of an aerial insectivore population.

Many species of birds have shown decline in abundance in North America. Most worrisome among them are aerial insectivores. For example, tree swallow (Tachycineta bicolor) abundance has declined by 4.2 % per year over the past 20 years in Québec. The goal of this project will be to expand a demographic model on tree swallow population dynamics, to integrate both local and global environment drivers and to quantify the relative role of these factors in driving the observed decline and forecast future population trends. The data available for this project come from a long-term individual monitoring of tree swallows in southern Québec, where survival and reproduction have been monitored in 400 nesting boxes since 2004.

Assets for this position include publications, a 'basic' knowledge of French (or a strong willingness to learn it), fieldwork experience, strong quantitative skills (e.g. CMR, Bayesian statistics, PVA). Canadian candidates will be preferred, but foreign candidates with a strong

publication record will be seriously considered. A scholarship is available, and financing for travel, fieldwork and lab expenses has been secured. The program can begin in September 2021 or January 2022. For information on my research, see https://labopelletier.weebly.com/ Interested candidates should e-mail a CV, a statement of research interests and the e-mails of two referees to Fanie Pelletier: fanie.pelletier@usherbrooke.ca

PhD: Snow and population dynamics of bighorn sheeps

We are looking for a student to start a PhD on the links between changing snow conditions, winter mass loss and population dynamics of the bighorn sheep. This project is part of a follow-up of individuals from birth to death that began in 1971 in Ram Mountain, Alberta. The student will have the opportunity to collect data (behavioral observations, capture, tagging and measurements of sheep, etc.) during 2 or 3 field seasons (May to September), in addition to being able to take advantage of the 'imposing dataset.

Assets for this position include a MSc in biology or ecology with publication(s), a 'basic' knowledge of French (or a strong willingness to learn it), fieldwork experience, strong quantitative skills. Canadian candidates will be preferred, but foreign candidates with a strong publication record will be seriously considered. A scholarship is available, and financing for travel, fieldwork and lab expenses has been secured. The program can begin in September 2021, January or May 2022. For information on my research, see https://labopelletier.weebly.com/ Interested candidates should e-mail a CV, a statement of research interests and the e-mails of two referees to Fanie Pelletier: fanie.pelletier@usherbrooke.ca

Audrey Sigouin Professionnelle de recherche, MSc écologie Département de biologie, Université de Sherbrooke

Audrey Sigouin <Audrey.Sigouin@USherbrooke.ca>

USouthFlorida TasmanianDevilEvol

The Margres Lab (www.margreslab.com) in the Department of Integrative Biology at the University of South Florida (Tampa campus) is looking for a highly motivated graduate student (Ph.D.) to study adaptation and coevolutionary dynamics between Tasmanian devils and a species-specific transmissible cancer. We use a combination of field work, 'omics, and bioinformatic approaches to answer fundamental questions in evolutionary biology related to adaptation, the genotype-phenotype relationship, and coevolution. Although the lab also studies venom evolution, currently the lab is only accepting a graduate student to work on the Tasmanian devil-cancer system.

Candidates should have a background in ecology, evolution, genetics and/or bioinformatics and be an independent learner with a strong work ethic. Familiarity with R, Linux/Unix, computing clusters, and the use of bioinformatic tools would be advantageous, but prospective students interested in establishing these skillsets are also encouraged to apply. Candidates should also have strong lab and interpersonal skills allowing them to work well in a laboratory setting and in a group. The Margres lab is committed to increasing diversity in STEM, and we encourage applications from underrepresented groups.

Interested applicants should contact Dr. Margres directly at margres@usf.edu. The desired start date is Fall 2022. See here for more details: https://www.usf.edu/arts-sciences/departments/ib/graduate/how-to-apply.aspx Mark Margres, Ph.D. Assistant Professor, Department of Integrative Biology University of South Florida Tampa, FL 33620 www.margreslab.com

"Margres, Mark" <margres@usf.edu>

UStrasbourg EvolutionaryBiol

"Phd position - University of Strasbourg :

Thesis subject open to the competitive examination of the Strasbourg doctoral school

Thesis jointly supervised with University of Turku, Finland

Thesis supervisor: Sylvie Massemin, Institut Pluridisciplinaire Hubert Curien, UMR 7178, Lecturer at the University of Strasbourg

Co-supervisor: Sophie Reichert, Researcher at the University of Turku, Finland

Application procedures:

A CV and a cover letter written in French or English must be sent before May 15, 2021 to:

sylvie.massemin@iphc.cnrs.fr   and   reichert.sophie@gmail.com

The candidate selected by the supervisors will be able to apply for the Doctoral School of Life and

Health of Strasbourg (ED 414) on the site: http://ed.vie-sante.unistra.fr/appel-a -candidatureau-doctoral-contract / application-file /

Interindividual variation of the response to thermal constrains: from underlying

mechanisms to evolutionary consequences.

The human footprint, including global changes, and their effects on ecosystems, is growing and widespread. Our ability to quantify and predict the magnitude of these effects represents one of the major challenges of 21st century. While climate change is characterized by a gradual increase of ambient temperature through time, it is also leading to an increased frequency of climate anomalies, such as heat waves, especially in urban areas. Strikingly, even small changes in ambient temperature within the ZNT of individuals can have significant effects on the performance of organisms. In birds, environmental parameters experienced during development and growth, including temperature, are of crucial importance and can have a significant influence on individuals' physiology and life history trajectories. However, relatively few studies have investigated the physiological and molecular mechanisms which underlie these effects and their consequences on the life history trajectories in individuals. Performing energetically costly activities (growth, reproduction, maintenance) under warm ambient temperatures might expose individuals to a risk of hyperthermia. This can lead to a reduced investment in such energetically-costly activities and may lead to reduced reproductive investment and success. Alternatively, organisms might maintain their energy investment in those essential activities under warm temperatures but suffer from various physiological costs related to heat stress. Moreover, thermal stress effects during development and / or growth can have transgenerational effects. Finally, the parents would change quickly their behaviour at the nest according the environment change. To expand our understanding of how bird species respond to temperature variation, we will investigate if parents can adjust the microclimate around the nestlings. Using a multidisciplinary and integrative approach, the aim of this project is to evaluate the effects of thermal disturbances on the physiology of organisms, in order to better understand and predict their ability to adapt to these effects, but also to determine their potential effects at the scale of life history trajectories.

Experiments To do so, we propose to set up two experiments, one in natura on the Great tit (Parus major) and in a controlled lab environment on the Zebra finch (Taeniopygia guttata), to address the following questions: 1) What are the effects of thermal disturbance on organisms' physiology? We will identify the underlying mechanisms involved in thermal adaptation by using crossing-over method (chick swap) between different sites. 2) What is the impact on individuals' life history trajectories? We will study evolutionary consequences of thermal disturbances. 3) What is the impact of thermal disturbance during the growth of nestlings? We will plan a "mis-match" experiment by modify temperature during prenatal development and postnatal growth of nestlings and evaluate the physiological and life history traits effects. 4) How parents adjust their parental effort during the thermo-dependence period of nestlings according to the temperature variation? We have to control if the time-budget of the parents linked to nest activities change to buffer the temperature increase. Physiological and molecular parameters To assess the impact on metabolism, we will measure metabolic activity in a portable metabolic chamber and mitochondrial density. To assess lifestyle effects and their impact on individuals' health, oxidative stress, telomere dynamics, and corticosterone will be measured. Oxidative stress will be evaluated from plasma samples with measures of oxidative damage (global and oxidative damage on DNA) and antioxidant defences (non-enzymatic OXY capacity and enzymatic superoxide dismutase activity). Telomere lengths are measured from blood samples by qPCR. From the same DNA extracted from these blood samples, mitochondrial density will be measured by qPCR as

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Vienna MolecularEvolution

Ph.D. student position in molecular evolution

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

Topic: Molecular evolution of coding sequences

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

Description: A major goal in evolutionary biology is to understand the forces that operate in the genomic se-

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

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

Starting date: Ideally, September 2021 or earlier

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

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

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

Application deadline: May 16, 2021

Questions about the project: Rui Borges (rui-borges23_at_gmail.com)

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

Rui Borges <ruiborges23@gmail.com>

Vienna PopulationGenetics

Reminder: Call for PhD students closes May 16th

Start date: Sept 2021 (or earlier)

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

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

Topics include:

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

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

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

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

www.popgen-vienna.at   https://twitter.com/-PopGenViennaPhD c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni

Vienna) Veterinärplatz 1, 1210 Wien

Current home office contact via Skype: julia.hosp

http://www.vetmeduni.ac.at/en/population-genetics/
https://twitter.com/PopGenVienna　　　　Julia　Hosp
<Julia.Hosp@vetmeduni.ac.at>

WashingtonStateU PlantMicrobeInteractions

The Porter lab at Washington State University seeks an MS student to join in investigating how wildfire and drought alter soil microbiomes and soil hydrology to facilitate or inhibit tree regeneration after fire. Over two years, the student will have the opportunity to study post-fire tree seedling regeneration and soil microbiomes using a greenhouse experiment and amplicon sequencing. Prior experience in Evolutionary Ecology, Environmental Science, Microbiology, Plant Science, or Bioinformatics would be useful. The successful candidate will join a collaborative WSU research team spanning plant-microbe interactions (Porter lab), ecohydrology (Moffett lab), and restoration ecology (Cheeke lab), so strong communication skills are a plus.

Project Background. Wildfire and climate change pose a risk of widespread forest conversion to shrub- or grass-lands. This conversion has already occurred in many locations around the world, but the contributing mechanisms remain a puzzling and active area of research. Key aspects of forest resilience, such as soil microbial ecology and hydraulic function, are critical drivers of tree seedling survival and drought tolerance. However, fire's impact on microbial and physical components of soils are rarely tested for their combined effects on post-fire regeneration and drought tolerance, especially outside of boreal forests. We aim to disentangle the disruptions that fire imposes on temperate montane conifer forest seedling-microbe-soil feedbacks at the microscopic scale and any impacts on seedling drought tolerance.

Lab Description. The Porter lab (https://labs.wsu.edu/-stephanie-porter/) investigates diverse projects on the Evolutionary Ecology of Plant-Microbe Interactions, ranging from how symbiotic plants and microbes adapt to environmental stresses to the ways in which plant-microbe cooperation shifts during crop domestication. We are housed in the School of Biological Sciences at Washington State University, Vancouver. The student will also have the opportunity to engage with Vancouver's Moffett lab on themes of water-soil-plant interactions in diverse settings, including post-fire systems. Located on a beautiful 351-acre campus across the Columbia River from Portland, Oregon, WSU Vancouver offers an excellent quality of life. Recognized by Insight Into Diversity Magazine as a top college for diversity, WSUV and this collaborative project team commit to inclusive excellence by advancing equity and diversity in all that we do.

How to Apply. A BS or BA in a relevant scientific field is required. Tuition, benefits, and stipend will be funded by a combination of research and teaching assistantships, guaranteed for two years. If interested, please email an inquiry with the subject header, "Plant-Microbe-Fire MS" with CV, GPA, relevant experience and coursework, and a short statement explaining your interest in the position to stephanie.porter@wsu.edu. Application review will begin on May 30th, 2021, and continue until the position is filled. Position could begin as soon as July 1st, 2021. For more information about the Masters of Science in Biology or Plant Biology in the School of Biological Sciences at WSU-Vancouver, please see: https://cas.vancouver.wsu.edu/science-graduate-programs/biology-and-plant-biology-ms-and-phd
Stephanie Porter <stephanie.porter@wsu.edu>

Jobs

AmherstCollege ResAssist EvolutionDisease

AmherstCollege.EvolutionDisease.ResAssist

RESEARCH ASSISTANT POSITION EVOLUTIONARY ECOLOGY OF INFECTIOUS DISEASE

The Hood Lab (https://www.amherst.edu/people/facstaff/mhood) in the Biology Department at Amherst College is seeking to fill a full-time research assistant position. The position is for one year, and there is the possibility to reappointment for a second year. Ongoing projects address the evolutionary ecology of infectious disease in natural plant populations, which extend off the recent AmNat paper, https://www.journals.uchicago.edu/doi/10.1086/715013. Activities in this lab span a wide range of approaches, including population biology and greenhouse/field work. The research assistant will gain experience and participate in each of these activities as well as in general lab maintenance and operation. Start date will be as early as July 1, 2021.

Qualifications: Bachelor's degree in biology or related field, previous laboratory experience, and motivation to engage in biology research are expected.

To apply online, please visit our web site at

https://amherst.wd5.myworkdayjobs.com/-Amherst_Jobs/job/Amherst-Campus/Research-Assistant—Biology_JR1065   Amherst College is an equal opportunity employer and encourages women, 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.

Michael E. Hood Professor of Biology Amherst College Amherst, MA USA 01002-5000 ph (413) 542-8538 email: MHood@amherst.edu https://-www.amherst.edu/people/facstaff/mhood Michael Hood <mhood@amherst.edu>

AstraZeneca Cambridge Bioinformatician

Are you a bioinformatician passionate about medical research and looking for an exciting and impactful new challenge? Do you have experience in analysing *genome-wide omics* data and *high-throughput molecular or genetic screens* for target identification and drug discovery?

We are currently seeking a talented *Senior Bioinformatician* to join our Data Sciences & Quantitative Biology team in *Cambridge, UK* and apply bioinformatics and computational solutions to help us evolve and extend our capabilities in our drive to find the medicines of the future. In doing so, you will be part of a multi-disciplinary team of bioinformaticians, data scientists, image analysts and statisticians providing quantitative insights to discover new therapies. Our group is committed to enhancing AstraZeneca's ability to enable effective target selection and hit identification.

We welcome applications no later than *Saturday 5th June*. For more details and to apply, use the following link:

https://careers.astrazeneca.com/job/cambridge/-senior-bioinformatician-molecular-screening-and-omics-research/7684/19348534   Sergio Martinez Cuesta <sermarcue@gmail.com> Sergio Martinez Cuesta <sermarcue@gmail.com>

online, and study abroad.

The Department supports faculty development at all ranks, and promotion through instructional ranks is expected for these renewable, non-tenure track positions. Salary level will be commensurate with education and experience, and a benefits package is included.

Department Description The Department of Biological Sciences at Clemson University harnesses faculty expertise across the areas of ecology, evolution, and organismal biology; microbiology; molecular, cellular, and developmental biology; and environmental toxicology to advance the University's discovery mission and provide strong educational programs at both the undergraduate and graduate levels.

The Department, located within the College of Science, is home to 50-plus full-time faculty, including 16 lecturers, supporting research and degree programs in Biological Sciences, Microbiology, and Environmental Toxicology. The department's student population includes ca. 70 graduate students in M.S. and Ph.D. programs in Biological Sciences, Microbiology, Environmental Toxicology and 200 in the online M.S. program in Biological Sciences for Science Educators. There are 1650-plus undergraduate students in B.A. and B.S. degree programs in Biological Sciences and Microbiology.

For additional information, see the full positionhereor contact Yanzhang (Charlie) Wei, Chair of the search committee (ywei@clemson.edu). To apply:https://apply.interfolio.com/88231. For full consideration, applications should be submitted by June 15, 2021. Review will continue until the position is filled.

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

Richard Blob Alumni Distinguished Professor Chair, Division of Vertebrate Morphology, SICB rblob@clemson.edu Web: https://sites.google.com/site/richardbloblab/ Pronouns: He, Him, His

Richard Blob <rblob@clemson.edu>

Bonn LepidopteraCurator JuniorScientistAward

Deadline extended to May 30, 2021:

Curator Lepidoptera CeNak (m/f/d) - Hamburg, Germany The Leibniz Institute for Analysis of Biodiversity Change (LIB) is looking for a scientist for a tenure track position of a Curator Lepidoptera (m/f/d) in Hamburg:

https://www.zfmk.de/en/job-portal Deadline extended to May 30, 2021:

Margarethe Koenig Award for international female junior scientists as a "stepping stone" for the further academic career:

https://www.zfmk.de/en/job-portal –

Dr. Karen Meusemann - Scientific Adviser Zoological Research Museum Alexander Koenig (ZFMK), Bonn - Leibniz-Institute for Animal Biodiversity - Adenauerallee 160, 53113 Bonn, Germany phone: +49 228 9122 - 307 email: k.meusemann@leibniz-zfmk.de www.zfmk.de Stiftung des öffentlichen Rechts; Direktor: Prof. Dr. Bernhard Misof Sitz: Bonn

Meusemann Karen <K.Meusemann@leibniz-zfmk.de>

ClemsonU 2 TeachingEvolution

The Department of Biological Sciences at Clemson University is seeking two full-time, 9-month Lecturers in Biological Sciences to begin August 15, 2021.We seek candidates who will contribute innovative teaching and student-centered learning in our B.A. and B.S. degrees in Biological Sciences and online M.S. in Biological Sciences for Science Educators.

Teaching responsibilities will include: 1) undergraduate lecture and lab courses, specifically introductory biology and possibly physiology, evolution, cell biology, microbiology, or other courses within the candidate's area of expertise, and may include 2) online M.S. courses, such as ecology, evolution, scientific writing, animal or plant biology, microbiology, cell biology, or teaching pedagogy-experimental design and analysis. There are summer salary opportunities available for teaching on-campus,

ColoradoStateU ResTech PlantMolecularEvolution

The Sloan lab at Colorado State University is recruiting a technician with experience in plant molecular genetics to join our group. Researchers with an M.S. (or B.S. and subsequent full-time lab research experience) in one or more of the following areas are encouraged to inquire.

–Plant growth and crossing –DNA extraction, PCR, and genotyping –Cloning and transformation –Mitochondrial and chloroplast isolation –Protoplast transfection – Fluorescence microscopy –Next-gen sequencing library construction

We are looking for an individual who is excited about developing their research career while contributing to a positive, diverse, and intellectual lab environment. Research in our lab focuses on genetic interactions among the multiple genomic compartments (nuclear, mitochondrial, and plastid) that exist within plant cells. More information about our research program can be found at our lab website: https://sites.google.com/-site/danielbsloan/ Inquiries can be e-mailed to Dan Sloan (dan.sloan@colostate.edu) and should include a resume/CV and a brief statement of research/career goals. Evaluation will begin June 1, but inquiries are still highly encouraged after that point.

Dan.Sloan@colostate.edu

Durham Bioinformatics

Avalo is a sustainable crop development company using AI and evolutionary theory to massively accelerate gene discovery and breeding. We are collaborating in major row crops and pioneering projects in understudied systems to create a new kind of crop breeding company. We'Âre a fast-growing, dedicated group of evolutionary scientists, gardeners, and engineers all rolled into one, and we'Âre looking for people passionate about linking science and practice to create the next generation of crops. We'Âre based in Durham, NC, but fully open to remote work, depending on the position and needs.

Please note: we'Âre eager to train the right candidates

for this role, and encourage those who meet at least two thirds of the criteria to apply.

Role & Responsibility

Apply genomics, statistical, and artificial intelligence concepts to conduct genome-wide analyses on DNA and RNA sequencing data Curate data from public and proprietary sequence databases to streamline inputs to computational pipelines Collaborate with the science team to create the future of genomic tools 'X e.g. algorithms, data structures, predictive models, software pipelines, or experimental approaches 'X that improve our ability to find targets of interest Troubleshoot technically complex design problems, and propose solutions or experimental plans to resolve or correct for them Prepare presentations and present data to an interdisciplinary technology team with diverse scientific backgrounds as well as external partners

Skills & abilities

Strong background in genomics, bioinformatics, population genomics, evolutionary biology, plant biology, or related field Basic familiarity with machine learning concepts preferred but not required Ability to work in a UNIX environment, ideally in a high-performance computing environment Expertise in next-generation sequencing data generation and processing Familiarity with data management and R/Python is a plus Good communicator and be comfortable with handling simultaneous tasks Strong organization skills are strongly preferred Comfortable working in a fast-paced and cross-functional environment Enthusiasm for Avalo'Âs mission

What we offer

Competitive salary with share options Flexible PTO and 25 paid holidays per year 90% work/10% personal scholarship time division Casual, flexible, and intellectually stimulating work environment

Brendan Collins <b.collins@avalo.ai>

EmbarkVeterinary BostonMA Bioinformatics

Senior Software Engineer, Bioinformatics

Apply here: https://embarkvet.applytojob.com/apply/-n8eybrL2ys/senior-software-engineer-bioinformatics/ Why you should join the Embark pack:

Embark is growing fast as we pursue our mission to improve the life and longevity of all dogs through science

and technology. Our DNA test is becoming a part of the global standard of pet care and enabling us to make advances in every area of care.

Our highly rated Dog DNA test allows you to discover your dog more than fur deep with the most comprehensive DNA test on the market. Designed by world leaders in dog genetics, in partnership with Cornell University, the Embark DNA test tells owners what breeds make up their pets, how to prevent future possible health problems, and what features and traits their pet might have. Behind the scenes, our scientists use the data people choose to share with us to create new advances to enable a better future for pets and the people who love them.

Interested in joining? We look for highly motivated and driven employees who will join us as Embark leads the cutting edge of creativity and innovation in the fast-growing consumer genetics space.

The team you'll join:

On the Ancestry team, you will work to improve and maintain the bioinformatics pipeline underlying Embark's breed and ancestry products. This pipeline transforms raw genetic data into a dog's breed mix and ancestry, doggy relatives, and more. It must run efficiently, reliably, and at a massive scale on AWS. You will work closely with Scientists, Engineers, and Product Managers to solve important scientific problems and develop the next generation of breed and ancestry products.

This year the team will:

- Evolve Embark's architecture and bioinformatics pipelines to enable Embark to continue to scale exponentially. - Bring to life new and exciting scientific ideas to improve Embarkâ euro s best in class Breed and Ancestry products. - Compound the delightful experiences we provide to our highly rated products.

This is one of the most exciting times to join Embark!

What you'll do:

Senior Software Engineers at Embark lead by example through development of high quality, easy to maintain features and enhancements. They have broad experience and excel in a few areas where they have deep, passionate experience.

- Deliver clean, efficient, maintainable code, as well as thorough tests and documentation - Mentor other software engineers to enable their growth - Leverage your deep knowledge of our stack to advise your technical leaders how to best tackle problems - Contribute to improving our technology and development practices via retrospectives and other means, with the goal of continuous improvement of quality and team efficiency

Who you are:

- At least a Bachelors in Computer Science or equivalent practical experience - Expertise in designing, building, testing, maintaining, and operating large-scale distributed data systems - Experience with systems in genetics/bioinformatics or a related field is preferred but not required - Deep knowledge of building large, type-annotated analytics codebases in Python - Knowledge of architectural patterns and experience making architectural decisions - Experience profiling and optimizing local and distributed systems - Experience with customer-centric product development - Expertise with SQL relational databases (PostgreSQL) - Experience with non-relational databases is preferred but not required - Expertise with AWS or similar cloud technologies - Understands DevOps, as well as Agile development philosophies - Willingness to participate in on-call rotation including some weekends and holidays - Excellent verbal and written communication skills - Strong people leadership skills and project leadership skills as well as strong technical leadership skills - Passion for dogs and genetics

What we can offer:

Embark is an employer who cares about your career and your wellness. We believe the best employees have a life outside work and we help you achieve balance and success. Some perks include:

- A flexible vacation policy that lets you take off the time you need when you need it - Paid maternal and paternal leave (for fur babies too) - Every other Friday off each summer - Dog-friendly office near South Station, Boston (when we got back to the office), with some flexibility (eg work from home 2 days a week, flexibility around child care needs, etc) - Perks tailored for dog lovers including subsidized pet insurance, dog-walking services, and paw-ternity leave - Startup perks with big-company benefits (401k match, commuter benefits, all-inclusive healthcare, HSA/FSA) - Competitive salaries and equity participation - every employee gets

— / —

EmbarkVeterinary IthacaNY 3 CanineGenetics

Senior Research Scientist, Population Genetics

Apply here: https://embarkvet.applytojob.com/apply/-RUzljXqGYa/senior-research-scientist-population-genetics/ Who we are:

Join Embark on our mission to improve the life and longevity of dogs everywhere. Our canine DNA test â euro " the highest-rated, most accurate on the market â euro " enables us to make scientific advances in personalized pet care. Recently named one of the fastest-growing private companies in America by Inc. Magazine, Embark is the only canine genetics company using research-grade technology, which allows us to make new scientific discoveries.

Designed by world leaders in dog genetics in partnership with Cornell University, the Embark Dog DNA Test provides information on genetic health risks and breed make-up, allowing dog owners, breeders, and veterinarians to make personalized care plans based on a dog's unique genetic profile. Embark is also home to the world's only canine DNA relative finder. No wonder The New York Times recently called Embark's Breed and Health Kit the best dog DNA test available!

Interested in joining our pack? We are looking for highly motivated and mission-driven employees who will join us as Embark leads the cutting edge of creativity and innovation in the fast-growing consumer genetics space.

About the role:

On the Ancestry team, you will work to improve and maintain the science and bioinformatics pipeline underlying Embark's breed and ancestry products. This pipeline transforms raw genetic data into a dog's breed mix and ancestry, doggy relatives, and more. It must run efficiently, reliably, and at a massive scale on AWS. You will work closely with other Scientists, Engineers, and Product Managers to solve important scientific problems and develop the next generation of breed and ancestry products. This year, the team will:

- Bring to life new and exciting scientific ideas to improve Embarkâ euro s best in class Breed and Ancestry products. - Evolve Embark's science and bioinformatics pipelines to enable Embark to continue to scale exponentially. - Compound the delightful experiences we

provide to our highly rated products.

What you'll do:

Senior Scientists at Embark lead by example through high quality data analysis and research that drives new products and product features or the improvement of existing products. They have a strong desire to share their knowledge, continuously learn, and excel in a few areas where they have deep, passionate experience. In this role, you will:

- Benchmark current methods and recommend new experiments, algorithms, and statistical methods to improve core Ancestry product outcomes (Ancestry Deconvolution). - Be an excellent individual contributor by delivering high quality data, data analysis, and code, as well as thorough scientific reports and documentation. - Work closely with software engineers to deliver clean, efficient, maintainable code, as well as thorough tests and documentation - Mentor other scientists to enable their growth - Leverage your deep scientific knowledge to advise leaders how to best tackle problems

What experience we're looking for:

- PhD in Population Genetics, Animal Breeding, Computational Biology, or a related field and 3+ years of experience. - Strong skills in applied population genetics (e.g. ancestry deconvolution, detection and characterization of population structure, etc.) - Experience working with whole-genome genotype array and/or whole genome sequence data - Excellent verbal and written communication skills - Comfort with Linux/Unix environments - Coding and data analysis experience in Python and/or R; Python skills preferred. - Excellent statistical proficiency. - Strong people leadership skills and project leadership skills - Experience working in and/or leading multidisciplinary research and development teams - Expertise with AWS or similar cloud technologies preferred - Experience with databases (SQL and non-relational) preferred - Experience with customer-centric product development preferred - Passion for dogs and genetics

What we can offer:

At Embark, we might be dog lovers, but we're passionate about people too. We're committed to building an inclusive culture where all employees can belong and flourish. Here are some of our benefits and perks:

- Working with the world's largest team of PhDs, DVMs and engineers focused on canine genomics and devoted to making the next generation of discoveries and technologies that will make the lives of dogs today and in the future longer and healthier - A flexible vacation policy so you can take off the time you need when you need it - Paid maternal and paternal leave (plus paw-ternity

leave for new pets)

<div align="center">— / —</div>

GeorgiaTech 2ResTech MulticellularEvolution

Full Time Research Technician at Georgia Tech in Atlanta- Experimental Evolution of Multicellularity / Synthetic Biology

The Ratcliff lab is hiring two full time research technicians to work on the evolution of multicellularity in our 'snowflake yeast' model system. Read more about our research here: https://ratclifflab.biosci.gatech.edu/ . This work will use a combination of synthetic biology, experimental evolution, and confocal microscopy / quantitative image analysis to study the de novo evolution of multicellular development, and evolution of increased multicellular complexity. We are open to either recently graduated students looking for a year of research experience before graduate school (often called a 'postbac'), or longer-term employment. A BS in biology and prior experience with cell culture or molecular biology are required, yeast experience would be a plus.

To apply for these jobs, visit hr.gatech.edu/careers and select "start your search here" under external applicants. Then select "View all jobs". Please make sure the business unit selected is "Georgia Tech" and you may search by requisition numbers 226739 and 226690.

You can also email Will Ratcliff (ratcliff@gatech.edu) to discuss the position prior to applying.

Interviews will start the week of 5.14.2021, and will continue until the positions are filled.

Associate Professor,Biological Sciences

Co-Director, Interdisciplinary Graduate Program in Quantitative Biosciences (QBioS)

Georgia Institute of Technology

Lab website:http://www.ratclifflab.biology.gatech.edu/ Google Scholar profile

Twitter: @wc_ratcliff

Phone:612-840-4983

Office: 331 Cherry Emerson

Lab: 330 Cherry Emerson

"Ratcliff, William C" <william.ratcliff@biology.gatech.edu>

HarvardU ResTech PlantSpeciation

The Hopkins lab at Harvard University is seeking a full-time research technician.

Please apply with your CV and cover letter here:

https://sjobs.brassring.com/TGnewUI/Search/-home/HomeWithPreLoad?partnerid=25240&siteid=-5341&PageType=JobDetails&jobid=1571375   Our research focuses on understanding the evolutionary forces driving adaptation and speciation. We use a variety of population genetic, molecular, greenhouse, and field techniques to study selection, gene flow, and adaptive mutations in plants. Much of our work focuses on characterizing reproductive isolation between species and mate choice within species. This position will involve assisting researchers with a variety of laboratory, field, and greenhouse tasks including:

§Performing basic plant care and propagation §Performing controlled crosses between plants §Performing basic microscopy on plant tissue §Recording results of experiments §Organizing and summarizing data, in collaboration with team §Under direction, performing standard laboratory techniques such as DNA extraction, PCR, and cloning §Working with senior scientists on design, planning, and optimization of experiments

We are looking for someone excited to learn more about evolutionary biology, plant biology, speciation, and population genetics. We would like to find someone organized, self-motivated, detail oriented, and with strong communication skills. Ideally, candidates will have some research experience or course work in evolution, genetics, or plant biology.

The Hopkins lab (http://hopkins-lab.org/) is part of the Organismic and Evolutionary Biology department at Harvard University, which is diverse and vibrant with a broad range of research and teaching interest. Our lab is located at the Arnold Arboretum research building in Boston.

In the Hopkins lab we believe the strength and excellence of our community stems from our diversity of identities, experiences, and perspectives. We are an equal oppor-

tunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability status, protected veteran status, gender identity, sexual orientation, pregnancy and pregnancy-related conditions, or any other characteristic protected by law.

Please contact Robin Hopkins (rhopkins@fas.harvard.edu) with questions

"Hopkins, Robin" <rhopkins@fas.harvard.edu>

Madrid Genetics

Assistant Professor in Genetics is available at Complutense University of Madrid (UCM).

Other positions in relation with evolutionary studies also include Zoology or Ecology.

Details can be found here:

https://www.ucm.es/convocatoria-publicada-en-el-bouc-de-20-de-mayo-de-2021 Last day for applications (can be done on-line): 10 June 2021.

Ro berto <geneticsstudies@hotmail.com>

MaxPlanckTuebingen RegulatoryGenomics

We are posting two exciting opportunities to join our effort to understand the non-coding regulatory genome in adaptation using threespine stickleback fish.

- Staff scientist in genomics (see below) - Postdoc in Genomics and Epigenomics of Gene Regulation (see ad under "Postdoc")

A major challenge in the field is understanding how the non-coding genome functions in natural populations under different environmental conditions. In our group we combine state-of-the-art facilities to manipulate environmental conditions and have been collecting a trove of chromatin, epigenomic and transcriptomic data from adaptively divergent stickleback fish ecotypes to map and quantify how the non-coding regulatory genome functions and evolves. In previous work we have shown the predominance of cis-regulatory differ-

ences in gene expression divergence (Jones et al 2012[1], Verta et al., eLife 2019, [2]), tracked allelic trajectories during adaptation over time (ancient DNA, Kirch et al., Curr Biol. 2021 [3], Kingman et al., Sci. Advances, in press/bioRxiv [4]. and Schluter et al., PNAS, 2020 [5]) and developed novel techniques to determine the recombination landscape in single individuals (Dreau et al., Nat Comm. 2019 [6]). We have recently generated a large multi-tissue, multi-omic dataset dubbed "StickleCODE" [unpub] to further dissect the molecular mechanism of adaptation (including environmental manipulations) in the system.

We are looking for a staff scientist to join as a core member of our team and support projects central to our groups' overall aims. You will actively generate genomic data in the molecular lab and/or apply pipelines in bioinformatic analysis of 'omic datasets. You will also provide research support to other team members. The successful candidate will have previous experience in areas related to gene regulation, genomics, epigenomics and evolution; and some experience with data analysis and bioinformatics (e.g., familiarity with Unix/linux, bash, Python, R).

The Max Planck Tübingen Campus is a leading research hub with world-class genomics and machine learning expertise. Our sequencing core features Illumina, PacBio and 10X Genomics platforms. English is the working language. All seminars and communications are in English.

We offer a varied and interesting job with the social benefits of the public service. Remuneration is in accordance with the TVöD (German public service salary scale). The positions are to be filled from June 2021 and is initially limited to two years.

The Max Planck Society is committed to employing more women in areas in which they are underrepresented. Qualified women are therefore particularly being encouraged to apply. The Max Planck Society strives to employ disabled people. Applications from disabled persons are expressly welcome.

Please send your application and contact details of three referees to:

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Max-Planck-Ring 9 D-72076 TuÃÂbingen

E-Mail: fcjones@tuebingen.mpg.de https://-fml.tuebingen.mpg.de/jones-group/ Application deadline: open until filled.

References: 1. Jones FC, Chan YF, Schmutz J., Brady SD, Southwick A, Myers RM, Schluter D, & Kingsley

DM. (2012) A genome-wide genotyping array reveals patterns of global and species-pair divergence in three-spine stickleback. Current Biology 22, 83-90. 2. Verta JP and Jones FC (2019). Predominance of cis-regulatory changes in parallel expression divergence of sticklebacks. eLife 8:e43785 doi: 10.7554/eLife.43785 3. Kirch et al., (2021). Ancient and modern stickleback genomes reveal the demographic constraints on adaptation. Curr Biol. 31, 20272036 4. Kingman GA, et al. (2020). Predicting future from past: The genomic basis of recurrent and rapid stickleback evolution. Science Advances. in press. bioRxiv doi: https://doi.org/10.1101/2020.11.13.382424 .5. Schluter D, Marchinko KB, Arnegard ME, Zhang H, Brady SD, Jones FC, Bell MA, Kingsley DM (2020) Fitness maps to a large-effect locus in introduced stickleback populations. PNAS. 118(3)e1914889118. 6. Dreau A, Venu V, Avdievich E, Gaspar L and Jones FC. (2019) Genome- wide recombination map construction from single individuals using linked- read sequencing. Nat comm. 10:4309-4320.

Dr. Felicity Jones

Max Planck Research Group Leader Friedrich Miescher Laboratory of the Max Planck Society Max-Planck-Ring 9 72076 Tuebingen Germany Ph +49 (0)7071 601 840

jones.floss@gmail.com

MedUni Vienna PartTimeTechnician HostMicrobeEvol

***** Part-time Research Technician at the Department of Cell & Developmental Biology, Med. Univ. Vienna *****

A part-time Research technician (30 hours/week) position is available in the group of Martin Kapun within the lab of Wolfgang Miller at the Department of Cell and Developmental Biology of the Medical University of Vienna. The main focus of our group research is deciphering how eco-evolutionary dynamics caused by host/microbe interactions between Drosophila and endosymbiotic Wolbachia bacteria affect the behavior and life history of the host. We are combining evolutionary genetics, molecular & cellular biology and microbiology in conjunction with cutting-edge NGS technologies.

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

This part-time post is expected to start June 15th, 2021 and is limited to one year.

The following responsibilities are expected from you:

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

Your profile:

We are looking for a highly organized and motivated candidate with good social and communication skills and practical experience in at least two of the three skills mentioned above, who is fitting the following profile: - Experienced technician with a Bachelor"£Âs degree in Evolutionary Biology, Genetics, Molecular Biology, or a related field - Excellent understanding of the theoretical and technical principles of common techniques in genetics and molecular & cellular biology. Experience with the Drosophila system will be highly valued - She/He should be willing to acquire further skills and contribute to the development of new analytic methods - Excellent written and spoken English skills; Computer know-how and experience in Microsoft Word, Excel and PowerPoint is essential

In case of interest, please contact either Martin Kapun (martin.kapun@meduniwien.ac.at) or Wolfgang Miller (wolfgang.miller@meduniwien.ac.at). The advertisement will be open until the position is successfully filled.

Martin Kapun <capoony@gmail.com>

Montpellier 1yrLabTech MicrobeEvolution

1-year laboratory technician position: Microbial ecology/ Microbiology/ Wetlab

In the ANR project E-SIASH we investigate spatial dynamics using microbes as model organisms. In this context, we are seeking a full time lab technician/ lab assistant for 1 year with experience in microbial ecology, microbiology and/or experimental evolution. We use experimental evolution (with the model organism Tetrahymena thermophila; e.g. Fronhofer et al. 2015,

Nature Commun.) to study life-history evolution and its consequences during experimental range expansions into abiotic gradients as well as eco-evolutionary dynamics of range expansions of communities. Ultimately, we want to understand the relative impact of abiotic gradients and species interactions on the ecological and evolutionary dynamics of species expanding their range.

Responsibilities of the lab technician include: - Overseeing and assisting in experimental evolution projects - Performing phenotyping assays to measure population growth - Entering and formatting data - Animal husbandry and media preparation - Ensuring normal day-to-day operations of the lab

Experience in a microbiology laboratory, working under sterile conditions, and familiarity with R is highly preferred. In addition, the qualified candidate will have excellent verbal and written communication skills (English; optimally also in French) and the ability to work accurately and with attention to detail.

The lab technician will work with Dr. Emanuel A. Fronhofer (https://www.emanuelfronhofer.net/) and his collaborators and is based at the Institut des Sciences de l' ÂEvolution de Montpellier (ISEM; http://www.isem.univ-montp2.fr/) and the University of Montpellier (UM; http://www.umontpellier.fr/), France. Montpellier offers a highly stimulating and international research environment, excellent research facilities and a lively and social working place. The University of Montpellier is ranked in the top 2 world-wide in ecology (Shanghai Ranking).

Applications should include a letter of motivation with a description of pertinent experience, a complete CV (incl. publication list), the names and e-mail addresses of two academic references, and copies of certificates of academic qualifications.

These documents should be uploaded to: https://bit.ly/3vfjAf9 Don' Ât hesitate to contact Emanuel Fronhofer (emanuel.fronhofer@umontpellier.fr) in case of questions.

Optimal starting date: Sept. 1 2021. The position is open until filled.

– Dr. Emanuel A. Fronhofer

Institut des Sciences de l'Evolution (ISEM, UMR 5554) | Universit Â Â de Montpellier (CC065) Place Eug Â Âne Bataillon | 34095 Montpellier Cedex 05 | France

+33 (0) 4 67 14 31 82 www.emanuelfronhofer.net emanuel.fronhofer@umontpellier.fr

Paris ResEngineer OriginOfSarsCoV2

Dear colleagues,

We are recruiting a "Research Engineer" (with a scientific PhD) in bioinformatics and molecular evolution for 1 year, with possible renewal of 1 year.

The last intermediate step between a non-human animal virus and the current human SARS-CoV-2 is still a major enigma. More precisely, i) the evolution from the ancestral (very likely bat) virus to the human strain, ii) the transport from tropical Yunnan bat caves to Wuhan more than 1000 km away, and iii) the contamination of the first human, are three distinct aspects of the proximal origin on which we have little to no information. Each aspect could, in various proportions, result from contributions due to natural, accidental or intentional mechanisms. Determining these contributions requires an observation-based scientific approach free of a priori.

We propose a state-of-the-art analysis of the available sequences of SARS-CoV-2 and related viruses, to examine whether the identity of the virus (bat-adapted/human-adapted, natural/artificial) has changed across generations. The expected outputs of this work are not only scientific publication(s), but more importantly scientific insights on the origin of the ongoing pandemic and therefore hints on how to prevent a future pandemic.

The work will be organized in order to develop open science bioinformatic tools in order to allow the inclusion of new sequence data in the analysis when available. We will investigate both small-scale and large-scale changes: synonymous and non- synonymous mutations, insertions/deletions of small or large sequence pieces, and finally recombinations of fragments from different viruses, as recombination is a key mechanism of coronavirus evolution.

The recruited engineer will share her/his working time between the Université $de Paris main Campus (V. Courtier; IJM and F. Graner, MSC) a$ $depth molecular evolution analysis of the relevant accessible SARS viral$

The ideal candidate (1) will be familiar with concepts of molecular evolution (i.e. phylogeny, detection of recombination, ratio of non-synonymous/synonymous mutations, codon usage, etc.) and (2) will have skills in computer programming (e.g. python 3, R and/or C language).

Salary: around 2 500 euro /month with taxes (~1 925 euro after taxes). The exact salary will depend on the candidate's experience.

Starting date: September 2021.

Application deadline: May 23th 2021. Later applications might be considered.

To apply, send a letter of motivation and a scientific CV to virginie.courtier@ijm.fr and guillaume.achaz@mnhn.fr. Furthermore, at least one mentor of the candidate should send a letter of recommendation directly to the same addresses.

- – Guillaume Achaz - Homo sapiens http://bioinfo.mnhn.fr/abi/people/achaz/ - Je connais une planète oÃ¹ il y a un Monsieur cramoisi. Il n'a jamais respiré une fleur. Il n'a jamais regardé une étoile. Il n'a jamais aimé personne. Il n'a jamais rien fait d'autre que des additions. Et toute la journée il répète comme toi: "Je suis un homme sérieux! Je suis un homme sérieux!" et ça le fait gonfler d'orgueil. Mais ce n'est pas un homme, c'est un champignon! - Un quoi? - Un champignon! Le petit prince était maintenant tout pâle de colère. - Il y a des millions d'années que les fleurs fabriquent des épines. Il y a des millions d'années que les moutons mangent quand même les fleurs. Et ce n'est pas sérieux de chercher à comprendre pourquoi elles se donnent tant de mal pour se fabriquer des épines qui ne servent jamais à rien? Ce n'est pas important la guerre des moutons et des fleurs? Ce n'est pas sérieux et plus important que les additions d'un gros Monsieur rouge? Et si je connais, moi, une fleur unique au monde, qui n'existe nulle part, sauf dans ma planète, et qu'un petit mouton peut anéantir d'un seul coup, comme ça, un matin, sans se rendre compte de ce qu'il fait, ce n'est pas important ça?

Guillaume Achaz <guillaume.achaz@mnhn.fr>

RoyalBotanicGardens Kew 3 Leaders

Scientific Priority Leader jobs at the Royal Botanic Gardens, Kew

The Royal Botanic Gardens, Kew is seeking to hire three new Scientific Priority Leaders, each responsible for driving our scientific agenda within a major area of research in accordance with our Science Strategy (Accelerated Taxonomy; Digital Revolution; and Unlocking Properties).Each Priority Leader will define, establish and

deliver major initiatives within their priority area; manage 4-8 research teams (collectively comprising up to 60 staff) assigned to their priority; and participate in RBG Kew???s senior scientific leadership team. They will contribute to the overall direction of RBG Kew???s scientific work, and nurture a culture of excellence, innovation and openness within their team and across the organisation. Salary: ??61,500 - ??73,439 per annum, depending on skills and experience. Closing date: 13 June. For further details, see https://careers.kew.org/vacancy/-priority-leader-x3-445385.html Dr Rhian J Smith

Senior Science Editor |Kew Science| Research Coordinator |Antonelli Research Group at Kew|

Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AE www.kew.org/science |https://antonelli-lab.net/ The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

Any views expressed in this email do not necessarily reflect the opinions of RBG Kew.

Rhian Smith <Rhian.Smith@kew.org>

SaintMarysU Canada PlantEvolutionaryBiologist

Tenure-Track Position

Assistant Professor in Biology: Plant Ecologist or Plant Evolutionary Biologist

The Department of Biology at Saint Mary's University (SMU) invites applications for a full-time, tenure-track faculty position at the rank of Assistant Professor to commence as early as January 1st, 2022. We are seeking applicants with research expertise in Plant Ecology or Plant Evolutionary Biology. Preference will be given to candidates combining field work with laboratory-based molecular or biochemical analyses to address their research questions. The candidate will support our undergraduate curriculum by teaching courses in Plant Biology, Ecology and Evolution, and potentially developing courses in their areas of research specialization.

Saint Mary's University is located in the historic port city of Halifax, Nova Scotia, a vibrant, urban community of over 430,000 people. Halifax is a major educational center for Atlantic Canada and is home to five universities. It is conveniently located to recreational areas and

to other major urban centers in Canada and the Northeastern United States. The Faculty of Science, which houses the Department of Biology, has gone through significant renewal, with many new and active faculty involved in teaching, research, and service activities. We are working to establish and build upon areas of distinct research strength and through those foster collaborations locally, regionally, and internationally.

At Saint Mary's University equity and diversity are integral to excellence and enrich our community. As an institution committed to fostering an environment of inclusion and respect, we welcome applications from women, Indigenous peoples, racialized persons/visible minorities, persons with disabilities and others who might contribute to the growth and enrichment of our community. All qualified candidates are encouraged to apply; however, preference will be given to Canadian citizens and permanent residents. If you require accommodations during the recruitment process, please contact Human Resources at hr@smu.ca.

The successful candidate must hold a Ph.D. in Biology and provide evidence of a strong research record or an emerging scholarly profile, have a record of a high standard of teaching in the field (preferably in the courses noted above), and have a strong commitment to collegial service. Qualified candidates must submit an application package consisting of:

i) A cover letter outlining how the applicant's background aligns with the desired qualifications, and which of the Department's current course offerings the applicant would most like to teach

ii) An up-to-date curriculum vitae

iii) A research statement including: i) A summary of the applicant's three most significant contributions to research (publications/presentations/reports/patents on a specific subject can be grouped into one contribution; maximum of 2 pages), ii) A short-term (5 years) and longer-term research plan (maximum of 2 pages)

iv) A teaching dossier that includes evidence of teaching effectiveness with student evaluations of past teaching (if available)

v) The names, addresses, and email contacts of three persons that are best able to describe your suitability for this position

The complete application should be sent as a single file in .pdf format to: Dr. Laura Weir Department Chair, Biology Department, Saint Mary's University, 923 Robie Street, Halifax, Nova Scotia, B3H 3C3, email: Laura.Weir@smu.ca. Complete applications must be received on or before July 15th, 2021. Only those selected

for an interview will be contacted.

All applicants also need to contact the Biology Department secretary at biology@smu.ca to request SMU's "Self-Identification Questionnaire". Once complete, the form should be emailed to SMU's Diversity and Inclusion Advisor, Ms. Deborah Brother-Scott- deborah.brothers-scott@smu.ca. Section I of this form is mandatory and relates to citizenship. The University must comply with federal government requirements regarding recruitment of foreign academics and give priority to qualified Canadian Citizens and permanent residents, whether in Canada or abroad. Section II is the voluntary self-identification information. The chair of the search committee only confirms the applicants' Canadian citizenship/permanent residency status with Ms. Brother-Scott.

Link: https://www.smu.ca/webfiles/Approved-Ap92021PlantEcologistorEvolutionaryBiologistTTJobAd.pdf
 Anne Dalziel <Anne.Dalziel@smu.ca>

StonyBrookU TeachingEvolution

Lecturer 10-Introductory Biology Department of Ecology & Evolution, College of Arts & Sciences, Stony Brook University

Description

The Department of Ecology and Evolution at Stony Brook University invites applications for a one-year non-tenure-track position at the rank of Lecturer. The lecturer position is anticipated to start in Fall 2021, for one year (10 month) temporary, renewable contract.

The successful candidate will co-teach active-learning sections of an introductory biology course (BIO 201 Organisms to Ecosystems) and work with undergraduate and graduate student teaching assistants. The successful candidate may also be asked to teach additional courses in areas such as evolution, genomics, and human genetics. Descriptions of the department's faculty and current facilities may be found at http://-www.stonybrook.edu/commcms/ecoevo/ . Preference will be given to candidates with knowledge of and/or experience with: implementing active learning in collaborative group settings, working with undergraduate and/or graduate teaching assistants, using Vision and Change in Undergraduate Biology (AAAS 2011) to guide instruction, addressing student misconceptions, teaching with educational technology, and aligning instruction

with equity and diversity goals.

Qualifications

Required Qualifications: Doctoral degree in ecology, evolution, biology education, or a closely related field. Experience teaching undergraduate biology majors and/or non-majors using active learning methods.

Preferred Qualifications: Experience addressing scientific misconceptions. Experience teaching in-person and/or online courses. Experience using educational technology (e.g., Blackboard, Google apps) to facilitate student learning. Experience using virtual conference technology (e.g., Zoom) to facilitate student learning. Experience working with undergraduate and/or graduate teaching assistants. Enthusiasm for innovative teaching approaches in large introductory biology courses. Familiarity with Vision and Change in Undergraduate Biology (AAAS 2011). Knowledge of and/or experience implementing collaborative learning. A strong commitment to equity and diversity in undergraduate education.

Application Instructions Those interested in this position should submit a cover letter indicating their interests and goals, curriculum vitae, a statement of teaching experience, and a diversity statement through Interfolio apply.interfolio.com/86510. Applicants should provide contact information for three confidential letters of recommendation to be submitted on their behalf to Interfolio. Finalists for the position will be asked to present a 30-minute teaching demonstration. Applications are due June 3, 2021.

The selected candidate must successfully clear a background investigation.

In accordance with the Title II Crime Awareness and Security Act, a copy of our crime statistics is available upon request by calling (631) 632-6350. It can also be viewed online at the University Police website at http://www.stonybrook.edu/police . Stony Brook University is committed to excellence in diversity and the creation of an inclusive learning, and working environment. All qualified applicants will receive consideration for employment without regard to race, color, national origin, religion, sex, pregnancy, familial status, sexual orientation, gender identity or expression, age, disability, genetic information,veteran status and all other protected classes under federal or state laws.

If you need a disability-related accommodation, please call the university office of institutional diversity and equity at (631) 632-6280.

Robert Thacker <robert.thacker@stonybrook.edu>

Sweden ProfessorBergianusChairInBotany

One of the oldest endowed Chairs in Sweden, and at the same time one of the most well-funded, is currently open - Professor Bergianus in Botany, at the Royal Swedish Academy of Sciences.

The position as Professor Bergianus is broadly defined as in botany. This may include, but is not limited to, research directions in systematics, biogeography, ecology, evolution, population genetics, and paleobotany. The successful candidate should have a very strong research profile within the field of botany, defined as above. The position will be placed at the Department of Ecology, Environment and Plant Sciences at Stockholm University.

Please see www.kva.se/bergianus for the full advertisement.

Deadline for application is June 21, 2021.

Hans Ellegren Vice-President, Royal Swedish Academy of Sciences

Hans Ellegren <hans.ellegren@ebc.uu.se>

TowsonU LecturerEvolution

Lecturer, Zoology and Biology Department of Biological Sciences The Jess and Mildred Fisher College of Science and Mathematics

Position: The Jess and Mildred Fisher College of Science and Mathematics invites applications for a non-renewable, non-tenure track, 10-month Lecturer in the Department of Biological Sciences beginning August 2021.

Qualifications: M.S. in Biology or a related field. Possess a strong commitment to excellence in teaching.

Responsibilities: Teach three 4 credit courses per semester which will include a lower level General Zoology lecture and associated lab, and either a non-majors general biology course (BIOL 120) or an upper level course depending on area of expertise and departmental

needs.

Towson University: Founded in 1866, Towson University is now recognized by U.S. News & World Report's as one of the top public universities in the Northeast and Mid-Atlantic regions. Towson is nationally recognized for its programs in the liberal arts and sciences, business, education, communications, health sciences, and the fine and performing arts. The University places a strong emphasis on service learning and civic engagement through such activities as internships, practica, clinical placements, course assignments and student events. As the Baltimore area's largest university and Maryland's Metropolitan University, Towson articulates its research and scholarship mission through partnerships that link the University to the economic, educational and cultural life of the state of Maryland and the mid-Atlantic region. Towson enrolls more than 21,800 undergraduate and graduate students in 64 undergraduate majors, 44 master's programs and four doctoral programs. Located on a rolling 328 acres, the striking campus is eight miles north of downtown Baltimore and 45 miles from Washington, D.C. The campus and its surrounding cities provide an excellent environment for teaching and supporting the academic pursuits of the 830 full-time faculty who work here.

Application Process: Review of applications will begin immediately and continue until position is filled. Send, electronically, a letter of application describing qualifications, a CV and a teaching statement describing previous teaching experience, and have two letters of reference sent to:

Ms. Brandi Mayo, Administrative Assistant Department of Biological Sciences Towson University 8000 York Road Towson, MD 21252-0001 Email: bmayo@towson.edu

Electronic submissions only

Questions about the position should be addressed to the search committee chair, Dr. Vanessa Beauchamp, vbeauchamp@towson.edu

Official copies of undergraduate and graduate transcripts, as well as a Criminal Background Investigation is required for the hired candidate and the results may impact employment.

Please be sure to visit http://www.towson.edu/odeo/-employment/resources/data.html to complete a voluntary on-line applicant data form. The information you provide will inform the university's affirmative action plan and is for statistical-related purposes only. The information will not be used for any other purpose. Please note that the search number for which you have applied is: *****

Towson University is an equal opportunity/affirmative action employer and has a strong institutional commitment to diversity. Women, minorities, persons with disabilities, and veterans are encouraged to apply.

Steve Kimble

Clinical Assistant Professor, Towson University

skimble@towson.edu

https://www.towson.edu/fcsm/departments/-biology/facultystaff/skimble.html "Kimble, Steven" <skimble@towson.edu>

UCalifornia SanDiego TeachingEvolution

Assistant, Associate, or Full Professor in Biological Sciences (Advancing Faculty Diversity) The Division of Biological Sciences at the University of California, San Diego (www.biology.ucsd.edu) is seeking applications from outstanding research faculty at assistant, associate, and full levels. UC San Diego is forging a new paradigm for engagement and collaboration between STEM/Public Health/Health Sciences and the Social Sciences/Arts & Humanities (https://af-amstudies.ucsd.edu/faculty-recruitment/index.html). This faculty line is one of 13 ladder-rank faculty positions that unites STEM/Public Health/Health Sciences departments and African American and the Black Diaspora Studies through innovative research, coordinated teaching, and targeted service. Faculty will have multiple opportunities to engage with scholars across UCSD disciplines to address issues of race and racism, access and equity, and social and political influences focused on STEM/Public Health/Health Sciences, while also working within their home departments and professional communities.

Faculty holding these positions will be expected to design and teach undergraduate courses that align with the African American Studies Minor (AASM). They may also demonstrate the equivalent through service to the AASM and by mentoring undergraduate students. We seek candidates whose research, teaching, and/or service advance anti-racism, anti-oppression, equity, and justice in STEM/Public Health/Health Sciences. We welcome candidates whose experiences have facilitated their understandings of traditionally underrepresented racial minority communities. Faculty are expected to have an inclusive stance on mentoring and advising that

incorporates working with women and underrepresented racial minority undergraduate and graduate students.

All candidates must have earned a Ph.D. or equivalent degree, and be pursuing innovative research in areas aligned with one of the four Sections within the Division of Biological Sciences (see below). In addition to excellence and creativity in biological research and scholarship, successful candidates must have demonstrated commitment to equity and inclusion at the undergraduate and/or graduate levels. We are especially interested in candidates who have created or contributed to programs that aim to increase access and success of underrepresented students and faculty in the sciences. Tenured candidates must demonstrate strong leadership skills.

The Division of Biological Sciences at UC San Diego is a renowned center of scientific discovery, innovation, and collaboration. Our large research base spans many areas of biology and has one of the most vibrant graduate programs in the country. We are committed to both academic excellence and diversity within the faculty, staff, and student body.

The Four Sections in the Division of Biological Sciences include:

Cell & Developmental Biology: Areas of study include mechanistic analysis at multiple levels of: cell structure and function, the developmental biology of multicellular organisms, cutting-edge investigations into plant biology, and pathogenesis. Ecology, Behavior, & Evolution:Areas of study are focused on investigating ecological and evolutionary processes operating at the level of individuals, populations, species, and communities. Molecular Biology: Areas of study include the mechanisms of gene expression and function at the cellular and organismal levels, the study of normal and pathogenic microbes, and the study of immunology.

Neurobiology: Areas of interest include multi-level analysis of brain circuits, neural networks, sensory receptors, neurotransmitter regulation, and computational models of behavior.

Strong candidates will have a research agenda easily related to factors of race/ethnicity, as well as previous experiences teaching, mentoring, and supporting the advancement of underrepresented racial minority students, and a record of service activities that promote diversity, equity, and inclusion. Strong candidates will also have experience with or the desire to engage in interdisciplinary conversations and scholarship across UCSD disciplines.

Salary is commensurate with qualifications and based on University of California pay scales.

Review of applications will commence on June 30, 2021 and will continue until all positions have been filled or close on May 5, 2022. Interested applicants must submit a cover letter, curriculum vitae, statement of research, statement of teaching, a statement describing their past leadership experience in fostering equity and diversity and/or their potential to make future contributions, and 3-5 publications. Applicants at the Assistant Professor level need to submit 3-5 references, and applicants at the Associate or Full Professor level need to provide

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UC London Fellowship EvolutionaryBiology

Research Career Development Fellowships: Expression of Interest for 2021 Research Department of Genetics, Evolution and Environment/Division of Biosciences, London, Grade 8 Salary (inclusive of London allowance) 44,737 - 52,764 per annum

Duties and Responsibilities The Research Department of Genetics, Evolution and Environment, (GEE) at University College London (UCL) invites Expressions of Interest from Early Career Researchers (ECRs) who wish to be sponsored for external fellowships to establish an independent research group. Successful candidates will be of the highest calibre, able to demonstrate an exceptional track record in relation to their career stage, and have the potential to submit competitive fellowship applications.

GEE offers a world-class, interactive and support research environment within the Division of Biosciences at UCL. We are strongly committed to recruiting and supporting the most promising ECRs who choose to secure a Group Leader Fellowship as their route to becoming a Principal Investigator. This policy applies to senior fellowships such as Wellcome Trust Henry Dale, MRC CDA, BBSRC David Phillips, NERC IRF, UKRI FLF, Royal Society URF, CRUK, ERC Starting Grants and equivalent fellowships. We provide support to ensure that fellows can successfully establish their own research group, have opportunities to gain teaching skills and play a full role in the running of the department. Our

commitment starts with academic and administrative support at the application and interview stages and continues throughout the tenure of the fellowship, with regular career development and mentoring programmes. We expect fellows to develop into strong candidates for Principal Investigator positions in the department or elsewhere. In line with this ethos, a large proportion of our past departmental fellows have progressed to permanent positions in GEE.

Areas of Research Interest

The GEE is organised into six Centres, with cross-cutting research interests, and close links with other organisations, including the Francis Crick Institute, the Natural History Museum, and The Zoological Society of London.

We especially welcome expressions of interest from ECRs with a strong track record in the following areas:

Institute of Healthy Aging: Ageing, age-related disease; interventions improving late-life health in model systems (e.g. cellular senescence); applying computational approaches to ageing and late-life disease (AI, big data, medical genomics).

Centre for Biodiversity and Environment Research: Nature's contributions to people (ecosystem services); community and/or behavioural ecology (especially relating to plants, insects and/or microbes).

Centre for Life's Origins and Evolution: Origins and early diversification of the animals; comparative genomics; evolution of cell types; invertebrate palaeontology.

UCL Centre for Computational Biology: Big data and computation; computational genomics; computational phylogenomics,

UCL Genetics Institute: Computational approaches to biology or medicine; computational tool development and applying them to genomic data; high-throughput bioinformatics, statistical genetics; metagenomics.

UCL East Nature Smart Centre: Cross-disciplinary solutions hub bringing together expertise from ecology, computer science, public health, built environment and social science to gather evidence on how we can best manage our natural resources for a sustainable and resilient future.

Commitment to Equality and Diversity We strongly encourage applications from women, disabled candidates, and those from an ethnic minority from the UK and internationally as part of our ongoing commitment to equality, diversity, and inclusion.

Further information and details for how to apply can be found here: https://www.ucl.ac.uk/biosciences/gee/-independent-fellowships Fiona Williamson Executive Assistant to Professor Chris Thompson, Head of Research Department Genetics Evolution & Environment University College London Room 111, Darwin Building Gower Street London WC1E 6BT

E: f.williamson@ucl.ac.uk

"Williamson, Fiona" <f.williamson@ucl.ac.uk>

UGuelph PlantEvolution

Position Title / Rank: Assistant Professor in Plant Ecology or Plant Evolution College: College of Biological Science Department: Integrative Biology Deadline: June 1, 2021 or until a suitable candidate is found

Position Description: The Department of Integrative Biology at the University of Guelph invites applications for a tenure-track position at the Assistant Professor level in the area of Plant Ecology and/or Plant Evolution.

A Ph.D. and relevant postdoctoral experience in plant ecology or evolution will be required, along with evidence of strong potential to establish a productive, externally-funded research program, including effective mentorship of graduate students. The successful candidate will pursue mechanistic, hypothesis-driven research in plant biology and may employ any number of research approaches, ranging from comparative to experimental studies in natural or human-managed field environments and in controlled-environment or lab settings. We welcome applications from candidates doing research in any area of plant ecology, plant evolutionary biology, and plant systematics, including, but not limited to, ecological and evolutionary responses to climate change and/or other anthropogenic effects on the environment, evolutionary processes responsible for the origins and diversification of plant biodiversity, the conservation and function of plant biodiversity, causes and consequences of plant invasions, and the ecology and/or evolution of plant interactions with competitors, herbivores and mutualists. The successful candidate will also demonstrate a commitment to effective and evidence-based teaching at the undergraduate level. The successful candidate will contribute to teaching in the Department' Âs organismal plant biology curriculum, which includes courses in plant diversity and systematics, plant evolution, and plant ecology, and contribute to teaching other ecology-and/or evolution-themed courses.

The successful candidate will be joining a dynamic, multidisciplinary department with ˜35 faculty and an excellent record in research in physiology, evolutionary biology, ecology, conservation biology, and biodiversity, encompassing a wide range of taxa and levels of biological organization from molecules to ecosystems. The successful candidate will have access to facilities and resources unique to the University of Guelph, including the Phytotron, the Herbarium, the Arboretum, and multiple field research sites.

In the Department of Integrative Biology, we value diversity and inclusivity because we know that diversity in experiences and perspectives is vital to advancing innovation, critical thinking, complex problem solving, and the creation of a modern, representative academic community. The Department is committed to developing and maintaining a culture that is positive, collegial, and respectful of all members, and in which wellness and healthy work-life balance are valued along with (and indeed, contribute to) excellence in research and teaching. To develop an inclusive and vibrant departmental culture, the Department maintains standing committees focused on Equity, Diversity, and Inclusion and Mental Health and Wellness and has developed specific recommendations for faculty hiring that incorporate these important issues.

The University of Guelph is the third largest employer in Guelph, a city of approximately 130,000 people, located about an hour drive west of Toronto, Ontario. University of Guelph is a top-ranked comprehensive university in Canada with an enrolment of over 30,000 undergraduate and graduate students across over 40 academic units. The University is known for its commitment to student learning, innovative research, and collaboration with world-class partners. It is a unique place, with transformative research and teaching and a distinctive campus culture. People who learn and work here are shaped and inspired by a shared purpose: To Improve Life. Reflecting that shared purpose in every experience connected to our university positions us to create positive change, here and around the world. Our University community shares a profound sense of social responsibility, a drive for international development, and an obligation to address global issues.

This position is one of several positions being advertised simultaneously in the Integrative Biology department and across the university.

Application Process Assessment of applications will begin June 1, 2021 and will continue until the position is filled. Interested applicants should submit the following materials: (1) cover letter; (2) curriculum vitae; (3) research statement; (4) teaching statement; (5) diversity statement, (6) three publications (preferably first-authored) that are representative of prior work, and (7) names and contact information of three references.

The research statement (2 pages max) should present a vision of the long-term goals of the research program as well as several short-term

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ULisbon ResTech PlantEvolution

A full-time Research Technician position is available within an ERC consolidator grant at the laboratory of Sara Magalhāes (https://mitesquad.weebly.com/) at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/), University of Lisbon, Portugal.

The candidate is expected to have a Master degree in Biology, to be fully independent in organizing his/her work. Preference will be given to candidates with experience in plant biology and/or in molecular techniques (DNA extraction for Next Generation Sequencing, diagnostic PCRs and qPCRs)

We are especially seeking a candidate who enjoys working in a group, respects the lab tidiness and appreciates learning tasks.

Applicants should follow the procedure in the following link: http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=135039   In case of doubt, please contact us at snmagalhaes@fc.ul.pt.

Application deadline: June 8, 2021 Starting date: flexible (ideally September 2021). Duration: 6-months with the possibility of an extension until the end of project. Place: Faculdade de Ciências da Universidade de Lisboa. Project title: Competition under niche construction (COMPCON) Funding: ERC Consolidator Grant.

Sara Magalhāes, Assistant Professor, https://mitesquad.weebly.com/ Centre for Ecology, Evolution and Environmental Changes http://ce3c.ciencias.ulisboa.pt/ Faculdade de Ciencias da Universidade de Lisboa http://www.fc.ul.pt/

Campo Grande Lisboa researcher ID: http://www.researcherid.com/rid/B-9673-2012 Sara Magalhaes <snmagalhaes@fc.ul.pt>

UMainz EvolutionaryEcology

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

The Institute of Organismic and Molecular Evolution (iomE) at the Faculty of Biology invites applications for the position of a University Professor of Evolutionary Ecology beginning at the earliest possible date.

Salary grade W 3 LBesG | Civil servant (tenured)

Tasks and expectations:

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

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

Requirements:

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

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

What we have to offer:

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

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

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

Disabled candidates with adequate qualification will be given priority. The interview symposium is tentatively planned for July 2021.

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

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

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

UPortsmouth TerrestrialEvolutionaryEcol

Lecturer or Senior Lecturer in Terrestrial (Evolutionary) Ecology -School of Biological Sciences, University of Portsmouth, UK

We seek an academic with a proven track record in Terrestrial Ecological research. As a senior lecturer the applicants should have a recognized HE teaching qualification (or equivalent experience) and have experience in coordinating both teaching and research. We would be particularly interested in applications from individuals able to contribute to the teaching of plant biology and interact productively with the evolutionary ecology research group within the School.

The successful candidate will have a proven track record of educating and supporting students at both undergraduate and postgraduate level.

The School is committed to promoting a fair, inclusive and diverse workplace. We offer a range of family friendly and flexible working practices alongside inclusive employment policies.

Closing date is 16 June for applications, interview is on 8 July 2021. Due to the current situation it is anticipated that recruitment will take place online; there will be a video submission task prior to the presentation/interview date.

For informal enquiries about the post, please contact (by email in the first instance) Dr. Darren Mernagh, Head of School - Darren.mernagh@port.ac.uk

Please see https://port.engageats.co.uk for additional details about the position and how to apply.

WS Armbruster University of Portsmouth, UK & University of Alaska Fairbanks, USA

W Scott Armbruster <wsarmbruster@alaska.edu>

Vienna TechAssist HostMicrobeEvolution

Full-time Research Technician (40 hours/week)

at the Department of Cell & Developmental Biology, Med. Univ. Vienna

A full-time Research technician (40 hours/week) position is available in the group of Wolfgang Miller at the Department of Cell and Developmental Biology of the Medical University of Vienna. The main focus of our group research is deciphering host'Vmicrobe evolution and interactions between Drosophila, endosymbiotic Wolbachia bacteria and other selfish genetic elements. We are combining genetics, molecular & cellular biology and microbiology in conjunction with cutting-edge NGS technologies.

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

This full-time post is expected to start June 15st, 2021 and is limited for 1-year with the possibility for further extension depending on successful evaluation.

The following responsibilities are expected from you:

1. Molecular genetics and cellular analyses, including isolation of DNA, RNA and proteins; standard, diagnostic and RT-PCR, primer design, NGS library preparation, cDNA synthesis and preferentially FISH and ISH techniques

2. Drosophila stock keeping, typing and crossing of sensitive lines

3. Lab organization and management

Your profile:

We are looking for a reliable, highly organized and motivated candidate with good social and communication skills and practical experience in at least three of the four skills mentioned above, who is fitting the following profile: - Experienced technician with a Bachelor'Âs degree in Biology, Genetics, Molecular Biology, or a related field

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

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

- Excellent skills in time management and lab organization and supervising undergraduates - Excellent written and spoken English skills; Computer know-how and experience in Microsoft Word, Excel and PowerPoint is essential

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

The advertisement will be open until the position is successfully filled. For further information please visit the Lab page: https://anatomieundzellbiologie.meduniwien.ac.at/group-miller Wolfgang J. Miller, PhD Lab Genome Dynamics, Dept Cell & Developmental Biology Center of Anatomy and Cell Biology, Medical University of Vienna,

Schwarzspanierstr. 17, Bauteil C, Hochparterre, Raum 36 A-1090 Vienna

AUSTRIA.

email: wolfgang.miller@meduniwien.ac.at

https://anatomieundzellbiologie.meduniwien.ac.at/group-miller Tel. 0043 1 40160 37750

Wolfgang Miller <wolfmanmiller@yahoo.com>

Other

Biodiversity CallForProposals FRB-CESAB

Dear Sir, madam,

I am contacting about the launch for the call for proposals on biodiversity in the netropical realms, that I think could be of interest for you. The call is organized by the CEntre for the Synthesis and Analysis of Biodiversity of the French Foundation for Biodiversity Research (FRB-CESAB < https://www.fondationbiodiversite.fr/en/about-the-foundation/le-cesab/ >), the Brazilian Synthesis Center on Biodiversity and Ecosystem Services (SinBiose < http://www.sinbiose.cnpq.br/web/sinbiose >), the Sāo Paulo Research Foundation (FAPESP < https://fapesp.br/en >) and the French Laboratory of Excellence CEBA < http://www.labex-ceba.fr/en/ > (CEnter for the study of Biodiversity in Amazonia).

Two projects will be selected and funded for a period of three years, including: the recruitment of a post-doctoral fellow based in Brazil and working on the project for two years, the organization of four meetings (two in France,

at CESAB in Montpellier and two in in Brazil in the state of Sāo Paulo) and the promotion and publication of the results. Logistical, technical and administrative support will also be provided.

The submitted projects can be in the fields of natural sciences and/or social and human sciences and should aim at developing the synthesis of ideas and concepts and/or the analysis of existing data. The call is restricted to terrestrial biomes only (i.e., excluding marine biology) and to tropical South America, Central America and/or Caribbean Islands.

Pre-proposals deadline: 30st July 2021, 12 :00 CEST

More information: https://www.fondationbiodiversite.fr/en/calls/appel-a-projets-synergy-frb-cesab-sinbiose-fapeps-ceba-la-biodiversite-neotropicale/ Don't hesitate sharing it to your colleagues!

Many thanks, Marie-Claire

[signature_701717591]

Marie-Claire Danner

SCIENCE OFFICER

IPBES TSU FOR THE ASSESSMENT OF SUSTAIN-

ABLE USE OF WILD SPECIES

CHARGÃE DE COMMUNICATION

CESAB (CENTRE DE SYNTHÃSE ET D'ANALYSE SUR LA BIODIVERSITÃ)

+33 (0)6 71 66 46 58

Siège de la FRB : 195, rue Saint-Jacques 75005 PARIS

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

Eelpout samples

Dear EvolDir community,

We are seeking eelpout (fish in the family Zoarcidae) samples for genome sequencing and comparative genome biology. We are specifically interested in samples from non-polar latitudes (roughly $60Å^oN$ to $60Å^oS$). Since we plan to do long-read sequencing (e.g., PacBio), it is important that samples have been sufficiently stored for extraction of high-molecular weight DNA. For instance, a flash frozen tissue that has been stored at $-80Å^o$is ideal.

We have funding to cover shipping costs, sample prep, and sequencing. We would also welcome those with tissues as collaborators on manuscripts. If you have tissue(s) you'd be willing to share or other ideas for how we can obtain them, please email Joanna Kelley at joanna.l.kelley@wsu.edu.

Thank you!

Joanna L. Kelley, PhD Associate Professor, School of Biological Sciences Washington State University joanna.l.kelley@wsu.edu   509-335-0037   http://labs.wsu.edu/genomes   "joanna.l.kelley@wsu.edu" <joanna.l.kelley@wsu.edu>

EvolutionaryEcolJ CallForPapers

Call For Papers for Special Issues / Topical Collection

1. CALL FOR PAPERS: Infectious disease: the ecological theatre and the evolutionary play Submission Deadline: July 31, 2021 | Expected 2022

2. CALL FOR PAPERS: The ecological and evolutionary implications of allometry Submission Deadline: August 31, 2021 | Expected 2022

3. CALL FOR PAPERS: Mimicry beyond natural selection on colour Submission Deadline: October 31, 2021 | Expected 2022

4. CALL FOR PAPERS: Fitness Effects of Mutations Submission Deadline: November 1, 2021 | Expected 2022

Featured Papers

1. Featured Paper: Supergroup F Wolbachia in terrestrial isopods: Horizontal transmission from termites? Freely accessible until May 31, 2021

2. Featured Paper: EyeÂ©\body allometry across biphasic ontogeny in anuran amphibians Open Access

3. Virtual Archive of Past Featured Papers (2018 - 2021)

Latest TOC

1. Volume 35, issue 2, April 2021

Author Services

1. Students & Early Career Researchers Incentive 2. In Review: Evolutionary Ecology'Âs Preprint Service 3. Evolutionary Ecology TOC Alerts

Social Media

1. Evolutionary Ecology journal dedicated Twitter account: https://twitter.com/evoecology Takeesha Moerland-Torpey Associate Editor | Medicine and Life Sciences - Journals Ecology and Conservation Springer Nature P.O. Box 17, 3300 AA Dordrecht, The Netherlands T +31 (0)78 657 6227 Takeesha.Moerland-Torpey@springernature.com www.springer.com www.springeropen.com Springer Nature is a leading research, educational and professional publisher, providing quality content to our communities through a range of innovative platforms, products and services. Every day, around the globe, our imprints, books, journals and resources reach millions of people ÂC helping researchers, students, teachers & professionals to discover, learn and achieve.

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Takeesha   Moerland-Torpey   <Takeesha.Moerland-Torpey@springer.com>   Takeesha   Moerland-Torpey <Takeesha.Moerland-Torpey@springer.com>

France)

christian.rellstab@wsl.ch

JMolEvol ClassicPapers

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

forsdyke@queensu.ca

Online EvoltreeSeminarSeries StephenPalumbi

EVOLTREE Online Seminar Series on Adaptation to Climate Change

The last seminar of the series will be held by Stephen Palumbi on 12th May 2021, 16:30-18.00 CEST. He will talk about "Ocean species and their capacity to adapt to climate change ? stories from corals and caves".

More information: http://www.evoltree.eu/index.php/-8-news/news-left/181-evoltree-online-seminar-series-2021-on-adaptation-to-climate

Registration: https://www.eventbrite.co.uk/e/evoltree-online-seminar-series-on-adapting-to-climate-change-tickets-148236899557   Seats in the live sessions are limited to 150. All seminars are recorded and available on the EVOLTREE YouTube channel afterwards (https://www.youtube.com/channel/-UCla0sRglK9UUPYp5Ks8hwFA).

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

Online SeminarSeries MarineOmics

Starting on May 7 at 11a US CST is a new virtual seminar series through the MarineOmics working group and the RCN for Evolution in Changing Seas. The MarineOmics working group was assembled to promote reproducible and robust genomic research in evolutionary biology and marine science.

The biweekly series will have virtual Q & A panel seminars with 3-5 experts on topics ranging from GBS/RADseq, population genomics with whole genome sequencing, and transcriptomics. Panelists will discuss each topic, with questions coming from the working group and the audience. Seminars are every two weeks, on Fridays from 11:00am-12:15pm US Central Time. The first panel seminar on GBS/RADseq is at 11am CST on Friday May 7.

For more information on the seminar series and to register for talks, please visit the website:

https://marineomics.github.io/   Katherine Silliman, Ph.D. Postdoctoral Fellow School of Fisheries, Aquaculture, and Aquatic Science Auburn University https://-ksilliman.weebly.com/ ksil91@gmail.com

Passing Marty Tracey

Dear colleagues,

Friends and colleagues mourn the passing of population geneticist, Martin L. Tracey, on February 23, 2021. Marty was born in Brookline, MA, March 3, 1943. He received his PhD under the supervision of Professor Masatoshi Nei, then at Brown University, where he developed a life-long interest in the roles of sex chromosomes and mating behavior in speciation. He did postdoctoral research at the University of California Davis, first with Professor Francisco J. Ayala, where he contributed to an understanding of genetic divergence during the speciation process in the Drosophila willistoni group, and then with Professor Robert A. Shleser, where, at the Bodega Marine Laboratory, he did seminal

work on the genetics of marine invertebrates. He held faculty positions at Brock University and at Florida International University. Over the last two decades of his career, he developed a strong interest in the use of DNA as forensic evidence and served as an expert witness in hundreds of cases.

Dennis Hedgecock, John McDonald, and Phil Hedrick dhedge@usc.edu (Dennis Hedgecock)

SMBE FacultyAwards CallForNominations DeadlineMay15

Dear SMBE Members:

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

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

SMBE Early-Career Excellence Award

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

SMBE Mid-Career Excellence Award

This award is intended for outstanding members of the SMBE community who are in the midst of their re-

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

SMBE Lifetime Contribution Award

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

SMBE Community Service Award

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

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

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

Early-Career Excellence Award https://-www.smbe.org/smbe/AWARDS/FacultyAwards/-SMBEEarlyCareerExcellenceAwards.aspx Mid-Career Excellence Award https://-www.smbe.org/smbe/AWARDS/FacultyAwards/-SMBEMidCareerExcellenceAward.aspx Lifetime Contribution Award https://-www.smbe.org/smbe/AWARDS/FacultyAwards/-SMBELifetimeContributionAward.aspx Community Service Award http://www.smbe.org/smbe/AWARDS/-FacultyAwards/CommunityServiceAward.aspx Best Regards, Marta L. Wayne

SMBE Past President

smbe@allenpress.com

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

Sweden 2 VolFieldAssist Birds

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

We are looking for 2 highly motivated, expenses paid field volunteers to join our long-term field project on Siberian jays (main responsible PD Dr. Michael Griesser, University of Konstanz, Germany).

For the upcoming field season (5 Aug 'V 8 Nov 2021) we are looking for 2 assistants to help with our work on social evolution in Siberian jays. The assistants will help with catching and ringing birds, do behavioural observations, do field experiments, and assist with data management. The work will be carried out in both pristine and managed boreal forests. Observe that temperatures in the end of the season can be as low as -15C, involves walking up to 15km per day, and that fieldwork can be physically strenuous at times.

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

Applications received before 6 June 2021 will be given full consideration.

If you wish to apply, send a motivation letter, CV, and two contacts for references (as a single PDF) to michael.griesser@uni-konstanz.de

Michael Griesser Heisenberg Fellow Department of Biology University of Konstanz

https://scholar.google.com/citations?user=-IEIH0xkAAAAJ Michael Griesser <michael.griesser@uni-konstanz.de>

PostDocs

BolzanoItaly BarkbeetleMicrobiome

A Postdoctoral position is being offered at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler. The project is funded for one year renewable for six months and aims to study the microbial and fungal community of the European spruce bark beetle Ips typographus.

The European spruce bark beetle Ips typographus is one of the most important forest pests in Europe. In addition to factors such as a high fecundity and the establishment of several generations per year, symbiotic associations with fungi and bacteria are responsible for its potential to cause forest mortality. The focus of this project is to study the associations of Central European bark beetle populations with symbiotic bacteria and fungi to obtain a more holistic understanding of the biology, ecology and harmful potential of this important pest species. The project is in collaboration with Martin Schebeck and Christian Stauffer (Boku, Vienna) and Massimo Faccoli and Andrea Battisti (University of Padova).

We are looking for an enthusiastic candidate with a strong background in molecular biology and experience with bioinformatic analyses of bacterial and/or fungal communities associated with insects. The candidate will be responsible to develop an amplicon-sequencing approach for fungi optimized for this species and perform PacBio full-length amplicon sequencing of both mycobiome and bacterial microbiome.

The Free University of Bozen-Bolzano is located in one of the most fascinating European regions, at the crossroads between the German-speaking and Italian cultures. Its trilingualism in teaching and research, its high level of internationalization as well as an ideal research environment guaranteed by its excellent facilities are some of the reasons why unibz regularly reaches top positions in national and international rankings. Our lab is part of the newly funded competence Centre for Plant Health within the Department

of Science and Technology https://www.unibz.it/en/-home/research/competence-centre-plant-health. We are a young and dynamic research group studying various aspects of insect-microbe interactions in a collaborative atmosphere http://hschuler.people.unibz.it General requirements for the position: A PhD degree in Biology or Evolution or related fields. The candidate should have excellent communication skills and should be fluent in English.

The project is expected to start in August 2021, but the starting date is negotiable.

Application deadline is 11.06.2021

All documents for the application procedure can be found at: https://www.unibz.it/en/home/position-calls/positions-for-academic-staff/5264-allgemeine-und-angewandte-entomologie-dr-schuler?group=
For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler hannes.schuler@unibz.it.

Dr. Hannes Schuler Competence Centre for Plant Health Faculty of Science and Technology Free University of Bozen-Bolzano Universitätsplatz 5 I-39100 Bozen-Bolzano Tel: +39 0471 017648 http://hschuler.people.unibz.it   Schuler Hannes <Hannes.Schuler@unibz.it>

ColoradoStateU ComparativeGenomics

The Sloan lab at Colorado State University is recruiting a postdoctoral researcher who is broadly interested in molecular evolution and comparative genomics to investigate interactions between plant nuclear, mitochondrial, and plastid genomes.

The position would primarily involve computational genomics and bioinformatics, with the opportunity to contribute to multiple ongoing projects on cytonuclear coevolution and mutation rates, as well as to develop

independent lines of investigation. More information about our research program can be found at our lab website: https://sites.google.com/site/danielbsloan/ We are looking for a researcher who is excited to contribute to a positive, diverse, and intellectual lab environment. Experience and interest in some or all of the following computational areas would be relevant: analysis of NGS datasets, comparative genomics, variant calling, molecular phylogenetics, and positive selection analyses.

Our lab is in the Department of Biology, which is housed in a state-of-the-art research facility that opened in 2017. The department includes numerous labs in the fields of both plant molecular biology and evolutionary biology, so there are ample opportunities for collaboration outside the lab group. The university is in Fort Collins, Colorado, which routinely ranks among the top locations in the country in terms of overall quality of life.

Inquiries can be e-mailed to Dan Sloan (dan.sloan@colostate.edu) and should include a CV and a brief statement of research/career goals. Evaluation will begin June 1, but inquiries are still highly encouraged after that point.

Dan.Sloan@colostate.edu

CPG Stockholm DeepTime Palaeogenomics

POSTDOC IN DEEPTIME PALAEOGENOMICS

The Centre for Palaeogenetics is looking to hire a postdoctoral researcher in palaeogenomics. The main goal of the project is to recover and analyze genome-wide data from specimens that range in age from one hundred thousand and up more than one million years old. The analyses will be aimed at developing a better understanding of evolutionary processes in wild mammals, such as speciation, introgression and adaptation. The primary methods used in the project will be ancient DNA laboratory analysis of prehistoric bones and teeth, as well as advanced computational analyses of the resulting data. The research group working on this project is international and interdisciplinary. The postdoc will be based in Love Dalén's research group at the Centre for Palaeogenetics (www.palaeogenetics.com), which is a joint venture between Stockholm University and the Swedish Museum of Natural History. The research group working on this project is international and interdisciplinary.

WORK TASKS

The position is mainly directed towards research, including recovering and and analyzing ancient genetic data collected with high-throughput DNA sequencing. It is also expected that the successful applicant will participate in the daily activities at the Centre for Palaeogenetics.

QUALIFICATION REQUIREMENTS

Postdoctoral positions are appointed primarily for purposes of research. Applicants are expected to hold a Swedish doctoral degree or an equivalent degree from another country.

ASSESSMENT CRITERIA

The degree should have been completed no more than three years before the deadline for applications. An older degree may be acceptable under special circumstances, which may involve sick leave, parental leave, clinical attachment, elected positions in trade unions, or similar.

In the appointment process, special attention will be given to research skills. A record of scientific achievement in bioinformatics and computational genomics is essential, as is previous experience in handling NGS data using scripts and analysis pipelines. Additional merits include proficiency in wet lab analyses of ancient or historical DNA samples.

Working experience from highly degraded DNA is essential. Experience with large-scale analyses of high-throughput DNA sequencing data will be considered a merit, as well as an interest and knowledge in paleontology or archaeology. Because the position involves integrating with other research groups, personal skills such as good collaborative and analytical skills, ability to work independently and take own initiatives, well-developed sense of responsibility and service mindedness, are considered additional merits.

Well-developed ability of oral and written communication in English are also considered as merits.

TERMS OF EMPLOYMENT

The position involves full-time employment for a maximum of two years, with the possibility of extension under special circumstances. Start date as per agreement.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

APPLICATION

Closing date: 24/05/2021 Ref. No. SU FV-1682-21

Full advertisement and application instructions via this link: https://www.su.se/english/about-the-university/-

work-at-su/available-jobs?rmpage=job&rmjob=-14989&rmlang=UK Love.Dalen@nrm.se

DalhousieU PhylogeneticModels

A fully funded, 2-3 year, postdoctoral research position in statistical phylogenetic modeling is available immediately to work with Andrew J. Roger and Edward Susko at Dalhousie University. The research project is focused on developing new phylogenetic models/approaches aimed at resolving deep tree of life relationship. Specifically, the successful candidate will develop, implement and apply novel phylogenetic statistical models/phylogenomic methods to determine billion-year relationships related to the origin of eukaryotes. Roger and Susko are part of the world-renowned Centre for Comparative Genomics and Evolutionary Bioinformatics (CGEB: http://cgeb.dal.ca) 'V a large collaborative group of faculty and trainees at Dalhousie university with shared research interests in deep evolution, comparative genomics, phylogenetics, microbiomics and computational biology.

The successful candidate will become part of an international collaborative team involving the Dalhousie group, Dr. Laura Eme in Orsay, France and Dr. Minh Bui in Canberra, Australia, creator of IQ-TREE) that will be addressing the difficult phylogenetic problems that are key to understanding the origin of eukaryotic cells (e.g. the root of the eukaryote tree, the positions of eukaryote nucleocytoplasm and mitochondria in the tree of life, etc.). The goals are part of our Moore/Simons Foundation-funded project to develop new more realistic phylogenetic models including approaches to model heterogeneity in the process of protein sequence evolution across sites and branches of phylogenetic trees and accommodate multiple different phylogenetic histories for different genes or sites. New models will be implemented in a maximum likelihood framework in IQ-TREE (http://www.iqtree.org/) and their statistical properties will be investigated.

The ideal candidate should have a Ph.D. evolutionary biology, phylogenetics, computational biology, or related disciplines. Knowledge and expertise in phylogenomics and implementation of phylogenetic models in a maximum likelihood or Bayesian framework are assets. Programming experience using C++ (or C) and the R statistical package are especially important qualifications.

For more information about the Roger and Susko labs and the CGEB Centre see http://rogerlab.biochem.dal.ca, https://www.mathstat.dal.ca/~tsusko/ and http://-cgeb.dal.ca To apply please send an application package consisting of:

1. a cover letter that describes why you are interested in this position and highlights your expertise,

2. your curriculum vitae (CV), and

3. the names and contact details of 2 or more individuals who have agreed to write reference letters.

The applications should be emailed to: Andrew Roger: andrew.roger@dal.ca Review of applications will occur continuously until the position is filled. Only those candidates chosen to continue on through the selection process will be contacted.

Dalhousie University is committed to fostering a collegial culture grounded in diversity and inclusiveness. We encourage applications from individuals from all equity-seeking groups including qualified people who identify as indigenous, African Nova Scotians, differently-abled, ethnic minorities, minority sexual orientations and gender identities, and all other qualified candidates who would contribute to the diversity of our community.

Andrew Roger <Andrew.Roger@Dal.Ca>

DukeU EvolutionaryMechanics

A postdoctoral position in evolutionary analyses of origins, transitions, and diversification rates is available at the Patek Lab in the Biology department at Duke University. The broad goal of the Patek Lab's research is to establish the principles by which biological systems navigate physics-based limits and transitions through scaling and evolutionary processes.

Requirements:

* Ph.D. in Biology * Journal publication record in organismal or evolutionary biology * Previous experience in at least one of the following areas: comparative biomechanics, comparative physiology, or phylogeny- based evolutionary analysis

The candidate should demonstrate:

* Experience in hypothesis testing through integration of phylogeny- based comparative analyses * Interest in physiological and mechanical principles of biologi-

cal movement in a rigorous evolutionary framework *
Experience engaging broader communities in research
or science. * Interest in developing broader impact
leadership skills through implementation of structural
changes in academic research to enhance inclusiveness,
specifically through the Muser program.

Applications will be processed rapidly until the position
is filled. Apply soon! The position is available immedi-
ately with the start date no later than September 1, 2021,
with a preference for an earlier start date this summer.
The initial appointment will be for 12 months with the
possibility for renewal contingent on performance and
continuing funding availability. Annual salary starts at
$53,760. Become part of a diverse and inclusive research
team and university, with outstanding job benefits in
a culturally diverse and affordable geographic region.
Contact Prof. Patek via email (snp2@duke.edu) for
inquiries about the position.

The job application must be submitted to https://-
academicjobsonline.org/ajo/jobs/18580 and include the
following information:

1. Cover letter including your specific research interests
in this position, how your previous research provides a
strong foundation for this position, and how this posi-
tion connects to your career goals. 2. C.V. 3. List of
three references including contact information and the
basis of the relationship to the candidate. Letters of
recommendation will be requested later in the review
process.

Duke University is an Affirmative Action/Equal Oppor-
tunity Employer committed to providing employment
opportunity without regard to an individual's age, color,
disability, gender, gender expression, gender identity,
genetic information, national origin, race, religion, sex,
sexual orientation, or veteran status.

Duke aspires to create a community built on collabora-
tion, innovation, creativity, and belonging. Our collec-
tive success depends on the robust exchange of ideas-an
exchange that is best when the rich diversity of our per-
spectives, backgrounds, and experiences flourishes. To
achieve this exchange, it is essential that all members
of the community feel secure and welcome, that the
contributions of all individuals are respected, and that
all voices are heard. All members of our community
have a responsibility to uphold these values.

snp2@duke.edu

DukeU FungalGenomics

Postdoc ad: Fungal genomics, Duke University

The Vilgalys Mycology Lab at Duke University seeks
a postdoctoral researcher in the area of plant-fungal
symbiosis and evolution. The selected candidate will
contribute to ongoing studies on evolution of forest fungi
and their interactions with trees including Populus, Pi-
nus and other species. We are especially interested
in linkages between phylogenetic diversity, population
structure, and molecular functioning of forest fungi,
including their effects on ecosystem processes. As a
team-member, you will have the flexibility to explore
your interests within the broad scope of fungal biology
and metagenomics.

Major Duties/Responsibilities: Design, conduct and in-
terpret laboratory and field based research; lead and
contribute to the development of scientific manuscripts
and proposals. The postdoc chosen for this position will
also have opportunities to interact with collaborating in-
stitutions in the US and abroad. Research is facilitated
by state-of-the-art equipment/facilities for microbiol-
ogy, molecular biology, and genomics, in a professional
environment with excellent technical support.

Qualifications Required: Ph.D. degree in mycology, ge-
nomics, molecular ecology, or related fields. Applicant
should have demonstrated expertise in modern molecular
methods including comparative genomics, phylogenetics,
as well as working with informatics tools for microbiome
and metagenomic studies. Demonstrated expertise must
include a track record of peer-reviewed publications.

Qualifications Preferred: Priority will be given to ap-
plicants with a successful history of interdisciplinary,
integrative, and innovative research in this area. Inter-
ested applicants should send a cv, research statement,
and names of 3 references (preferably in a single pdf)
to Dr. Rytas Vilgalys, fungi@duke.edu. The position
is available immediately and will remain open until a
suitable candidate has been hired. For more informa-
tion on the Vilgalys Lab see: http://sites.duke.edu/-
vilgalyslab/ Rytas Vilgalys, Professor Biology Depart-
ment, Duke University Durham, NC 27708-0338 USA
phone: (work) 919-660-7361 (cell) 919-672-0403 email:
fungi@duke.edu https://sites.duke.edu/vilgalyslab/ Ry-
tas Vilgalys <fungi@duke.edu>

DurhamU AncientDNA

Applications are invited for a 3 yearsPostdoctoral Research Associate in Ancient Human Genomicsuntil the 31st of May 2021. The successful candidate will join a team of researchers to work in the Leverhulme Research Project "What'Âs in a house?: exploring the kinship structure of the world'Âs first houses"(RPG-2019-362). Employment dates: August/September 2021-July/August 2024.The research team will comprise the PI Dr Eva Fernandez-Dominguez at Durham University (UK) and the Co-I Dr. Jessica Pearson at Liverpool University (UK) and two postdoctoral research associates: one based at Durham University and specialised in human ancient DNA (this post) and one based at the University of Liverpool specialised in human bioarchaeology and stable strontium and oxygen isotope analysis. The post-holder will be based in the Department of Archaeology at Durham University and will work closely with Dr. Eva Fernandez-Dominguez and the research team in Liverpool.You can find details about the post, including how to apply at:https://durham.taleo.net/-careersection/du_ext/jobdetail.ftl?job=21000441&tz=-GMT%2B01%3A00&tzname=Europe%2FLondonFor enquiries about this job, please contacteva.fernandez@durham.ac.uk

Dr. Eva FernÂ'ndez-DomÂÂnguez Associate Professor in ancient DNA Manager of the ArchaeoDNA Laboratory Dp. Archaeology. Durham University. Dawson Blg. South Road. Durham DH1 3LE email:eva.fernandez@durham.ac.uk Tf: 01913341141

https://www.dur.ac.uk/directory/profile/?id=14218

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https://www.researchgate.net/profile/-Eva_Fernandez_Dominguez   "FERNANDEZ-DOMINGUEZ, EVA" <eva.fernandez@durham.ac.uk>

GriffithU Australia 2 6mnth HumanEvolution

The Australian Research Centre for Human Evolution at Griffith University In Queensland, Australia (https://www.griffith.edu.au/centre-planetary-health-food-security/research-centre-human-evolution) is recruiting two postdoctoral researchers who have expertise in ancient and modern genomics and human evolution generally. Each of these appointments will be for a period of 6 months. At a broad level, the research is aimed at an improved understanding of the relationships among the hundreds of different language groups of Aboriginal Australians. More specifically our ancient and modern genomic studies are focused on the identification of the origins of the large number of ancient remains of our Indigenous people that are held in museums and other research institutions in Australia and abroad. Many of these remains are not associated with any collection details, hence they cannot be returned to their ???Place and Country???. We need to expand our full genome sequencing of modern and ancient remains and hence require Postdoctoral Fellows with genomic experience and with bioinformatic skills. We have a number of long-term collaborators in this research including Assoc Prof Craig Millar in the School of Biological Sciences at the University of Auckland, Dr Sankar Subramanian at the University of the Sunshine Coast in Queensland, plus collaborators at the Centre for GeoGenetics at the University of Copenhagen as well the University of Cambridge, UK. Enquiries should be e-mailed to Prof David Lambert and should include a CV and a brief statement of research/career goals. Applications should be sent before June 15th although enquiries will still be encouraged after that time. The positions will be at the Australian Research Centre for Human Evolution at Griffith University at Nathan, Brisbane. Applications should be sent directly to Prof Lambert at ARCHE at the following email address d.lambert@griffith.edu.au

Prof David Lambert Australian Research Centre for Human Evolution Griffith University, 170 Kessels Road, Nathan 4000 Voice (61) 37355298 Email: d.lambert@griffith.edu.au

Australian Research Centre for Human Evolution

18-20 May, 4-6 pm. Chat with our specialists and find a study path to suit you. Reserve your place

www.griffith.edu.au   Prof David Lambert Australian Research Centre for Human Evolution Environmental Futures Research Institute Griffith University Nathan Queensland 4111

Phone (office) +61 7 37355298 Email: d.lambert@griffith.edu.au

Griffith University - CRICOS Provider Number 00233E

http://www.remarkablegriffith.com.au/ David Lambert <d.lambert@griffith.edu.au>

HarvardU ComputationalGenomicsStatistics

We are hiring two postdoctoral fellows to work on comparative and population genomics of conserved non-coding elements in birds. The successful candidates will develop statistical methods and computational tools to infer evolutionary forces acting on non-coding sequences, building on our published work on PhyloAcc (https://doi.org/10.1093/molbev/msz049). These are NIH-funded positions, which will be based at Harvard University in the groups of Scott Edwards < https://edwards.oeb.harvard.edu/ > (Organismic and Evolutionary Biology), Jun Liu < http://sites.fas.harvard.edu/~junliu/ > (Statistics), and Tim Sackton < https://scholar.harvard.edu/tsackton/home > (Bioinformatics).

Funding is available for 1 year, renewable up to 3 years contingent on successful performance. Funding from NIH grant 1R01HG011485-01 https://reporter.nih.gov/search/t-rz1eSGekuvtUF5P5w4iA/project-details/10098556 Qualifications

The preferred candidates will have a PhD in statistics, computational genomics, population genetics, computer science, or a related field, with a demonstrated record of research achievement (via publications or preprints). They will be experienced with Bayesian statistics, computational method development (using Python, C, C++, or a related language), or both. Experience with population genetics, comparative genomics, phylogenetics, shell scripting, computing cluster environments, and/or experience working with whole genome datasets will be beneficial, but is not required.

Working Environment

The successful candidates will be based in one or more of the PI labs (Jun Liu < http://sites.fas.harvard.edu/~junliu/ >, Scott Edwards < https://edwards.oeb.harvard.edu/ >, Tim Sackton < https://scholar.harvard.edu/tsackton/home >). The exact logistics are flexible and will depend on the candidate's interests and experience, but the postdoctoral associate(s) will have opportunities to gain experience and training in bioinformatics, statistics, population genetics, comparative genomics, developmental genetics, and ornithology. In addition, the successful candidates will have the opportunity to interact with collaborators Emma Farley (UCSD) and Cliff Tabin (Harvard Medical School). The combined experience of our groups spans a wide range of topics and provides an outstanding opportunity for training, collaboration, and scientific growth. The larger scientific environment in Boston is unparalleled and provides numerous opportunities for engagement, including the Boston Area Evolutionary Supergroup (https://evogen.hms.harvard.edu) and numerous seminar series and journal clubs.

Contact

Review of applications will begin on July 15, 2021. Preferred start date as soon as possible but flexible. To apply, please send a CV and cover letter with contact details of three potential references and describing interest and previous experience to Tim Sackton (tsackton@g.harvard.edu), Scott Edwards (sedwards@fas.harvard.edu), and Jun Liu (jliu@stat.harvard.edu).

We are committed to diversity and especially encourage members of underrepresented communities to apply.

sedwards@fas.harvard.edu

HongKongU PathogenEvolution

Applications are invited for appointment asPostdoctoral Fellowin the HKU-Pasteur Research Pole of the School of Public Health(Ref.: 503788), to commence as soon as possible for one to two years, with the possibility of renewal subject to satisfactory performance.

Applicants should possess a Ph.D. in epidemiology, computational biology, virology, microbiology, antimicrobial resistance, genomics, bioinformatics, biostatistics or a related discipline. Preference will be given to those with a strong background in phylogenetics, population genetics, microbial evolution, or epidemiology. They should have experiencein next-generation sequence analysis using programming languages such as R or python. They should have a good command of written and spoken En-

glish, strong communication skills, and a demonstrated record of publishing academic research papers. They should be organized, highly motivated, and able to work independently as well as in an interdisciplinary team.

The appointee will join Dr. Dhanasekaran's research team to study the molecular epidemiology and evolution of infectious diseases.He/She will analyse genomic data from surveillance activities, linking clinical, epidemiological and genomic data for prediction of disease severity, transmission modelling and comparative genomic evolution in a phylodynamic framework.He/She will contribute to the design and implementation of virus surveillance and genome sequencing projects in collaboration with international experts in the field.

A highly competitive salary commensurate with qualifications and experience will be offered, in addition to annual leave and medical benefits.

The University only accepts online applications for the above post.Applicants should apply online and upload an up-to-date C.V. via the link below.Review of applications will start on May 12, 2021 and continue untilJuly 31, 2021, or until the post is filled, whichever is earlier.

https://jobs.hku.hk/cw/en/job/503788/postdoctoral-fellow kedwards <kedwards@hku.hk>

ImperialC 3 ComputationalBiology

Job Summary: We are seeking three Postdoctoral Research Associate positions in computational ecology. The project is to create a virtual rainforest: a general ecosystem model replicating all physical and biotic components of the ecosystem and their interactions, with a view to understanding system-level emergent properties. We are particularly interested in finding applicants with an interest in systems ecology and experience in process-based modelling. However, this project requires team members who provide complementary and diverse technical skills and disciplinary knowledge, so applicants from any ecological background and/or with any relevant skillset are encouraged to apply. Positions are open to full or part-time applicants, and you will be given time, resources and encouragement to pursue your professional development.

Project Description: We are building a team to create a virtual rainforest: a general ecosystem model replicating all physical and biotic components of the ecosystem and their interactions, with a view to understanding

system-level emergent properties. The virtual rainforest will link all of the biotic and abiotic system components through nutrient cycling, stoichiometric and metabolic processes. It will track the birth, growth and death of cohorts of plant, animal and soil microbial functional groups, and the movement of carbon, nitrogen, phosphorus, water and energy through the ecosystem. At its heart, the virtual rainforest will be an individual-based simulation of plants, animals, microbes and their interactions with the abiotic environment, and which rests upon the key individual-based processes of metabolism, respiration, reproduction and mortality. The virtual rainforest will be used to gain insight into the processes that govern three key, emergent properties of rainforests: their stability, resilience and sustainability.

Ecosystems cannot be understood through piecemeal studies of their individual components. The discipline of tropical forest ecology has at its disposal ever-accumulating datasets examining all aspects of rainforest ecosystems giving insight into everything from the population dynamics of plants through to the scavenging behaviour of ants. This knowledge allows us to understand much of how the ecosystem operates and the ecosystem services it generates, but in a disjointed fashion. As a Postdoctoral Research Associate in Computational Ecology, you will be part of an attempt to tie that knowledge into a single, comprehensive understanding of how the ecosystem operates in its entirety.

Duties and responsibilities:

The primary role of successful applicants will be to develop one of the four modules of the virtual rainforest: plant, animal, soil microbial or abiotic processes. You will be assisted in this by additional team members, including your peers, a separately appointed scientific programmer and postgraduate students. The project provides a generous budget for placements and secondments to give you the freedom to work with, and harness the expertise of, research groups beyond our own. The virtual rainforest will lean heavily on data collected from the SAFE Project (www.safeproject.net), and you will be required to help with the management of these datasets. All team members will be expected to help develop the skills and competencies of their peers through the sharing of tasks and knowledge. As part of a research group and environment that extends beyond the virtual rainforest team, you will contribute to the supervision of undergraduate and postgraduate student projects. You will be given time, resources and encouragement to pursue your professional development, along with opportunities to gain teaching experience in the form of tutorials, lectures, practical classes and field trips.

Essential requirements: We require team members who

provide complementary technical skills and disciplinary knowledge, so applicants from any ecological background and with any relevant skillset are encouraged to apply. No individual team member is expected to have more than a small subset of this list of topics and skills, and we specifically encourage applicants to clearly identify the subset of skills that they could bring to the team. Among the team members, we will need understanding of plant, animal and microbial ecology, along with functional ecology, metabolic ecology, ecological stoichiometry, biogeochemistry, hydrology and microclimate processes. Candidates with an interest in systems ecology and the concepts of stability, resilience and sustainability are particularly encouraged to apply. Some programming experience - preferably in Python - is necessary for all applicants. Experience with either process-based or numeric simulation modelling is desirable, as is experience with error propagation and ecological statistics. We are also seeking experience with version

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IowaStateU PlantEvolutionaryGenomics

The Wendel lab at Iowa State University (https://-www.eeob.iastate.edu/faculty/wendel/) is recruiting a postdoctoral researcher who is broadly interested in evolutionary genomics with an emphasis on allopolyploidy. The conceptual direction of the position encompasses cytonuclear coevolutionary and homoeologous recombinational processes set in motion by allopolyploidization. Experience and interest in some or all of the following computational areas would be relevant: analysis of NGS datasets, comparative genomics, variant calling, molecular phylogenetics, and selection analyses. The initial appointment will be for one year from the date of hire, with the possibility of renewal beyond the initial term. This work is highly collaborative, with the possibility of contributing to additional projects in Dan Sloan's lab at Colorado State University and Dan Peterson's lab at Mississippi State University. More information about our research program can be found at, https://sites.google.com/-site/danielbsloan/ and www.igbb.msstate.edu. Inquiries

can be e-mailed to Jonathan Wendel and should include a CV and a brief statement of research/career goals. Evaluation will begin June 1, but inquiries are still highly encouraged after that point. The position is at Iowa State University, a premier land-grant university, in the intellectually vibrant Department of Ecology, Evolution, and Organismal Biology. Apply at: https://isu.wd1.myworkdayjobs.com/IowaStateJobs/-job/Ames-IA/Postdoc-Research-Associate–Plant-Evolutionary-Genomics_R5065 . Jonathan F. Wendel, Distinguished Professor Department of Ecology, Evolution, & Organismal Biology, Iowa State University Ames, IA 50011 Voice (515) 294-7172; FAX 515-294-1337; jfw@iastate.edu https://www.eeob.iastate.edu/faculty/-wendel/ http://www.eeob.iastate.edu/ (Department home page)

"Wendel, Jonathan F [EEOB]" <jfw@iastate.edu>

KielU AntibioticResistanceEvolution

Postdoc Position on Antibiotic Resistance Evolution in Kiel, Germany

Deadline for applications: 16 June 2021 The position will be based in the Schulenburg group, located at Kiel University. The position is available from 1. August 2021 (or soon afterwards) onwards, initially for 18 months with the possibility of an extension for another 3 years.

Area of work: Analysis of antibiotic resistance evolution using experimental evolution, genome analysis, and/or functional genetics of the human pathogen Pseudomonas aeruginosa. The postdoc project focuses on an assessment of negative hysteresis and/or evolved collateral sensitivity to minimize resistance evolution. The project links basic research to clinical application and involves collaborations with clinicians from several clinics in Northern Germany. For further information, see our publications by Roemhild et al. 2018 PNAS, Barbosa et al. 2017 Mol Biol Evol, or Barbosa et al. 2019 eLife (see also: https://www.evoecogen-kiel.de/). The postdoc project is part of the Excellence Cluster "Precision Medicine in chronic Inflammation" (PMI; https://-www.precisionmedicine.de/en/) and thus provides many opportunities for interactions with scientists working on related topics.

Expectations and Requirements: PhD with a focus on evolutionary biology and/or microbiology, ideally already on the analysis of antibiotic resistance evolu-

tion. Competences and experience in microbiological techniques and statistical data analysis. Ideally competences and experiences in the performance of evolution experiments, and/or bacterial genome sequence analysis, and/or bacterial functional genetic analysis. High competence in English and writing of manuscripts. We are looking for someone with creative ideas, enthusiasm for research, and the ability of performing large-scale experiments.

Kiel University: Kiel University considers itself to be a modern and cosmopolitan employer. We welcome your application regardless of age, gender, cultural and social background, religion, ideology, disability or sexual identity. We promote equality of the sexes. Women are given priority in case of equal qualifications and professional performance. Kiel University is committed to the employment of people with disabilities: Applications from severely disabled persons and persons of equal status will be given preferential consideration in case of suitable qualification. We expressly welcome applications from people with a migration background.

Applications: Deadline for applications is 16 June 2021. Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant's work), and copies of certificates (MSc, PhD). Applications should be sent as a single pdf-document by email to: Prof. Dr. Hinrich Schulenburg, hschulenburg@zoologie.uni-kiel.de

Hinrich Schulenburg

Evolutionary Ecology and Genetics Christian-Albrechts-Universitaet zu Kiel 24098 Kiel, Germany Tel: +49-431-880-4143/4141 Email: hschulenburg@zoologie.uni-kiel.de

https://www.evoecogen-kiel.de/ https://transevo.de/ http://www.evolbio.mpg.de/3248501/antibioticresistance www.kec.uni-kiel.de www.metaorganism-research.com www.evolbio.mpg.de/imprs evolung.fz-borstel.de

Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

Krakow JagiellonianU AdaptationGenomics

PostDoc:Krakow_JagiellonianU. Adaptation_Genomics

We are looking for a postdoctoral researcher to join Genomics and Experimental Evolution Group at Jagiellonian University, Institute of Environmental Sciences. The position is offered for two years and is funded from the Polish National Science Centre grant Environment-dependent balancing selection in a gene involved in sexual conflict. The position is available from autumn, but the starting date is flexible. Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland (www.eko.uj.edu.pl/en) is one of the strongests centres of research in evolutionary biology in Central Europe. Krakow is a beautiful medieval city with a rich history and a lively cultural life.

The project The maintenance of genetic variation, enabling populations to adapt to novel environments, is one of the greatest puzzles in evolutionary biology, because ubiquitous directional selection should lead to depletion of genetic variation in selected traits. This is especially the case with sexually selected traits, in which directional selection is particularly strong. Yet, substantial genetic variance in these traits is maintained. A potent force proposed to maintain genetic variation is balancing selection, but cases of a detailed dissection of the mechanisms of that maintain balanced polymorphisms are extremely rare. The project will likely provide a textbook example of balancing selection in action.

We aim to investigate the maintenance of polymorphism in Phosphogluconate dehydrogenase (6Pgdh), a sexually selected gene associated with sexual conflict in the bulb mite Rhizoglyphus robini. 6Pgdh polymorphism (with two alleles, S and F) is associated with differences in male reproductive success. The S-bearers have advantage in male-male competition, but decrease fecundity of their partners. Previous studies suggest that the nonsynonymous polymorphism defining F and S alleles is under (relatively) long-term environment-dependent balancing selection. The project is aimed at identifying mechanisms driving this selection and investigating its molecular signitures.

Responsibilities A PostDoc will look for the molecular signatures of balancing selection around the 6Pgdh gene

and attempt to estimate the age of the 6Pgdh. We expect a strong signal of long-term balancing selection within the genomic region centered on the F/S defining nonsynonymous polymorphism. The PostDoc will also be involved in gathering/analyzing field data to evaluate the levels of 6Pgdh polymorphism in natural populations and determine environmental factors affecting 6Pgdh allele frequencies in the field. This second task will be realized with the cooperation of a PhD student and PI.

Requirements

The successful candidate will have a PhD in biology, or other relevant field acquired no sooner than in 2014. The candidate will have experience in the analyses of population genomics data, including searching for the signals of balancing selection in the genome. We are looking for a candidate with a strong publication record, strong background in Evolutionary Biology and skills in data analysis. Excellent English, organizational and communication skills are also required.

Salary

The salary is 100 000 PLN/year gross (ca. 23000 euro; before taxes and insurances). Note that living costs in Poland are substantially lower than in the west of the EU, so this amount of money ensures a sufficiently good life standard.

Documents

Please send a CV including contact details for two references and a cover letter to Agata Plesnar-Bielak (agata.plesnar@uj.edu.pl). The applications should be sent until June 10 th 2021. For more information, please e-mail Agata Plesnar-Bielak.

Agata Plesnar-Bielak <agata.plesnar@gmail.com>

Krakow PlasticityTranscriptomics

Institute of Nature Conservation PAS Krakow Poland.PlasticityTranscriptomics

Postdoc position in the project 'Integrating effects of anthropogenic and natural stressors: phenotypic and genetic expression approach' at the Institute of Nature Conservation PAS, Krakow, Poland in collaboration with the Jagiellonian U. U of Lodz, Norwegian Institute for Nature Research and Norwegian Veterinary Institute.

Cities as 'heat islands' are often hot spots for alien invasive species that can drastically alter population dynamics of native species. In addition, natural stressors such as seasonal time and thermal constraints at high latitudes can strongly affect organism fitness. The aim of the project is to understand how anthropogenic and natural stressors: urbanization, native and invasive alien predators, and latitudinal gradient affect traits linked to fitness down to gene expression level in a common bluetail damselfly.

Requirements: PhD in biology, ecology or related field (PhD defense not earlier than 7 years before the year of employment in the project); Experience in field and laboratory work on aquatic/semi-aquatic invertebrates; An experience in using molecular methods to address ecological or evolutionary questions, with an appropriate publication track record; Good working knowledge of R environment, including advanced skills in statistical modelling; Working knowledge of standard bioinformatics tools in the Linux environment; Publication record including articles in leading ecological and evolutionary journals; Involvement in work during irregular working hours (during field work); Strong motivation for work in the project; Fluency in English, written and spoken; Valid driving license; Experience in and enthusiasm for working in an international team would be an asset.

I have funding from Norway grants under the Norwegian Financial Mechanism 2014-2021.

Principal investigator: Dr hab. inÂ¿. Szymon Âniegula, http://www.iop.krakow.pl/-pracownicy,102,szymon sniegula.html Feel free to contact me at ecopond@iop.krakow.pl

The posting is here https://www.iop.krakow.pl/files/-327/jsz call 2021 en 2.pdf Closing date: 21 May 2021

Starting date of employment: 1 June 2021

– Szymon Sniegula Institute of Nature Conservation Polish Academy of Sciences Mickiewicza 33 31-120 Krakow, POLAND

phone: +48 602 152996 e-mail: szymon.sniegula@gmail.com my personal website < http://www.iop.krakow.pl/-pracownicy,102,szymon sniegula.html >

Szymon Sniegula <szymon.sniegula@gmail.com>

London 2 EvolutionaryEpigenomics

Two open post-doctoral positions in the laboratory of Dr. Alex de Mendoza at Queen Mary University of London (United Kingdom). These are European Research Council funded positions under the project METHYLEVOL, aimed at understanding the evolution of DNA methylation in animals and other eukaryotes. Both positions are for 2 years and can be extended up to 4 years.

For one position, the candidate must have previous experience in bioinformatics (fluent in Unix and R or Python), comparative genomics, epigenomics and genome-analysis of gene regulation. Expertise on Transposable Elements will be a plus. Additionally, the capacity to perform molecular biology techniques would be highly advantageous (e.g. cloning, NGS library construction). Find link to the application and salary/conditions details here:

https://webapps2.is.qmul.ac.uk/jobs/-job.action?jobID=5627   For   the   other   position, the candidate should have previous experience in molecular biology of cnidarian model systems (specifically Nematostella vectensis), including lab culture, genetic manipulation, spawning. Alternatively, experience in functional EvoDevo techniques of other non-traditional model systems is also welcome. Bioinformatics experience would be a plus, but we can train the candidates in this aspect. Ample opportunities for training in functional genomics. Find link to the application and salary/conditions details here:

https://webapps2.is.qmul.ac.uk/jobs/-job.action?jobID=5631   Applications   close   on May 20th. All you need is:

1.- Curriculum vitae (CV).

2.- Motivation letter.

3.- Names and contact details of two references.

Potential candidates should not hesitate to get in touch with a.demendozasoler@qmul.ac.uk to discuss your interest in the posts and the projects, even if you cannot make it to the deadline.

More information on the group, publications and research topics in the group can be found in the laboratory website: https://www.demendozalab.com/   Research environment:

Queen Mary University of London and the School of Biological and Chemical Sciences are in London's East End, and hosts a vibrant community of researchers with complementary expertise in evolutionary genomics and EvoDevo (https://www.qmul.ac.uk/sbcs/about-us/our-departments/biology/), with access to state-of-the-art computational resources and genomics facilities. Furthermore, we are part of the Epigenetics Hub, a highly integrated group of researchers with different expertise in different aspects of epigenetics, from basic to applied research: http://qmulepigenetics.com/home   Alex de Mendoza Lecturer | Queen Mary University of London School of Biological and Chemical Sciences Mile End Road. Fogg Building 5.14 E1 4NS London UK

Lab website: https://www.demendozalab.com/   Alexandre de Mendoza Soler <a.demendozasoler@qmul.ac.uk>

LoyolaChicago PlantEvolutionaryGenomics

A research/teaching postdoctoral position is currently available at Loyola University of Chicago in the Grillo lab (https://grillolab.weebly.com/). The postdoc will work on research projects in plant evolutionary genomics involving plant-microbe interactions. Research in the Grillo lab focuses on the classic mutualism between legume plants and nitrogen-fixing bacteria (rhizobia). Current projects involve genetic mapping of symbiosis traits in the model legume, Medicago truncatula, and population genomics in Astragalus, the single most species-rich genus of plants. Moving forward, projects are expanding beyond rhizobia to examine legume interactions with the broader host-associated microbial communities (microbiome). The post-doc will also be responsible for teaching one course a year in the topic of introductory biology or genetics in the Department of Biology. The position will be open until filled and applications will be reviewed on a continual basis. Contact Mike Grillo, mgrillo1@luc.edu, with interest or questions. To apply visit:

https://www.careers.luc.edu/postings/15468   Michael A. Grillo, Ph.D. Assistant Professor Department of Biology Loyola University Chicago 1032 W. Sheridan Road Life Sciences Bldg, Rm 225 Chicago, Illinois 60660 USA https://grillolab.weebly.com/   "mgrillo1@luc.edu" <mgrillo1@luc.edu>

MaxPlanck Tuebingen RegulatoryGenomics

We are posting two exciting opportunities to join our effort to understand the non-coding regulatory genome in adaptation using threespine stickleback fish.

- Postdoc in Genomics and Epigenomics of Gene Regulation (see below) - Staff scientist in genomics (see ad posted under "Jobs")

A major challenge in the field is understanding how the non-coding genome functions in natural populations under different environmental conditions. In our group we combine state-of-the-art facilities to manipulate environmental conditions and have been collecting a trove of chromatin, epigenomic and transcriptomic data from adaptively divergent stickleback fish ecotypes to map and quantify how the non-coding regulatory genome functions and evolves. In previous work we have shown the predominance of cis-regulatory differences in gene expression divergence (Jones et al 2012[1], Verta et al., eLife 2019, [2]), tracked allelic trajectories during adaptation over time (ancient DNA, Kirch et al., Curr Biol. 2021 [3], Kingman et al., Sci. Advances, in press/bioRxiv [4]. and Schluter et al., PNAS, 2020 [5]) and developed novel techniques to determine the recombination landscape in single individuals (Dreau et al., Nat Comm. 2019 [6]). We have recently generated a large multi-tissue, multi-omic dataset dubbed "StickleCODE" [unpub] to further dissect the molecular mechanism of adaptation (including environmental manipulations) in the system.

We are looking for a motivated postdoc to join our team to both analyze our rich set of genomic data (RNA-, ATAC- and ChIP- and CHRO-seq, including from single-cell platforms) and develop and lead new projects investigating evolutionary divergence in regulatory genome function using cutting edge techniques such as single cell 'omics, spatial transcriptomics and 3D genomics.

The Max Planck Tübingen Campus is a leading research hub with world-class genomics and machine learning expertise. Our sequencing core features Illumina, PacBio and 10X Genomics platforms. English is the working language. All seminars and communications are in English.

We offer a varied and interesting job with the social benefits of the public service. Remuneration is in accordance with the TVöD (German public service salary scale). The positions is to be filled from June 2021 and is initially limited to two years.

The Max Planck Society is committed to employing more women in areas in which they are underrepresented. Qualified women are therefore particularly being encouraged to apply. The Max Planck Society strives to employ disabled people. Applications from disabled persons are expressly welcome.

Please send your application and contact details of three referees to:

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Max-Planck-Ring 9 D-72076 Tuebingen

E-Mail: fcjones@tuebingen.mpg.de https://fml.tuebingen.mpg.de/jones-group/ Application deadline: open until filled.

References: 1. Jones FC, Chan YF, Schmutz J., Brady SD, Southwick A, Myers RM, Schluter D, & Kingsley DM. 2012) A genome-wide genotyping array reveals patterns of global and species-pair divergence in threespine stickleback. Current Biology 22, 83-90. 2. Verta JP and Jones FC (2019). Predominance of cis-regulatory changes in parallel expression divergence of sticklebacks. eLife 8:e43785 doi: 10.7554/eLife.43785 3. Kirch et al., (2021). Ancient and modern stickleback genomes reveal the demographic constraints on adaptation. Curr Biol. 31, 20272036 4. Kingman GA, et al. (2020). Predicting future from past: The genomic basis of recurrent and rapid stickleback evolution. Science Advances. in press. bioRxiv doi: https://doi.org/10.1101/2020.11.13.382424 .5. Schluter D, Marchinko KB, Arnegard ME, Zhang H, Brady SD, Jones FC, Bell MA, Kingsley DM (2020) Fitness maps to a large-effect locus in introduced stickleback populations. PNAS. 118(3)e1914889118. 6. Dreau A, Venu V, Avdievich E, Gaspar L and Jones FC. (2019) Genome- wide recombination map construction from single individuals using linked- read sequencing. Nat comm. 10:4309-4320.

jones.floss@gmail.com

MichiganStateU MolBiolQuantGenet

A postdoctoral position is immediately available immediately in molecular biology/quantitative genetics and genomics in the Department of Animal Science at

Michigan State University in the laboratory of Wen Huang (https://qgg-lab.github.io). Our laboratory is broadly interested in the genetics of complex quantitative traits, using Drosophila, livestock animals, and human data as models. Laboratory approaches include classical genetics, molecular biology, genomics, statistics, and bioinformatics therefore trainees will receive training in these areas.

Applications are invited from candidates with background in molecular biology/genetics. Candidates with a recent Ph.D. and experience in molecular biology or molecular genetics are strongly encouraged to apply; prior Drosophila experience is not required but a plus. Projects that can be immediately started include mapping developmental and environmental regulatory variation for translational control in early Drosophila embryos; development of massively parallel reporter assays to assess effects of regulatory variation for translation. Postdocs are also encouraged to develop projects that fit their own interest and align with directions of the lab. Candidates are encouraged to inquire and/or apply by sending current CV and a brief introduction explaining background, experience and career plan to the PI (Wen Huang: huangw53@msu.edu). References will be checked when there is mutual interest to move forward. Salaries and benefits will be commensurate with experience and follow NIH guidelines.

"huangw53@msu.edu" <huangw53@msu.edu>

MississippiStateU CloseKin MarkRecaptureMethods

Title: Post-Doc 'V Developing Close-Kin Mark-Recapture Methods to Monitor Black Bear Populations

Agency: Department of Wildlife, Fisheries and Aquaculture, Mississippi State University

Location: Starkville, Mississippi (remote work currently negotiable) Job Category: Post-doctoral Research Salary: $55,000+/year (dependent on experience) Last Date to Apply: June 1, 2021 Start Date: August 16, 2021 (negotiable)

Description: We are seeking a post-doctoral scientist to develop and validate Close-Kin Mark-Recapture models to monitor black bear populations. The successful candidate will be housed within the Carnivore and Population Ecology Lab at Mississippi State University (https://www.carnivore.fwrc.msstate.edu/index.php) and collab-

orate with Drs. Dana Morin (MSU), Robert Lonsinger (US Geological Survey), and Lisette Waits (University of Idaho). Funding is available for two years and includes travel to Michigan to present results and train agency scientists on implementing validated methods.

Qualifications: PhD in Wildlife Science, Ecology, Math, Statistics, or a related field. Applicants must have completed all the requirements for their doctoral program by start of employment, with demonstrated research accomplishments and publications in the primary research literature. Required experience includes advanced knowledge, development, and application of Bayesian hierarchical models for population parameter estimation OR population genomics and close-kin mark-recapture methods. Candidates with some experience in both areas of expertise will be preferred.

To APPLY: Please submit a combined PDF including 1) cover letter discussing your qualifications and career goals, 2) curriculum vitae, 3) complete contact information for three professional references to dana.morin@msstate.edu.

Contact Person: Dana Morin

Contact Phone: 662-325-8577

Contact Email: dana.morin@msstate.edu

EQUAL EMPLOYMENT OPPORTUNITY STATEMENT: MSU is an equal opportunity employer, and all qualified applicants will receive consideration for employment without regard to race, color, religion, ethnicity, sex (including pregnancy and gender identity), national origin, disability status, age, sexual orientation, genetic information, protected veteran status, or any other characteristic protected by law. We always welcome nominations and applications from women, members of any minority group, and others who share our passion for building a diverse community that reflects the diversity in our student population.

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

President National Association of University Fisheries and Wildlife Programs 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>

MontpellierU-IRD 2 EvolBiology

Post-doctoral position in association genetics and functional genomics

A 2-year post-doctoral position is available in the

Cereal Roots Systems team at the French National Research Institute for Sustainable Development (IRD)/Montpellier University in Montpellier, France (http://diade.ird.fr/en/teams/ceres-team.html). This post-doctoral position is open in the frame of an ANR project that will explore adaptive root plasticity in response to drought in pearl millet in close collaboration with the DYNADIV team of IRD Montpellier (http://diade.ird.fr/en/teams/dynadiv-team.html), and two teams in Senegal and the UK.

Pearl millet is key for food security in arid and semi-arid regions of West Africa and India. In these regions, increased extreme climatic events due to climate change (dry spells and heat waves in particular) are threatening pearl millet cultivation and varieties more adapted to climate uncertainties are needed. Root plastic traits could improve the plant ability to adapt to these conditions by stabilizing yield only under extreme events without negative trade-off in the absence of stress.

The work of the post-doc will aim at identifying the genetic determinants controlling adaptive root plasticity in pearl millet. Original approaches will be developed to calculate root plasticity and correlate this plasticity with agronomical traits. Association genetics (GWAS) combined with functional genomics approaches will be deployed to identify new QTLs/genes controlling plasticity of key root traits.

We are seeking a highly motivated and independent postdoc with skills in molecular biology and genetics with basic knowledge in quantitative genetics, R and command-line interface. The candidate should have good writing and communication skills, and be comfortable working in a collaborative, multi-disciplinary environment.

The post-doc would ideally start in fall 2021. Gross salary will be around 2800âÂÂ¬per month according to experience.

Applications including CV, cover letter and contact of three referees should be send in one PDF file to Drs Alexandre Grondin (alexandre.grondin@ird.fr) and Philippe Cubry (philippe.cubry@ird.fr) before May-30 2021.

Recent lab publications Varshney et al 2017 Nat Biotech (https://doi.org/10.1038/nbt.3943) Burgarella et al 2018 Nat Ecol Evol (https://doi.org/10.1038/s41559-018-0643-y) Debieu et al 2018 PLOS One (https://doi.org/10.1371/journal.pone.0201635) Grondin et al 2020 PLOS One (https://doi.org/10.1371/journal.pone.0233481) Rhone et al 2020 Nat Comm (https://doi.org/10.1038/s41467-020-19066-4)

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Bioinformatic Research associate/ Post-doctoral position in genomic data analysis of domestication

A 20 months position is available at French National Research Institute for Sustainable Development (IRD) in Montpellier, France (http://diade.ird.fr/en/teams/dynadiv-team.html) to study plant genomic diversity associated with 14 plant domestication events. The project is co-jointly led by M Tenaillon, S Glémin, C Dogimont and Y Vigouroux to study impact of domestication on cultivated genome diversity.

Wild relatives of crop species represent an untapped reservoir of adaptive diversity to sustain plant breeding and improvement. However, little has been done to understand the extent and nature of reproductive barriers between wild and cultivated forms, and the underlying evolutionary processes. The project aims at characterizing the evolutionary and molecular determinants of the establishment of genetic barriers that can be 'caught in the act' between recently diverged wild and domesticated lineages.

The candidate will set up a pipeline and make it available for the four scientific teams involved in the project. He/She will carry SNP detection in several systems. He/she will also contribute to the characterization of diversity and divergence patterns along genomes. He/She will test different methods for the characterization of deleterious mutation mutations, thereby contributing to build a comparative dataset across the 14 different species. He/she will be working in close collaboration with members of the four teams, including a PhD student currently working on statistical pipelines for data analysis. He/She will participate to all scientific meetings among the partners of the project, playing a pivotal role on the development of common and accessible tools and workflows. The position is open in the frame of the ANR DOMISOL project and will be based at Montpellier, France.

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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

NaganoU EelConservation

Postdoctoral Researchers (temporary job)

Nagano University - Nagano, Japan

Nagano University is planning to seek a few trained postdoctoral researchers (Statistician and/or Pop-up Argos tag researcher) to work with a team on a study about the population dynamics and fisheries management of Japanese eel (Project Head: Professor Hiroshi Hakoyama). The project is supported by the Fisheries Agency of Japan, and is going to last for at least several years. The outcome of the project is expected to contribute to discussions at FAO, IUCN and CITES and policy design and implementation on the management of Japanese eel.

Duties & Responsibilities

(1) Statistician (frequentist, time-series analysis, mixed-effects models, fisheries management, mathematical modeling): analyzing spatiotemporal multivariate time-series of fisheries and environmental data of Japanese eel in frequentist approaches; developing statistical and mathematical methods for fisheries management.

(2) Pop-up Argos tag, experimental researcher, field-worker: conducting field experiments to track silver eels using pop-up Argos tags at several locations in Japan; conducting laboratory experiments using yellow eels for developing the new pop-up Argos tag cooperating with Little Leonardo Co.

Moreover, all postdoctoral researchers should cooperate with each other, write papers with co-workers, participate in team discussions, assist the members of the team and the lab in all respects, and accept other duties as assigned.

Information

Minimum education: Ph.D. in a related field

Applications: When applying for this position, please send a CV/cover letter and letters of recommendation from the research supervisor or the department head to Hiroshi Hakoyama,hiroshi.hakoyama@nagano.ac.jpby e-mail with the title \$B!H(BNagano_2021\$B!I(B.

Deadline to apply: Ongoing (Open until filled)

Location: 1088 Komaki, Ueda, Nagano 386-0031, Japan

Employment period: from 2021/04/01 (if possible, as soon as possible) to 2022/03/31. The employment period may be extended based on performance and availability of funding.

Regular work hours: 8:30-17:30 (Break time 12:00-13:00), Monday-Friday

Salary: 360,000–470,000 yen a month (according to research experience and achievements). The absence deduction will be calculated based on the amount of absence hours/days in accordance with the laws on employment.

Employee benefit: Employee must join the Japanese national social (health) insurance and pay employment insurance in accordance with laws of Japan. A part of the costs are borne by Employee and deducted from the monthly post-tax remuneration each month on payday (inquiry e-mail address:soumu@nagano.ac.jp). Nagano University will pay the cost of the LCC ticket from your country to Japan at the start of contract , and also pay the cost of the return ticket at the end of contract. Nagano University will pay the cost of a registered guarantor for your apartment.

URL: https://www.nagano.ac.jp/artis-cms/cms-files/-20210521-132945-1132.docx   \$BH";3MN(B <hiroshi-hakoyama@nagano.ac.jp>

NewYorkBotanicalGardens MelastomataceaePhylogenomics

A two-year postdoctoral position in phylogenetics and evolution is available at The New York Botanical Garden for an NSF-Funded project on Phylogenomics of Melastomataceae working with Dr. FabiÂ'n A. Michelangeli. This research is part of a collaborative project with Dr. Lucas Majure, Dr. Nico Cellinese and Dr. Walter Judd at the University of Florida. Qualified candidates should have a Ph.D. in Botany, Biology or Evolutionary Biology by the start date and demonstrable experience working with bioinformatics pipelines for the analysis of different types of next generation sequencing data (particularly Hyb-seq and genome skimming), experience generating and analyzing plant morphological data, and a track record of collaborative work and publishing. Experience organizing and carrying out field work in tropical environments is highly desirable.

Duties will include leading phylogenetic analyses for spe-

cific clades of Melastomataceae using phylogenomic data, coordinating and leading the assembly of family-wide morphological data, and taking the lead on manuscript preparation for specific aspects of the project while also collaborating with other PIs, postdocs and students on additional manuscripts. The position also offers opportunities for training and supervision of graduate and undergraduate students. The successful applicant will also be expected to support, through actions and conduct, NYBG'Âs Inclusion, Diversity, Equity and Accessibility initiatives and actively help to build and maintain an inclusive organization culture.

For more details on the position or informal inquiries please contact FabiÂ'n A. Michelangeli (fabian@nybg.org), but all applicants should apply through the NYBG website (http://www.nybg.org/-employment/) and include a curriculum vitae, a one-page statement of research interests, up to three reprints if available, and arrange for three letter of recommendation to be sent to hr@nybg.org).

Applications will be reviewed, starting on June 15th, until the position is filled. Starting date is negotiable but no later than January 2022.

The New York Botanical Garden is an Equal Opportunity Employer.

"Michelangeli, Fabian" <fabian@nybg.org>

NorthCarolinaStateU PopulationGeneticsModeling

Postdoc: Modeling Gene Drive and Evolution of Insecticide Resistance in Mosquitoes

OVERVIEW: We have funding from NIH for a project titled "Combining Aedes aegypti genomics and modeling to improve gene drive strategies and our understanding of insecticide resistance evolution". Aedes aegypti is the primary vector of dengue, Zika, chikungunya, and urban yellow-fever. We are searching for a postdoc to work on the modeling aspects of the project.

PROJECT DESCRIPTION: The idea of using selfish genetic elements to drive specific transgenes into a mosquito population either to reduce its size or to render it unable to transmit a particular pathogen was proposed over 40 years ago. It is only recently, however, with the advent of CRISPR-based gene editing technology, that this approach has gained broad attention from researchers and the news media. The need for this new technology is in part due to evolution of mosquito resistance to insecticides.

The most straightforward approaches for building gene drives using CRISPR/Cas9 technologies are theoretically expected to result in spread of the gene drive to individuals in all populations that are connected by even minimal gene flow. These approaches are appropriate in some cases, but detailed mathematical models are needed to understand the dynamics of spread and the potential for resistance evolving to the gene drive mechanisms. Our group and others have proposed more complex approaches for developing gene drives that are spatially and/or temporally limited. Novel molecular approaches accompanied by modeling are needed for development of these limited gene drives.

We currently have a detailed spatial model that simulates the population dynamics and population genetics of Ae. aegypti in a city, Iquitos, in the Amazonian region of Peru. There are rich data sets on both mosquito dynamics and dengue epidemiology that have been collected in this city. One important characteristic of this mosquito is limited among house movement and strong population structure. A main goal of our NIH grant is to modify this model to explore how and to what extent population structure will impact insecticide resistance evolution and the performance of novel gene drive strategies.

Dhole S, Lloyd AL, Gould F. 2020. Gene drive dynamics in natural populations: the importance of density-dependence, space and sex. Annu. Rev. Ecol. Evol. Syst. 51:505'V31

JOB DESCRIPTION: The postdoc in this position will lead efforts on modifying the detailed model and utilizing it to test hypotheses. The postdoc will have the option of also conceptualizing and developing general models to evaluate novel approaches for building spatially/temporally limited gene drives. Our project is strengthened by collaborations with a number of labs in the US and in Peru, and activity in the Genetic Engineering and Society Center at NC State that examines societal aspects of novel genetic technologies. The postdoc will interact with members of these other research groups. If desired, there will be an opportunity for some work in Peru and for mentoring undergraduate and graduate students. The appointment is for two-years with the potential to write new grants for extension beyond that period.

QUALIFICATIONS: We are looking for a postdoc with a solid background in population biology and population genetics who has experience with modeling and who wants to do applied research. Experience with C++ or related languages is desirable. Ability to work indepen-

dently and to communicate effectively as a member of a team is essential.

To apply: email a cover letter and CV to Fred_Gould@ncsu.edu AND Alun Lloyd@ncsu.edu

Fred Gould <fgould@ncsu.edu>

RutgersU FishEvoDevo

Postdoctoral Position in Evolutionary Developmental Biology of Fish, Rutgers the State University of New Jersey, NJ

The Nakamura lab in Department of Genetics at Rutgers university has a postdoctoral position available. The long-term goal of Nakamura lab is to identify the genetic mechanisms underlying fish diversity and their contribution to the fish-to-tetrapod transition. We are particularly interested in how fish fin skeletons diversified and evolved into tetrapod limbs. To this end, we bridge functional genomics, genetics, and embryology using model and non-model organisms, including zebrafish, skates, and sharks. More information about ongoing research projects can be found on the lab website (http://nakamuralab.com/).

Candidates should have strong research records in any of the following areas: evolutionary biology, developmental biology, genomics, or other relevant fields. Our lab is a highly interdisciplinary environment, therefore, scientific curiosity and strong communication skills are necessary. Experience in zebrafish embryology, high-throughput sequencing, or bioinformatics data analysis is preferred, but not required.

Rutgers University is located in New Brunswick, NJ, which is only 45 minutes away from NYC by train. Many competitive research universities and institutes are in the Northeast area, offering remarkable opportunities for collaboration and research conferences. The Nakamura lab regularly visits the American Museum of Natural History (https://www.amnh.org/) and the Marine Biological laboratory (https://www.mbl.edu/) for the purpose of analyzing unique specimens and educating students.

Candidates should send a curriculum vitae, brief statement of current research, and contact for 3 references to nakamura@dls.rutgers.edu (Tetsuya Nakamura).

Tetsuya Nakamura <tn241@rutgers.edu>

StonyBrookU NY Paleogenomics

Postdoctoral Position in Paleogenomics, Stony Brook University

The Veeramah Lab at Stony Brook (https://you.stonybrook.edu/veeramahlab/) has an opening for a postdoctoral researcher to begin in Fall 2021 to conduct research using paleogenomics as part of an ERC Synergy project, HistoGenes (https://www.histogenes.org/).

The position is funded for five years and will involve the bioinformatic processing and population genetic analysis of paleogenomic data from 5th9th century Europe being generated in collaboration with labs in Leipzig (Germany) and Budapest (Hungary). The individual's primary task will be to perform population genetic analysis of this data and potentially develop new methods (for example approaches capitalizing on rare-variants in whole genome data, that integrate temporal-spatial information or that take advantage of novel machine learning frameworks). They will work under close collaboration with senior population genetics researchers in the US and German teams. As well as primary research duties, applicants will be expected to write papers, help in grant writing and train/mentor graduate students.

All applicants are required to have a PhD or equivalent foreign degree in the areas of population, evolutionary or anthropological genetics (or related fields) in hand by August 2021. Ideally candidates will have experience in processing 2nd generation sequencing data and analyzing paleogenomics data, knowledge of python or equivalent or programming languages and excellent English skills as demonstrated by peer-reviewed scientific manuscripts. Applications should also be able to work as part of a team and think creatively.

Applications will be accepted until June 16th 2021. Applications should apply online at tinyurl.com/2pdf3y7a < https://t.co/enc3Qu4Tyz?amp=3D1 >

The official REF# is: 2101300

Applicants should submit a State employment application, a cover letter, CV and a one page research statement. At least two letters of recommendation will be requested of candidates selected for interview, so please include contact information for references in your cover letter.

Inquiries about the job can be made by email to Kr-

ishna.Veeramah@stonybrook.edu.

Stony Brook University is an equal opportunity/affirmative action employer.

"krishna.veeramah@stonybrook.edu"
<krishna.veeramah@stonybrook.edu>

SUNYDownstateHealth GeneFamilyEvolution

A Postdoctoral Research Fellow position is available in Sergios-Orestis Kolokotronis' research group at the Department of Epidemiology & Biostatistics in the School of Public Health and the Institute for Genomic Health at SUNY Downstate Health Sciences University in Brooklyn, NY. The successful applicant will join a large, collaborative NSF-funded project to disentangle the genome evolution of gymnosperms, the oldest surviving lineage of seed plants. Three of the four extant gymnosperm lineages contain species which Darwin termed "living fossils." These have been present since the Devonian Era and have survived an incredible range of climatic changes, mass extinction events, and adaptation challenges. The genomes of almost all the gymnosperms are extremely large and complex and have been somewhat refractive to genomic characterization as a result. Through the use of nanopore sequencing, transcriptomics, and epigenetics, we have been characterizing the genomes of these species, asking questions on evolutionary radiations and genome resilience. In this project, we interact with the genome assembly and annotation group, and contribute to orthology assessment. We investigate gene family evolution by adopting macroevolutionary phylogenetic methods, phylotranscriptomics, as well as natural selection scans. Our wider interests draw from population genetics, phylogenetics and community ecology, using bioinformatics — and computational biology to understand organismal diversification and adaptation across landscapes and time scales. Our group is located in the new Public Health Academic Building on the SUNY Downstate campus in Central Brooklyn. We interact with a diverse group of health research investigators in the Institute for Genomic Health, and through our affiliations in the School of Public Health and the Division of Infectious Diseases in the College of Medicine. Our lab is outfitted with an Illumina NovaSeq 6000 instrument for high-throughput sequencing, and we have been expanding our HPC capacity on site and on the cloud. HPC access is also available at partner institutions through the PI. More information can be found at http://kolokolab.org and https://scholar.google.com/citations?user=u3i_xH4AAAAJ&hl=en . — Candidates should have a doctoral -or equivalent- degree in life or computational sciences. A training background in bioinformatics, computational biology, molecular evolution and comparative genomics is required. A keen interest in plant biology and infectious disease systems is desirable. The successful candidate must be capable of working independently in an interdisciplinary, diverse, collaborative environment, and have strong analytical, quantitative, and English writing skills, evidenced by scholarly peer-reviewed publications. In addition to formal collaborations with our partner institutions in this project (CSHL, NYBG, NYU, AMNH, JHU, Purdue, NY Plant Genomics Consortium), opportunities exist to branch out in research on genomic epidemiology of infectious and chronic diseases (funded by NIH and NSF), grant proposal writing, mentoring of students, and teaching. — Salary is commensurate with experience. Start date is ASAP. Applications should include in this order: 1) a Statement of Research Interests, 2) a CV, 3) two (2) manuscripts, and 4) the contact information of 3 referees in a single PDF file emailed to sok@downstate.edu with this Subject line "Postdoc-NSF Plants". Referees should be notified that they might be contacted.

— SUNY Downstate Health Sciences University is an affirmative-action, equal-opportunity employer and does not discriminate on the basis of race, color, national origin, religion, creed, age, disability, sex, gender identity or expression, sexual orientation, familial status, pregnancy, predisposing genetic characteristics, military status, domestic violence victim status, criminal conviction, and all other protected classes under federal or state laws. Women, minorities, veterans, individuals with disabilities and members of underrepresented groups are encouraged to apply. If you are an individual with a disability and need a reasonable accommodation for any part of the application process, or in order to perform the essential functions of a position, please contact Human Resources at 718-270-3025.

Sergios-Orestis Kolokotronis <koloko@amnh.org>

Switzerland ClusterHire BlueGreenDiversity

Cluster hire of multiple postdoc and PhD positions to work on the Blue-Green Biodiversity (BGB2021-2024) research initiative of Eawag and WSL

The loss of biodiversity is, next to climate change, one of the biggest challenges humanity is facing. Research and action to reverse and mitigate the loss of biodiversity and associated ecosystem functions and services are thus crucially needed. In order to tackle this scientifically and societally urgent topic, the ETH Board has funded a research program on Blue-Green Biodiversity (BGB, www.eawag.ch/bgb and www.wsl.ch/bgb). Its goal is to strengthen interdisciplinary biodiversity research of WSL and Eawag in order to find answers to urgent social challenges of species loss as quickly as possible.

The BGB program started in 2020, with a series of projects. In its second phase, from 2021-2024, the program is now funding a series of projects including both postdoctoral and PhD student positions. All of these positions will be set in a highly collaborative framework at both institutions. Postdocs and PhD students will be employed at WSL or Eawag and will profit from a highly dynamic and international research community in biodiversity, ecology, evolution, environmental and social sciences.

The funded projects belong to a research or implementation track, respectively. Candidates for all positions will be selected to ensure strong complementarity among projects. We are also very committed to hire people from a diverse background, ensuring cultural, ethnic, and gender diversity. We invite interested candidates with a background and interest in biodiversity sciences (ecology, evolution) or related fields to apply. Postdoc positions are generally funded for two years. PhD positions are funded for four years, and will be accompanied with enrollment at a degree granting university (e.g., ETHZ, UZH, UniBE). Generally, positions are expected to be filled this summer. Salary and benefits are very competitive. Candidates interested in multiple positions can apply for several projects, but should cross-reference this in their applications. Details about individual projects can be found at the respective links; questions can be addressed to the respective project leaders. Both WSL and Eawag offer unique research and working environment and are committed to pro-moting equal opportunities for women and men and to support the compatibility of family and work. For more information, see www.wsl.ch and www.eawag.ch, respectively.

The positions listed below are opening now and selection of candidates will start from end-May onwards until all positions are filled. During the coming two years, there will be further positions opening and they will be announced in due time/individually. For more information on the BGB initiative, see: www.eawag.ch/bgb and www.wsl.ch/bgb.

For the following projects, we are now looking for competitive candidates:

Research track Project 1 - Blue-Green Stormwater Infrastructure Meets Biodiversity in the City [Benefit] Project lead: Dr. Lauren M. Cook (Eawag) and Dr. Marco Moretti (WSL) Information for interested postdocs: https://apply.refline.ch/673277/0848/-pub/1/index.html Information for interested PhD students: https://apply.refline.ch/673277/0849/pub/1/-index.html Project 2 - Food-webs across aquatic-terrestrial environments in forests in the face of climate change Project lead: Prof. Dr. Martin Gossner (WSL/ETHZ) and Prof. Dr. Carsten Schubert (Eawag/ETHZ) Information for interested postdocs: https://apply.refline.ch/273855/1164/pub/-1/index.html Information for interested PhD students: https://apply.refline.ch/273855/1165/pub/1/-index.html Project 3 - Species interactions in beaver engineered habitats link land-water ecosystem processes Project lead: Dr. Anita C. Risch (WSL) and Dr. Francesco Pomati (Eawag) Information for interested PhD students: https://apply.refline.ch/273855/1163/-pub/1/index.html Project 4 - Blue-Green Cyanobacteria: Diversity, Toxins and alpine Tourism Project lead: Prof. Dr. Christoph Scheidegger (WSL) and Dr. Elisabeth Janssen (Eawag) Information for interested postdocs: https://apply.refline.ch/273855/1161/-pub/1/index.html Information for interested PhD students: https://apply.refline.ch/273855/1162/pub/1/-index.html Project 5 - Assessing and designing blue-green conservation

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UArizona PlantMicrobeInvasions

POSITION: Postdoctoral Research Associate in the laboratory of Dr. Katrina Dlugosch in the Department of Ecology and Evolutionary Biology at the University of Arizona, Tucson, AZ, USA.

POSITION DESCRIPTION: This postdoctoral research position is funded by the National Science Foundation to work with the Dlugosch lab group (http://dlugoschlab.arizona.edu/) on the evolution and ecological genomics of plant-microbe interactions in the invasive plant yellow starthistle (Centaurea solstitialis). We are using greenhouse experiments, microbial culturing, plant immune function assays, microbiome sequencing, plant population genomics, plant QTL mapping, plant RNAseq analyses, and selection experiments to study the evolution of species interactions during range expansion and their impact on the spread of invading plant populations. This position will join the project described here, which is ongoing, https://www.ograntss.org/grants/dlugosch_katrina_2017 . The successful candidate will have the opportunity to lead publications related to the culmination of this multi-year project.

In addition, there will be opportunities for the postdoc to propose their own research directions, and to be involved in the mentoring of undergraduate students.

The successful candidate will join an active lab of undergraduates, graduate students, and postdocs, focused on the rapid evolution of plants in response to novel environments.

DUTIES & RESPONSIBILITIES: The successful candidate will be responsible for leading greenhouse-based plant-soil feedback and selection experiments, with associated plant RNAseq and microbial genomic studies and bioinformatic analyses.

The position is for one year initially, with reappointment for up to two additional years, subject to satisfactory performance. Duties will be located in Tucson, Arizona, USA, and the start date is negotiable as early as Aug 2021 or as late as Jan 2022.

MINIMUM QUALIFICATIONS: *PhD in Biology or a related field *Experience producing and analyzing molecular genetic data *Authorship of peer-reviewed publications of research in a field related to the position

DESIRABLE EXPERIENCE (Any of the following): *Experience rearing plants in a greenhouse or growth chamber *Experience preparing plant DNA for next-generation sequencing *Experience with QTL mapping / GWAS *Experience with RNA extraction and RNAseq library preparation *Experience with microbiome sequencing *Experience with bioinformatic analyses of genomic data *Experience culturing bacteria or fungi *Experience with assays of plant defense functions

TO APPLY: Submit a CV and a cover letter that describes your qualifications for this position, your career interests, and how this position would advance your career goals, to the open listing 5123 at https://talent.arizona.edu/ .Further details about pay and benefits are detailed in the position listing. (Direct link to position here: https://arizona.csod.com/ux/ats/careersite/4/home?c=arizona&sq=req5123)

Further inquiries about the position may be directed to Dr. Katrina Dlugosch (kdlugosch@arizona.edu).

Review of applications will begin May 17 and the position will remain open until filled.

Katrina M. Dlugosch katrina.dlugosch@gmail.com

Katrina Dlugosch <katrina.dlugosch@gmail.com>

UCalifornia Berkeley MosquitoLandscapeGenomics

POSTDOC POSITION IN MOSQUITO SURVEILLANCE & LANDSCAPE GENOMICS

The Marshall Lab (https://www.marshalllab.com/) at the UC Berkeley School of Public Health is seeking to hire a postdoctoral scholar to work on mathematical and ecological aspects of gene drive systems in mosquito vectors of malaria, dengue and other mosquito-borne diseases. The position is initially for one year, with the possibility of extension, and is available mid-2021. Salary is commensurate with experience, and full benefits are included.

The successful candidate will work on exciting collaborative projects with a consortium of mathematical modelers, molecular biologists, ecologists and epidemiologists, mostly throughout the University of California system. Molecular biology labs that we collaborate with include the Akbari Lab (https://www.akbarilab.com/), Bier Lab (http://bierlab.weebly.com/) and Gantz Lab (http://www.gantzlab.org/) at UCSD, and the

James Lab at UC Irvine. Ecology labs that we collaborate with include the Vector Genetics Lab (https://vectorgeneticslab.ucdavis.edu/) at UC Davis and the Mosquito Control Lab at QIMR Berghofer in Australia. We also collaborate with TIGS-UCSD (https://tigs.ucsd.edu/) and the Debug Project (https://debug.com/) at Verily Life Sciences (https://-/verily.com/), and serve as modeling lead for the UC Irvine Malaria Initiative (https://ucimi.org/).

Tasks that we are seeking help with include: * Developing methods to infer mosquito movement patterns and demography from landscape genomic data, * Informing mosquito monitoring and surveillance protocols to assess intervention efficacy and unintended spread, * Contributing to development of our modeling framework, the Mosquito Gene Drive Explorer (MGDrivE) (https://marshalllab.github.io/MGDrivE/), & * Mentoring PhD, Masters and undergraduate students.

An ideal candidate will have: * A strong background in applied mathematics, statistics and/or computer science, * Experience with population genetics, genomics or ecological and epidemiological modeling, * An interest in mosquitoes and/or mosquito-borne diseases, & * An interest in mentoring students and promoting diversity, equity and inclusion in research.

If you are interested in the position, please send: i) your CV, including a list of publications and the names and email addresses of three potential referees, ii) PDFs of your two most significant publications or manuscripts to date, and iii) a cover letter describing your research interests and motivations for joining our lab to John Marshall at john.marshall@berkeley.edu. Inquiries are also welcome. Additional information about the research in our lab can be found at https://www.marshalllab.com/. The position will remain open until filled. The first review date will be May 21st 2021.

UC Berkeley has large and vibrant public health, ecology and computational biology communities spanning the School of Public Health, the Department of Integrative Biology, the Department of Environmental Science, Policy and Management, the Center for Computational Biology, the Innovative Genomics Institute, and more. UC Berkeley offers competitive salaries, excellent benefits and is an equal opportunity employer. The City of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

"Marshall, John M." <john.marshall@berkeley.edu>

John Marshall <john.marshall@berkeley.edu>

UCalifornia Berkeley PupfishSpeciationGenetics

Postdoctoral position on the genetics, development, and origins of adaptive radiation in Caribbean pupfishes

The Martin Fish Speciation Lab at the University of California Berkeley Museum of Vertebrate Zoology seeks a postdoc for functional genetic and quantitative genetic studies of adaptive craniofacial traits in a sympatric radiation of trophic specialist pupfishes. Pupfishes present a rare opportunity to investigate the 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 lake environments.

A multi-year position is available (initial 12 month appointment with the possibility of renewal for at least one more year). This research is funded by both NIH and NSF grants. Start date is flexible, but ideally around August 2021. Salary starts at $54,540/year.

We are seeking postdoctoral applicants with interests/expertise in any of the following areas: *functional genetics (CRISPR experience preferred), quantitative genetics, craniofacial development, or speciation genomics*.

We have identified several candidate causal variants in craniofacial regulatory networks that warrant further functional investigation. See our recent PNAS paper for additional context: www.pnas.org/content/118/20/-e2011811118 The postdoc will have the opportunity to participate in short fieldwork excursions to the Bahamas starting in 2022, but previous field experience is not necessary and participation is not required.

Required qualifications:

Ph.D. or equivalent degree in biology, evolution, genetics, or related field. Publication of work based on dissertation. Programming experience in R or python. BIPOC applicants are especially encouraged to apply.

UC Berkeley contains a world-class community of integrative biologists studying adaptive radiation and speciation spanning the Department of Integrative Biology, the Museum of Vertebrate Zoology, the Department of Environmental Science, Policy, and Management, the Department of Molecular and Cell Biology, the Center for Theoretical Evolutionary Genomics, and more.

UC Berkeley offers competitive salaries, excellent benefits, and is an equal opportunity employer. The city of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

The University of California is an Equal Opportunity/Affirmative

Action Employer. All qualified applicants will receive consideration

for employment without regard to race, color, religion, sex, sexual

orientation, gender identity, national origin, disability,

age, or protected veteran status.

Interested candidates should send an email detailing their interest in the position and relevant experience along with their CV, PDFs of two recent publications, and contact information for three references to Chris Martin at chmartin@berkeley.edu

This position is open until filled, but please apply within the next two weeks for full consideration. Please feel free to contact me at the above email address with any questions.

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

christopher.h.martin@gmail.com

UCalifornia Davis PopulationAdaptationGenomics

Background Info: Research in the Whitehead lab (https://whiteheadresearch.wordpress.com/) focuses on evolutionary change in human-altered environments. We seek applicants for a Postdoctoral Research Associate to study population genetic change through space and time in Pacific herring. The causes of the collapse of the Prince William Sound (PWS) Pacific herring stock are controversial, and the reasons for the lack of recovery remain a mystery. We hypothesize that interactions between the 1989 Exxon Valdez oil spill and a subsequent viral epidemic were influential. We have collected whole genome sequences from ~1,300 individual fish from across Alaska and across time (four times spanning three decades), and throughout the rest of their range, to explore genomic change associated with the collapse and the period since; with these data we seek to explore and test hypotheses about the causes and consequences of the collapse, and test hypotheses about the genetic basis of parallel local adaptation. This huge population genomics dataset is ready for the right candidate to make rapid progress. Data are collected, and curated; we have a filtered variant data set where summary population genetics statistics have been estimated. Collaborations are in place with scientists in academia and with State and Federal agencies. The ideal candidate has experience in population genetics, statistical genetics, and computational biology. We are especially interested in candidates with a passion for open science and for connecting their work to decision makers, the public, and the broader conservation biology and evolutionary biology communities. There is funding for one year, with possibility of extension. We are open to the candidate working remotely. Our group is committed to creating a safe, inclusive, diverse, optimistic, and equitable work environment.

Responsibilities: Contribution to analysis strategy, code development, data analysis and interpretation, review of relevant literature, preparation of project reports and manuscripts for publication in peer-reviewed journals, presentation at professional conferences.

Minimum qualifications: PhD in genetics, population biology, evolution, genome science, data science, or another relevant field.

Preferred qualifications: Preference will be given to applicants with 1) expertise in population genomics and computational biology; 2) strong communication and organizational skills; 3) can code in R and python and have an interest in transparent and reproducible science; and 4) strong publication records, or the potential for developing one. Our team believes in and values the power of diversity; candidates from groups that have historically been underrepresented in science are strongly encouraged to apply.

Salary: Commensurate with qualifications and experience.

Application: Interested candidates should submit:

a one-page cover letter, your CV, and names and contact information of at least three references familiar with your work.

Please submit materials to Andrew Whitehead (awhitehead@ucdavis.edu) with "Popgen Postdoc" in the subject. Applications will be reviewed as they arrive, interviews will be over Zoom, and the position will remain open until filled. The position is available immediately,

with preferred start dates between late spring and early summer 2021.

Email any questions to Andrew Whitehead (awhitehead@ucdavis.edu)

Andrew Whitehead, Ph.D. Department of Environmental Toxicology 4121 Meyer Hall University of California, Davis, CA 95616 530-754-8982 <tel:530-754-8982> http://whiteheadresearch.wordpress.com/ Andrew Whitehead <awhitehead@ucdavis.edu>

UCalifornia LosAngeles AnthroGenomics

Postdoctoral Researcher in Biological Anthropology Description The Bigham Lab in the Department of Anthropology at UCLA invites applicants for a Postdoctoral Researcher Position. The Bigham Lab for Anthropological Genomics is focused on understanding human genetic adaptation to environmental pressures and how these adaptations affect the range of modern human phenotypic diversity. We are looking for a postdoctoral scholar to lead and perform bioinformatic analysis of whole genome and genotyping array data to identify genes under selection, identify putative causal variants for adaptive phenotypes through genotype-phenotype analysis, and conduct field work in Latin America. In addition, the scholar will prepare manuscripts for scientific journals, mentor graduate students in data analysis, present data at scientific meetings, and prepare grant applications.

The candidate must hold a PhD in Biological Anthropology, Evolutionary Biology, Human Genetics, Bioinformatics, or related discipline. Applicants will have strong quantitative backgrounds and experience in bioinformatics including programming in R and Python/Perl as well as cluster computing. In addition, applicants will display excellent interpersonal and writing skills.

The initial appointment is for 12 months with a possibility of renewal. Terms and conditions of employment are subject to UC policy and any appropriate collective bargaining agreement. Salary based on qualifications.

Please submit your application through UCLA Academic Recruit at: https://recruit.apo.ucla.edu/-JPF06448. Applications should include a letter of introduction, a curriculum vita, a research statement and names and contact information for three references.

Review of applications will begin June 16, 2021 and continue until the position is filled. Mailed or emailed submissions will not be accepted. Informal inquiries are welcome. Please contact Dr. Abigail Bigham (awbigham@ucla.edu).

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, age, sexual orientation, gender identity, or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: UC Nondiscrimination & Affirmative Action Policy.

Obed Aram Garcia <oagc@stanford.edu>

UCaliforniaSantaCruz GenomicEpidemiology

PROJECT DESCRIPTION: We seek an enthusiastic postdoctoral fellow with experience in computer science, bioinformatics and/or virology to work on approaches for large-scale phylogenetic inference and interpretation.

POSITION DESCRIPTION: The Genomics Institute at the University of California, Santa Cruz (UCSC) invites applications for the Postdoctoral Scholar in Genomic Epidemiology who will work under the direction of Drs. David Haussler and Russell Corbett-Detig. The postdoctoral scholar will have a background and demonstrated excellence in genomic epidemiology or related fields. The postdoctoral scholar will collaborate on a large-scale California-wide SARS-CoV genomic epidemiology public health initiative. Key responsibilities will be to develop approaches for rapid computational analysis of viral genomic datasets to extract public health immediately actionable data and write up the research results with the goal of publication. This postdoctoral scholar will work as a part of a large multidisciplinary team to support diverse efforts to leverage genomic sequence data to make epidemiological inferences.

Applicants with expertise in the computational aspects of viral genomic data, phylogenetics, and epidemiology, are particularly valued and are strongly encouraged to apply.

BASIC QUALIFICATIONS: Ph.D. (or equivalent foreign degree) in Epidemiology, Bioinformatics, Biology, Computer Science, Genetics, Engineering, Virology, or related field. Ph.D. must be in hand at time of the

initial appointment.

APPLICATION REQUIREMENTS: All documents and materials must be submitted as PDFs and should be forwarded to genomicshr@ucsc.edu by May 15, 2021. Please refer to Position title, Postdoctoral Scholar in Genomic Epidemiology in all correspondence.

REQUESTED DOCUMENTS/MATERIALS: Letter of application that briefly summarizes your qualifications and interest in the position. Curriculum vitae.

QUALIFICATIONS: Basic qualifications (required at time of application)

SALARY RANGE: Commensurate with qualifications and experience. Minimum annual salary rate of $62,000 is made based on the individual's Experience Level, which is determined by the number of months of post-doctoral service at any institution. See current salary scale for Postdoctoral Titles at https://apo.ucsc.edu/-compensation/salary-scales/index.html Percent time: Full-time (100%)

Anticipated start: As soon as possible after initial review of the applications. Ph.D. must be in hand at time of the initial appointment.

Position duration: Postdoctoral Scholar appointments are full-time; the initial appointment is for a minimum of one year, with the possibility of reappointment. Reappointment will be contingent upon positive performance review and availability of funding. The total duration of an individual's postdoctoral service may not exceed five years, including postdoctoral service at any institution. Under limited circumstances, an exception to this limit may be considered, not to exceed a sixth year.

APPLICATION Timeline Open April 13th, 2021 through Saturday, May 15, 2021 at 11:59pm (Pacific Time) Submit Applications at: https://-recruit.ucsc.edu/JPF01012 QUESTIONS: Contact rucorbet@ucsc.edu with any questions.

russcd@gmail.com

UChicago AncientDNA

Postdoctoral Fellow at Rank of Instructor University of Chicago, Oriental Institute

Apply here: https://academicjobs.uchicago.edu/-positions/72605 Description This is a twenty-four-month, non-renewable appointment. During this appointment, the Post-Doctoral Fellow will work closely with University of Chicago faculty members from the Oriental Institute and the Department of Human Genetics to do extraction and analysis of ancient DNA from Bronze Age human remains excavated at archaeological sites in the Middle East as part of a research project entitled "Genomes, Migrations, and Culture in the Early Civilizations of the Middle East." They will also assist in publishing the results of the research as a co-author and will help to organize quarterly workshops and an international conference on archaeogenetic research concerning the ancient Mediterranean and Middle East. They will also teach one quarter-length course per year on ancient DNA/archaeogenetics.

Core Responsibilities

* Perform tasks related to the extraction and analysis of ancient DNA from remains housed in the Oriental Institute Museum and the Field Museum of Natural History; the laboratory work will be conducted primarily in the "GenSCAPE" ancient DNA laboratory of the Dept. of Human Genetics under the supervision of Prof. Maanasa Raghavan. * Perform tasks related to the computational management and statistical analysis of ancient genomic data under the supervision of Profs. John Novembre (Human Genetics) and David Schloen (Oriental Institute). * Organize quarterly workshops at the University of Chicago's Neubauer Collegium for Culture and Society for participants in the "Genomes, Migrations, and Culture in the Early Civilizations of the Middle East" project; and also organize a concluding international conference for this project to be held in Spring 2023. * Teach one quarter-length course per year on ancient DNA and archaeogenetics.

Preferred Qualifications

* Ph.D. in anthropology with a specialization in archaeogenetics * Lab experience in extracting and analyzing ancient DNA * Expertise in some aspect of the archaeology of the ancient Mediterranean and/or Middle East

Competencies

* Knowledge of both archaeology and human genetics and awareness of the interpretive issues raised by the study of genetic variation in ancient human populations * Knowledge of how genomic data bear upon the archaeological reconstruction of ancient population movements and cultural change * Laboratory skills relevant to ancient DNA research * Strong skills in academic research, writing, and communication

Applicants should submit:

* Cover Letter * Curriculum Vitae * Three letters of reference

Review of applications will begin on Friday, April 2, 2021, and will continue until the position is filled. Start date is July 1, 2021. Inquiries can be directed to oi-administration@uchicago.edu with the subject heading Postdoctoral Fellow (archaeogenetics).

We seek a diverse pool of applicants who wish to join an academic community that places the highest value on rigorous inquiry and encourages diverse perspectives, experiences, groups of individuals, and ideas to inform and stimulate intellectual challenge, engagement, and exchange. The University's Statements on Diversity are at https://provost.uchicago.edu/statements-diversity. The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer and does not discriminate on the basis of race, color, religion, sex, sexual orientation, gender identity, national or ethnic origin, age, status as an individual with a disability, protected veteran status, genetic information, or other protected classes under the law. For additional information please see the University's Notice of Nondiscrimination < https://www.uchicago.edu/-about/non_discrimination_statement/ >. Job seekers in need of a reasonable accommodation to complete the application process should call 773-702-1032 or email equalopportunity@uchicago.edu with their request.

Maanasa Raghavan <mraghavan@uchicago.edu>

UCologne Wageningen ExperimentalEvolution

Postdoc position in experimental evolution of antibiotic resistance

We seek a postdoc for a collaborative project between the groups of Prof. Joachim Krug, Prof. Tobias Bollenbach (both at the Institute for Biological Physics, University of Cologne) and Prof. Arjan de Visser (Laboratory of Genetics, Wageningen University) on predicting evolutionary pathways to beta-lactam resistance. The project combines theory and experiments and is part of the Collaborative Research Center 1310 "Predictability in Evolution" funded by Deutsche Forschungsgemeinschaft (DFG) and coordinated at the University of Cologne. The aim of the project is to identify key predictors of the evolution of beta-lactam resistance across time scales and levels of organization. The postdoc will perform evolution experiments with E. coli and TEM-1 beta-lactamase to develop and test predictions about the effect of genetic and ecological constraints on the choice and repeatability of evolutionary trajectories. The experimental work will be done in close collaboration with a theoretical postdoc appointed within the same project. The position is available immediately and will initially be until 30 June 2022, with possibilities for extension.

Profile: We seek a highly motivated person with a PhD in molecular evolutionary biology, microbial genetics or enzyme engineering. Solid experience with microbiological and molecular genetics and genome analyses are absolute requirements; experience with evolutionary theory and quantitative models are an asset. Experimental work will be carried out at the University of Cologne (lab of Tobias Bollenbach) and Wageningen University (lab of Arjan de Visser). Travel between Cologne and Wageningen takes a bit more than two hours by train. Salary will be paid according to level E13 of the German public service salary scale (TV-L). The project can start as soon as we have found a suitable candidate.

Applications: Submit enquiries and applications (including CV, letter of motivation and names and contact information of two references) before 1st June 2021 to Arjan de Visser or Joachim Krug. The University of Cologne is one of the leading German institutions in molecular and evolutionary genetics. Wageningen University is a leading university in the field of the life sciences. The University of Cologne is an equal opportunity employer in compliance with the German disability laws. Women and handicapped persons are therefore strongly encouraged to apply.

Prof. Arjan de Visser Laboratory of Genetics Wageningen University, Radix building Droevendaalsesteeg 1 6708 PB Wageningen The Netherlands P: (+)31 317 483144 M: arjan.devisser@wur.nl W: https://-arjandevisserlab.wordpress.com Prof. Joachim Krug Institute for Biological Physics Zülpicher Strasse 77 50937 Köln Germany P: (+)49 221 470 2818 M: jkrug@uni-koeln.de W: www.thp.uni-koeln.de/krug/ "Visser, Arjan de" <arjan.devisser@wur.nl>

UConnecticut EvolutionaryBioinformatics

University of Connecticut: Postdoctoral researcher in evolutionary genomics and transcriptomics

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 research group studies the evolution of species interactions, adaptation, and trait variation, merging expertise in ecology, genetics, and immunology, with stickleback-cestode interactions as a dominant focus. In recent years we have generated multiple large genomic and transcriptomic datasets concerning gene expression responses to cestode infection, both stickleback and cestode population differentiation, and QTL mapping. We seek an individual with experience in bioinformatics relevant to population genetic and/or transcriptomic analyses of genetic data, to contribute to analyses and publications of existing data. Opportunities exist to pursue side-projects along with the core project task.

The position is funded by a NIH and NSF grant.

The postdoc will join an ongoing NIH-funded project to use CRISPR/cas9 gene editing of threespine stickleback to evaluate the phenotypic effect of candidate genes on host immune phenotypes and resistance to cestode infection. The postdoc may also begin work on a related question of how cestode genotype affects infection outcome.

Tasks: The postdoctoral researcher will conduct analyses of existing population genomic and transcriptomic datasets and publish peer-reviewed articles reporting results arising from these data.

Duration: The position is currently funded for one year. The position could extend longer, contingent on availability of additional grant or fellowship funds, which the PI is actively applying for. The postdoc should be able to start in summer or fall of 2021, exact dates to be negotiated.

Compensation: Starting salary will be $54,000, plus health benefits.

Qualifications: Applicants must have a PhD in evolutionary biology, genetics, computational biology, or a closely related field. Prior experience with analyses of genomic or transcriptomic data is essential. Expertise in population genetics is strongly preferred. Previous research experience and publications should demonstrate a commitment to basic research, good work ethic, computational skills, organizational ability, and publication productivity.

Applications should electronically submit a single pdf file containing the following, in order: 1) A statement of past research achievements, including relevant skills (1-2 pages) 2) A statement of what you can contribute to the Bolnick Lab's research (1 page) 3) CV 4) A copy of two publications or submitted manuscripts.

3) 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), though applicants will eventually need to also submit materials via the University of Connecticut job site once the position is posted (URL to be determined, inquire from Dr. Bolnick). Include the subject line "Evolutionary bioinformatics Postdoc: <YOUR NAME>". Application review will begin on June 1 2021, though late applications will be accepted 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=-cfwxm0AAAAAJ&hl=en).

The University of Connecticut is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Texas Disability Services Office (http://sites.utexas.edu/disability/). 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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UCopenhagen WeedEvollution

Postdoc in Weed Evolution and Population Genomics

Department of Plant and Environmental Sciences,Faculty of Science, University of Copenhagen, Denmark.

Description of the scientific environment

The Department of Plant and Environmental Sciences conducts fundamental research and has a strong focus on applying basic science to solve real world challenges, primarily within the plant, soil and environmental sciences. Research and teaching cover natural resources, agriculture, biotechnology and synthetic biology from the molecular to landscape scales.

The weed ecology and evolution group investigates the eco-evolutionary processes that dictate the adaptation and persistence of weedy and invasive plants in agroecosystems. We have a gene to landscape focus using approaches from population and evolutionary genetics, evolutionary biology, plant ecology, modelling and epidemiology and crop science. Our basic research recognises that weedy plants are excellent models for studying rapid plant adaptation. We apply these insights to develop sustainable weed management strategies using eco-evolutionary principles.

Project description

The position is funded by a Novo Nordisk Foundation start package "Basic research on ecology, evolution and sustainable management of weedy plants in agroecosystems"awarded to Professor Paul Neve. The post holder will work closely with another postdoc (plant/weed ecology) and a PhD student (plant/weed evolutionary ecology) in the weed ecology and evolution group.

You will address the questions 'what is the ecological and genetic (genomic) basis of weediness inAlopecurus myosuroides' and 'why has the species rapidly emerged as a weed in some agroecosystems and not others?' You will have access to a large collection of blackgrass accessions from around the world, including areas where the species is non-native and weedy, native but not a major weed and non-native and non-weedy. We have also recently completed the assembly and annotation of a high-quality reference genome for blackgrass. Classical plant ecological approaches will establish phenotypic and trait variation for common weedy traits within and amongst these accessions (via your interaction with a PhD studentship). As a molecular population biologist, you will use population genomics type approaches to address the genetic basis of the rapid evolution of weediness. Approaches used could encompass (i) genomic scans to identify areas of the genome under selection, (ii) studies of variation in genome size/structure and variation in large gene families implicated in resistance to herbicides and adaptations to biotic and abiotic stress and (iii) mapping and GWAS type approaches to explore the genomic basis of identified weedy trait variation.

The postholder will work closely with collaborators in the International Weed Genomics Consortium at Colorado State University, USA (https://www.weedgenomics.org), and with other labs with expertise in plant evolutionary genomics. Funds are available for lab visits to build and enable these collaborations.

Research group leaderis Professor Paul Neve, Department of Plant and Environmental Sciences,pbneve@plen.du.dk, Phone: +45 29611199.

Further details of the application and selection procedurecan be found at https://jobportal.ku.dk/videnskabelige-stillinger/?show4037   Paul Neve <pbneve@plen.ku.dk>

UFlorida ButterflyMothCRISPR

The Kawahara Lab at the University of Florida and the Florida Museum of Natural History in Gainesville, FL is seeking a postdoctoral fellow to conduct CRISPR-based DNA detection of Lepidoptera (butterflies and moths). The project and position are for 1 year but could be extended based on available funding.

Preferred Qualifications include: 1) Familiarity with CRISPR-Cas; molecular approaches such as DNA isolation and quantification, PCR, primer and guide RNA design; and high-throughput amplicon sequencing. 2) Bioinformatic experience in handling sequence data and computer programming/scripting. 3) An interest in applied entomology and/or molecular diagnostics.

The position centers around developing CRISPR-based

diagnostics to streamline DNA detection and identification of the invasive tomato leaf miner moth, Tuta absoluta. The project will use the CRISPR-Cas diagnostic method SHERLOCK (Specific high-sensitivity enzymatic reporter unlocking) to detect species-specific nucleotide motifs. Detection of tomato leaf miner DNA with the CRISPR-based SHERLOCK method is being tested as a model approach for other high-risk pest species that are difficult to identify. This approach has the potential to prevent biological invasions by improving one of the highest-risk steps in preventing a pest introduction: rapid identification.

Responsibilities include project management, data analysis, sample preparation for sequencing, and publishing a paper. The successful candidate will work closely with a technician and students in the lab. Position available September 1, 2021, or until the position is filled.

The Kawahara Lab values equity, accessibility, inclusion in its research, and outreach, and is committed to creating a supportive community with equitable opportunities for learning and advancement. Prospective candidates from diverse cultural, economic, and ethnic backgrounds, and of diverse gender, neurological, and differently-abled identities and abilities, are encouraged to apply. To ensure full consideration please send following materials to Akito Kawahara at kawahara@flmnh.ufl.edu. Please include a CV, Cover Letter explaining your interest and how your prior experience makes you an ideal candidate for the position, and list three references that we can contact. The subject line should read "CRISPR Postdoc Application." Learn more about the Kawahara Lab at: http://www.flmnh.ufl.edu/mcguire/kawahara/, about being a postdoc at UF: http://postdoc.aa.ufl.edu/, and current UF postdocs: https://sites.google.com/ufl.edu/ufpda/home?authuser=0 . "Akito Y. Kawahara" <kawahara@flmnh.ufl.edu>

UFlorida MarineInvertStemCell CompBiol

University of Florida, Whitney Lab: Postdoctoral Associate in Marine Invertebrate Stem Cell Biology

JOB DESCRIPTION The University of Florida, Whitney Laboratory for Marine Bioscience, Schnitzler Lab (https://www.whitney.ufl.edu/people/current-research-faculty/christine-e-schnitzler-phd/) seeks a highly motivated postdoctoral researcher to work on our NIH-funded stem cell heterogeneity project in the marine hydroid Hydractinia, using modern experimental and computational biology techniques. The project includes characterizing subpopulations of adult stem cells including investigating how stem cells are maintained and how progenitor populations are specified in different contexts, including regeneration. The postdoctoral associate will be expected to lead research activities related to these topics, including designing and performing experiments, developing and executing protocols, performing data analysis, and writing manuscripts and grants. The position will involve performing research as part of a team, as well as training and mentoring other lab members.

The ideal candidate will have extensive experience in molecular and cellular biology techniques such as: DNA and RNA extraction, molecular cloning, in situ hybridization, quantitative PCR, epifluorescence and confocal microscopy, and fluorescence activated cell sorting (FACS). Experience with gene manipulation or gene editing techniques and microinjection or electroporation is preferred. Experience with generating and processing bulk and single-cell RNA-sequencing or similar transcriptomic datasets, and Unix/command line and programming skills is preferred. Experience with cnidarians or other marine invertebrate organisms would also be advantageous.

Further information about the Whitney Laboratory for Marine Bioscience can be found at http://www.whitney.ufl.edu/. Interested individuals are asked to submit an application at: https://facultyjobs.hr.ufl.edu/posting/87338 Minimum requirements: Candidates should have or be close to obtaining a Ph.D. in developmental biology, cell and molecular biology, evolutionary developmental biology or a related subject. We are a lab that supports diversity and inclusion. Candidates from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply. Preference will be given to those who can start by September 2021 or earlier.

INSTRUCTIONS Special instructions to applicants: Please upload your curriculum vitae with publication list, a detailed letter of interest, a one-page summary of your Ph.D. thesis, and contact information for three professional references with your online application form.

ADDITIONAL INFORMATION The University of Florida is an equal opportunity institution dedicated to building a broadly diverse and inclusive faculty and staff.

The University of Florida is An Equal Employment Opportunity Institution. If an accommodation due to a disability is needed to apply for this position, please call 352/392-2477 or the Florida Relay System at 800/955-

8771 (TDD). Hiring is contingent upon eligibility to work in the US. Searches are conducted in accordance with Florida's Sunshine Law.

The Whitney Laboratory for Marine Bioscience (http://-/www.whitney.ufl.edu/) is a University of Florida research center. Founded in 1974, the Whitney Lab is dedicated to using marine model animals for studying fundamental problems in biology and applying that knowledge to issues of human health, natural resources, and the environment. The Laboratory is situated on a narrow barrier island with both the Atlantic Ocean and the Intracoastal Waterway within a few hundred feet of the facility. It is located in Marineland, about 18 miles south of St. Augustine and 80 miles from Gainesville. The academic staff of the Whitney Laboratory consists of 9 tenure-track faculty members, together with approximately 60 associates, students, and visiting scientists. Dr. Mark Q. Martindale is the Director. Fields of research conducted at Whitney Laboratory include biomechanics, neuroethology, sensory physiology, neurogenomics, comparative marine genomics, biodiversity, regenerative biology, and the evolution of development. The lab also has a NSF-funded undergraduate research training program (REU) and an active K-12 STEM education outreach program.

Apply here: https://facultyjobs.hr.ufl.edu/posting/-87338 Questions? Contact Dr. Schnitzler with questions at: christine.schnitzler@whitney.ufl.edu

"Schnitzler, Christine" <christine.schnitzler@whitney.ufl.edu>

ULaval QuebecCity DuplicationEvolution

Postdoctoral position

Two to four years

Investigating the impact of gene duplication on protein evolution.

Job Description A postdoctoral position is available in the Landry Laboratory at Universite Laval in Quebec City under the Canada Research Chair in Cellular Systems and Synthetic Biology. The selected candidate will work on projects aimed at dissecting the impact of gene duplication on protein evolution. These include experimental work aimed at determining how newly formed genes can interact with each other to alter their evolutionary trajectories and others aimed at studying the co-fitness landscapes of gene duplicates. See recent publications associated with the project below.

Qualifications The candidate is expected to have a PhD in biology or a related discipline, and a solid background in biochemistry and molecular biology with at least basic skills in bioinformatics and statistics.

Starting date The position is funded for two years and could be extended to 3 or 4 years depending on the funding situation. The starting date could be as early as September 2021. The position will remain open until a candidate is selected.

Research environment

The Landry lab is located at the Institut de Biologie Integrative et des Systemes (IBIS) of Universite Laval and is part of the Quebec Network for Research on Protein Function, Engineering, and Applications (PROTEO).

The Landry lab is an international team of 20 students, postdoctoral fellows and research associates from diverse backgrounds (microbiology, biology, bioinformatics, biochemistry) addressing questions in evolutionary cell and systems biology.

How to apply The application package (1 single PDF file) should include a motivation letter demonstrating the interest of the candidate for the field and the candidate'Âs ability to perform this type of research, reprints of the candidate'Âs most important contributions, a CV and the contact information of three people who can provide letters of reference. The file should be sent to landrylaboratory@gmail.com

Recent publications associated with the project

1: Ascencio D, Diss G, Gagnon-Arsenault I, Dubé AK, DeLuna A, Landry CR. Expression attenuation as a mechanism of robustness against gene duplication. Proc Natl Acad Sci U S A. 2021 Feb 9;118(6):e2014345118. 2: Després PC, Dubé AK, Seki M, Yachie N, Landry CR. Perturbing proteomes at single residue resolution using base editing. Nat Commun. 2020 Apr 20;11(1):1871. 3: Hallin J, Landry CR. Regulation plays a multifaceted role in the retention of gene duplicates. PLoS Biol. 2019 Nov 22;17(11):e3000519. 4: Dandage R, Landry CR. Paralog dependency indirectly affects the robustness of human cells. Mol Syst Biol. 2019 Sep;15(9):e8871. 5: Marchant A, Cisneros AF, Dubé AK, Gagnon-Arsenault I, Ascencio D, Jain H, Aubé S, Eberlein C, Evans-Yamamoto D, Yachie N, Landry CR. The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs. Elife. 2019 Aug 27;8:e46754 6: Eberlein C, Nielly-Thibault L, Maaroufi H, Dubé AK, Leducq JB, Charron G, Landry CR. The Rapid Evolution of an Ohnolog Contributes to the Ecological Specialization of Incipient Yeast Species. Mol Biol

Evol. 2017 Sep 1;34(9):2173-2186. 7: Diss G, Gagnon-Arsenault I, Dion-Coté AM, Vignaud H, Ascencio DI, Berger CM, Landry CR. Gene duplication can impart fragility, not robustness, in the yeast protein interaction network. Science. 2017 Feb 10;355(6325):630-634.

Christian Landry, PhD Professeur/Professor

Canada Research Chair in Cellular Systems and Synthetic Biology

http://landrylab.ibis.ulaval.ca/   Téléphone: 418-656-3954 Poste interne: 403954 Télécopieur: 418-656-7176

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

UMemphis InsectBioinformatics

A two-year postdoctoral position is available in the McKenna lab in the Department of Biological Sciences at the University of Memphis (www.duanemckenna.com)

Position Summary: The position will be supervised by Dr. Duane McKenna and Dr. Seunggwan Shin, as a part of a large international collaborative project funded by the National Science Foundation titled "Integrating phylogenomics, biophysics, and functional genomics to unravel the evolution of hearing and singing in Ensifera (katydids, crickets and relatives)." The position will also be remotely advised by Dr. Hojun Song (https://schistocerca.org/SongLab/) in the Department of Entomology at Texas A&M University, who is the PI of the overall project.

The goal of this project is to generate phylogenomic data and undertake phylogenomic analyses of target enrichment, transcriptome and genome sequencing data. Experience with bioinformatics, including analysis of phylogenomic data is desired; however, experience with more traditional multi-gene molecular phylogenetics and evolution is acceptable. The position offers opportunities for mentoring students and for being mentored, writing high-impact scientific papers, learning/developing/implementing cutting-edge analytical methods/pipelines/tools, and engaging in international collaboration.

Candidates should have strong 'wet-lab' skills, ideally including genomic DNA library preparation, and experience with managing, processing and analyzing next-generation sequencing data. Experience with Orthoptera evolution or insect phylogeny and evolution is an advantage, but is not required. Strong communica-

tion and interpersonal skills are critical for success in this position.

Desired Qualifications: (Ideal applicant; applicants without these skills will be considered) - Proficiency in bioinformatics related to phylogenomic analysis. - Wet lab experience with target enrichment. - Experience with genomic DNA library preparation and genome assembly.

The McKenna Lab: Lab members study insect systematics, genomics, evolution and diversity, including the evolution of insect-plant interactions. The lab hosts a highly-collaborative group of postdocs, PhD research associates, a research assistant professor, graduate and undergraduate students, and volunteers. We are part of a large community of biodiversity scientists associated with the Center for Biodiversity Research (www.umbiodiversity.org) in the Department of Biological Sciences (https://www.memphis.edu/biology/) at the University of Memphis a leading metropolitan research and teaching institution in Memphis, TN, U.S.A.

Application deadline: The position is open until filled. For more info. and to apply, visit: http://workforum.memphis.edu/postings/27058 Contact for questions: Duane McKenna (dmckenna@memphis.edu)

Duane McKenna PhD William D. Hill Professor of Biology Department of Biological Sciences University of Memphis Director, Center for Biodiversity Research Director, Agriculture & Food Technologies Research Cluster, FedEx Institute email: dmckenna@memphis.edu   http://duanemckenna.com www.umbiodiversity.org "Duane McKenna (dmckenna)" <dmckenna@memphis.edu>

UMilano Italy ConservationGenomics

The Ficetola lab at the Univ. of Milano is recruiting one postdoctoral fellow. The successful applicant will take a leading role in the project "HybrInd: Global changes, hybridization, and the tyranny of the golden mean: A tale of tails". Our project combines population genetics, genomics, analysis of performance and species distribution modelling to understand the drivers of biodiversity in some species of endemic reptiles from the Mediterranean, and to assess potential responses to global changes.

Research description

Mediterranean reptiles have amazing levels of diver-

sity and endemism, with some island endemic species restricted to a few small islands. However, we have a limited knowledge on the processes underlying the evolution of these species, and on their potential interactions with introduced invasive species. The HybrInd project combines the expertise of multiple researchers to understand the processes that determine the genetic diversity and performance in a set of model species from the Mediterranean basin. Emphasis will be given on the potential effects of interactions and hybridization between native and invasive species of reptiles.

We are looking for both young and experienced candidates with experience in the analysis of population genetics and genomic data (e.g. RAD-sequencing) to address evolutionary and ecological questions. Applicants for the position will be hard-working, enthusiastic, independently motivated and willing to lead a significant part of the HybrInd Project, and will join a highly-dynamic work group, with a strong emphasis on research excellence.

Key prerequisite include experience in the data analysis of genomic data (e.g. RAD-seq), and interest in the use of numerical ecology to address evolutionary and ecological questions. Experience in spatial ecology or in the biology of amphibians and reptiles will be welcomed.

Details on the application

The pre-call will be open until we will find the figure best fitting our needs.

The post-doctoral position is available for 12 months, renewable up to a total of 24 months. Salary will be proportional to the experience of candidates

Possible starting dates are from September 2021. No deadline for application, the positions will remain open until filled.

Applications should include: CV with list of publications in peer-reviewed journals; a letter explaining research interests and two academic references. Applications should be sent to Francesco Ficetola

For informal inquiries, please do not hesitate to contact me:

Francesco Ficetola, francesco.ficetola@unimi.it

G.F. Ficetola

Department of Environmental Science and Policy

Univ. of Milano-Italy

f.ficetola@libero.it

UMontana EvolutionaryGenomics

Postdoctoral Research Associate - Evolutionary Genomics, University of Montana

A joint postdoctoral position on evolutionary genomics is available to work with the Good and Cheviron research groups at the University of Montana, Missoula.

We seek a postdoctoral colleague interested in collaborating on several ongoing evolutionary genomic projects focused on adaptation, speciation, and molecular evolution. Current projects in our groups focus on comparative and population-level questions in several mammalian systems, with emphases on reproductive genomics and environmental adaptation. Candidates for this position would also have opportunities to collaborate with the UNVEIL research network (unveilnetwork.org) and the UM Genomics Core (UMGC) and contribute to phylogenomic analysis of local SARS-CoV2 genome evolution. The successful candidate will have the opportunity to lead analysis on several large existing genomic datasets, and to develop new research directions that complement our current research projects. A strong background in evolutionary genetics, analysis of large-scale genomic data, and a Ph.D. in biology or a related field is required. This position is available immediately, with flexibility for remote employment during the start of the appointment.

The University of Montana offers a vibrant research community. The Good and Cheviron labs share newly constructed molecular space along with the UMGC and three other outstanding research groups, as part of an entire floor dedicated to evolutionary genomics research. Missoula is a great college town located in the heart of the Rocky Mountains of western Montana. For further information on this position and our research please visit our lab websites (thegoodlab.org; chevironlab.org) and email Drs. Good and/or Cheviron directly at jeffrey.good@umontana.edu; zachary.cheviron@umontana.edu. All applicants are encouraged to contact us prior to applying.

To apply, please visit http://bit.ly/2923umjobs. Candidates must apply online, and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Applications will be reviewed upon receipt. Candidates should apply by June 14, 2021 for full consideration, and

the position will remain open until filled. The position start date will be flexible contingent on the needs of the preferred candidate.

ADA/EOE/AA/Veteran's Preference Employer

Jeffrey M. Good, Ph.D. (he/him) Associate Professor Division of Biological Sciences The University of Montana 32 Campus Drive, HS104 Missoula MT 59812 Phone: 406-243-5771 Fax: 406-243-4184 Website: http://-www.thegoodlab.org/   The Good Lab acknowledges that the University of Montana is in the aboriginal territories of the Salish and Kalispel people. We honor the path they have always shown us in caring for this place for the generations to come.

Jeffrey.Good@mso.umt.edu

UNebraska Lincoln EvolutionaryGenomics

A Postdoctoral position is available in the Evolutionary Genomics and Bioinformatics lab (http://bcb.unl.edu/) of University of Nebraska - Lincoln (UNL) to work on plant/microbial genomics projects. The lab is affiliated with the Department of Food Science and Technology (FDST) and Nebraska Food for Health Center (NFHC). We have ongoing genome sequencing projects funded by USDA, NSF and JGI and need an expert in plant comparative genomics, phylogenetics, and DNA sequencing data analysis. These genome projects are collaborative with research groups in USDA and in Europe. The lab is also funded by NIH to develop bioinformatics tools for genomic data mining in microbiomes. The postdoc researcher will have opportunities to work with collaborators and have the choice to participate in different projects depending on his/her interests. The lab also encourages members to explore/develop their own research projects within the broad Evolutionary Genomics and Bioinformatics research domain.

Duration: The initial appointment is for one year, with renewal based on performance. Funding is available for three years.

Qualifications: Applicants should have a PhD or will have completed a PhD before the position starts in bioinformatics, genomics, evolutionary biology, plant genetics, or a related discipline. The applicants are expected to have published first-authored research papers in reputed journals, and are proficient with programming in Python/Perl and R and UNIX. The candidate should

have extensive experience working with plant/microbial genome data and gene family analysis using phylogenies. Experience in machine learning and software development is desired but not required.

Working Environment: UNL is a leading research and land grant University in Nebraska. Its Agriculture Science ranks 51, Biotechnology and Applied Microbiology ranks 149, and Plant Science ranks 151 in the world according to U.S News. NFHC (https://-foodforhealth.unl.edu/) is a center established in 2016 with researchers from the University of Nebraska-Lincoln, the University of Nebraska Medical Center and the University of Nebraska at Omaha to tie gastrointestinal and biomedical research to agriculture, plant and animal breeding, and genetics. Lincoln is among top 10 state capital cities to live in according to https://-wallethub.com/edu/best-state-capitals/19030: #4 overall rank, #9 in affordability and #9 in quality of life.

Start Date: August 2021 but flexible.

Salary: A highly competitive salary plus medical benefits will be offered.

How to apply: Please send a CV (with contact information for three references), cover letter describing research interests and skills, and copies of publications to Yanbin Yin (yyin@unl.edu). Review of applications will begin immediately and continue until the position is filled.

Yanbin Yin, PhD Associate Professor Department of Food Science and Technology Nebraska Food for Health Center 253 Food Innovation Center University of Nebraska - Lincoln yyin@unl.edu yanbin.yin@gmail.com http://bcb.unl.edu/   yanbin.yin@gmail.com

UOxford PhytoplanktonEvolution

University of Oxford, United Kingdom Postdoctoral position (3yr) in Evolutionary genetics, genomics and biogeochemistry of marine phytoplankton

This is a collaborative project between Profs Rosalind Rickaby (Earth Sciences, Oxford UK), Dmitry Filatov (Plant Sciences, Oxford UK) and James Mccullagh (Organic Chemistry, Oxford UK), funded by NERC UK. The project aims to understand evolutionary and mechanistic bases of calcification process in marine phytoplankton and its biogeochemical implications affecting global carbon cycle and climate. This postdoctoral position will be focusing on evolutionary genetic processes in extremely large populations of marine phytoplankton,

as well as on identification of candidate genes likely involved in calcification process. Deadline for applications: 25th June 2021. For more details see URLs below

Relevant recent papers: Krasovec M, Rickaby REM, Filatov DA.(2020) Evolution of Mutation Rate in Astronomically Large Phytoplankton Populations. Genome Biol Evol. 12(7):1051-1059. doi: 10.1093/gbe/evaa131

Bendif EM, Nevado B, Wong ELY, Hagino K, Probert I, Young JR, Rickaby REM, Filatov DA. (2019) Repeated species radiations in the recent evolution of the key marine phytoplankton lineage Gephyrocapsa. Nature Communications 10(1):4234. doi: 10.1038/s41467-019-12169-7.

Filatov DA. (2019) Extreme Lewontin's Paradox in Ubiquitous Marine Phytoplankton Species. Mol Biol Evol. 36(1):4-14. doi: 10.1093/molbev/msy195.

McClelland HL, Bruggeman J, Hermoso M, Rickaby RE. (2017) The origin of carbon isotope vital effects in coccolith calcite. Nature Commun. 8:14511. doi: 10.1038/ncomms14511.

McClelland HL, Barbarin N, Beaufort L, Hermoso M, Ferretti P, Greaves M, Rickaby RE. (2016) Calcification response of a key phytoplankton family to millennial-scale environmental change. Sci Rep. 6:34263. doi: 10.1038/srep34263.

Rickaby, R.E.M., Hermoso, M., Lee, R.B.Y., Rae, B.D., Heureux, A.M.C., Balestreri, C., Chakravarti, L., Schroeder, D.C., and Brownlee, C. (2016). Environmental carbonate chemistry selects for phenotype of recently isolated strains of Emiliania huxleyi. Deep-Sea Research II 127, 28-40

More details can be found here: https://my.corehr.com/pls/uoxrecruit/-erq_jobspec_version_4.display_form?p_company=-&p_internal_external=E&p_display_in_irish=-N&p_process_type=&p_applicant_no=-&p_form_profile_detail=&p_display_apply_ind=-Y&p_refresh_search=Y&p_recruitment_id0798 or https://www.jobs.ac.uk/job/CFV227/postdoctoral-research-assistant-in-evolutionary-genetics-and-biochemistry-of-calcifying-phytoplankton Prof. Dmitry A. Filatov, PhD Professor of Evolutionary Genetics, Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB United Kingdom

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

UPennsylvania HumanEvolution

Postdoc. University of Pennsylvania Perelman School of Medicine. Philadelphia USA, The Kamberov lab is recruiting to fill a postdoc position in the field of evolutionary and developmental human genetics. Our lab investigates the genetic pathways and cis-regulatory mechanisms controlling the development and evolutionary divergence of the major organs found in human skin: sweat glands, hair and mammary glands. We use genetic manipulation in mice, human and mouse cell culture, xenograft and organotypic culture as well as high-throughput single transcriptomics and comparative genomics for discovery and functional testing. A postdoctoral position is available leading a project on the mechanisms underlying the developmental specificity and the evolutionary variation of enhancers controlling the formation and patterning of skin appendages in humans and related primates. The position is supported by NIH funding. Applicants should hold a Ph.D. in biology or related field. Applicants with a background in developmental biology, mouse genetics, evolutionary genetics and genomics, enhancer biology, and/or bioinformatics are especially encouraged to apply. Interested applicants should send a letter detailing your interest in the position and a CV to Yana Kamberov (yana2@pennmedicine.upenn.edu).

yana2@pennmedicine.upenn.edu

UTexas Gaveston FunctionalGenomics

Postdoc Position in Population and Evolutionary Genomics

University of Texas Medical Branch, Galveston, USA

The Ward Lab at the University of Texas Medical Branch in Galveston is seeking a Postdoctoral Fellow to lead core projects focused on cardiovascular functional genomics (https://www.ward-lab.org/). The goal of the Ward Lab is to dissect the global role of regulatory elements, including those derived from transposable elements, in directing gene expression in healthy, stressed

and disease states in cardiovascular disease-relevant cell types. We use a variety of population and evolutionary genomics approaches and induced pluripotent stem cell-based tools to tackle this problem.

Projects are available in several areas including: -understanding gene regulatory dynamics during differentiation to cardiovascular cell types -investigating gene regulatory processes in response to perturbation within and between species -measuring the impact of interindividual variation on cardiovascular disease-relevant cell types

We are looking for a highly motivated, enthusiastic individual to join our growing team. Candidates should have received their Ph.D. within the last year in Molecular Biology, Evolutionary Biology, Genetics, Systems Biology, Computational Biology, Cell Biology or a related field. They should have excellent communication skills and a good track record of productivity, including a first-author paper.

The University of Texas Medical Branch, located on the island of Galveston, is a member of the University of Texas System, the Texas Medical Center (the largest medical center in the world based in Houston -approximately 50 miles away), and the Gulf Coast Consortia in Quantitative Biomedical Sciences, thereby providing a vibrant research community. There are excellent Core facilities on campus including Next Generation Sequencing, Flow cytometry and Proteomics.

Please apply by sending a cover letter, C.V., and contact information for three references via email to Dr. Michelle Ward (miward {@} utmb {.} edu). Review of applications will begin immediately and continue until the position is filled. Informal enquiries are welcome.

UTMB Health strives to provide equal opportunity employment without regard to race, color, national origin, sex, age, religion, disability, sexual orientation, gender identity or expression, genetic information or veteran status. As a VEVRAA Federal Contractor, UTMB Health takes affirmative action to hire and advance women, minorities, protected veterans and individuals with disabilities.

Recent related publications:

Ward, M.C.*, Banovich, N.E.*, Sarkar, A., Stephens, M. and Gilad, Y. Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. eLife doi.org/10.7554/eLife.57345 (2021).

Ward, M.C. and Gilad, Y. A generally conserved response to hypoxia in iPSC-derived cardiomyocytes from humans and chimpanzees. eLife doi.org/10.7554/eLife.42374 (2019).

Ward, M.C., Zhao, S., Luo, K., Pavlovic, B.J., Karimi, M.M., Stephens, M. and Gilad, Y. Silencing of transposable elements may not be a major driver of regulatory evolution in primate induced pluripotent stem cells. eLife doi.org/10.7554/eLife.33084 (2018).

"Ward, Michelle" <miward@UTMB.EDU>

UVictoria FishGenetics

Title: UVic.SalmonGenomics University of Victoria, Department of Biology The Owens and Koop Labs at the University of Victoria are currently seeking a post-doctoral fellow (PDF) to work on a project entitled "Landslide Impact on Flow Dynamics, Fish Migration and Genetics of Fraser River Salmon". The PDF will lead an effort to understand the impacts of the 2018 Big Bar Landslide on the genetics of Fraser River Salmon (see Executive Project Summary: https://www.sfu.ca/content/dam/sfu/evsc/PDFs/-Employment/Executive%20Project%20Summary.pdf). The landslide blocked the Fraser River to salmon passage, potentially having significant impacts to salmon populations in the Northern Basin. The project is led by a large group of multi-disciplinary investigators from Simon Fraser University, University of Northern British Columbia, University of Victoria, Durham University, and University of Massachusetts-Amherst, working in collaboration with the Department of Fisheries and Oceans Canada, Hakai Institute, Fraser Basin Council, and the Fraser Salmon Management Council.

We seek a candidate who can lead research on the following topic: Genetic selection by hydraulic barriers. The post-doc will lead molecular genetics work to prepare hundreds of Pacific salmon samples for whole genome resequencing. They will also lead bioinformatic analyses that use the resulting sequence data. The goal of this work is to understand the effect landslides may have had on population genetic composition of sites above the landslide, and to find specific alleles that may have been selected for or against from this migration blockage.

The PDF will be part of a larger cluster of post-docs and research staff appointed at Simon Fraser University investigating the impacts of landslides and flow dynamics on salmon migration and evolution. Other PDFs on the project will lead research on i) The chronology of landslides in the Fraser Basin; ii) Linkages between

bedrock canyon geometry and landslide susceptibility; iii) Flow dynamics in bedrock canyons; iv) Linkages between flow dynamics and fish migration; and v) Fish migration and hydraulic barriers.

Funding is available for one year with a possible extension for up to three years. Candidates should have experience with molecular genetics, genomics, next-generation sequencing data, and bioinformatics. The project provides opportunities for candidates to gain experience working at the intersection of genomics, evolutionary biology, salmon ecology and life history, and geomorphology, within a large group of 15 research collaborators. With this comes additional opportunities to mentor graduate students, lead presentations and discussions within a variety of settings and platforms, and gain experience communicating complex science with real-world implications.

UVic is a short walk from the beach, and minutes from both downtown Victoria and temperate rainforest hiking trails. UVic has a long history of fisheries research and salmon genomics and is a stimulating environment in which to learn and do research.UVic is an equity employer and encourages applications from all qualified individuals including women, persons with disabilities, visible minorities, Indigenous Peoples, people of all sexual orientations and gender identities, and others who may contribute to the further diversification of the university. We acknowledge with respect the Lkwungen peoples on whose traditional territory the university stands and the Songhees, Esquimalt and WSÃNEÃ peoples whose historical relationships with the land continue to this day.

To apply for a position please send a cover letter describing your interests and experience, CV and a list of three references toEVSCHire@sfu.ca. Informal inquires and questions may be addressed to Gregory Owens at-grego@uvic.ca.

Review of applications will begin immediately and continue until the positions are filled.

Start date is negotiable, but we hope to have the full team in place before the end of 2021.

Gregory L. Owens PhD Assistant Professor, Department of Biology, Faculty of Science, University of Victoria Office: 040 Cunningham Building Website: owensgl.github.io

"Gregory Owens, PhD" <grego@uvic.ca>

Valencia SARS-CoV-2 Evolutionary

BIOINFORMATICS POSTDOC IN SARS-CoV-2 EVOLUTIONARY GENOMICS

Institute for Integrative Systems Biology (I2SysBio), UV-CSIC, Valencia, Spain

A postdoctoral position (1.5 years) is available immediately in the PathoGenOmics group of Mireia Coscolla in Valencia (Spain) www.uv.es/pathogenomic We are seeking enthusiastic applicants with skills in computational biology/bioinformatics and with experience in data mining and comparative or evolutionary genome analyses. Skills in Bayesian phylogenetics and phylodynamics, and pathogen evolution is a plus.

The project: Strategic initiative for genomic surveillance and assessment of the impact of SARS-CoV-2 mutations in real time. The aim of the position is to investigate molecular epidemiology dynamics, mutations surveillance, and to collaborate with a multidisplinary team to explore the functional impact of the different SARS-CoV2 variants. The project is highly linked to the ongoing project http://seqcovid.csic.es/ . The tasks of the postdoc will be in sequence and evolutionary analyses of SARS-CoV-2 sequences within a consortium with eight research groups ranging from virology to mathematics and protein structure. The position is based in Valencia, at the Institute for Integrative Systems Biology (I2SysBio), a mixed institute between university of Valencia and CSIC. The Pathogenomics group is part of the Pathogen Systems Biology program, and we study microbial pathogens in the context of their host and disease. To approach this, we use a range of different omics technologies where genomics is our main approach to study the evolution and molecular epidemiology of the pathogen. But we also perform experimental infections to discover which genomic determinants are involved in different virulence readouts, using among other approaches transcriptomic of host and pathogen To apply send CV and e-mail of two references to Mireia.coscolla@csic.es

Mireia Coscollá Devís: www.mireiacoscolla.com Principal investigator: www.uv.es/pathogenomic I2SYSBIO, Parc Cientific - Universitat de València C/Agustín Escardino, 9, 46980 Paterna (Valencia) Telephone.: 0034 963543317 e-mail: mireia.coscolla@uv.es

Mireia <mireia.coscolla@uv.es>

matics Viral Genetics and Emerging Diseases Virus-Host Interactions CNTS contractor in support of the Viral Diseases Branch, Walter Reed Army Institute of Research Room 3A06 503 Robert Grant Ave Silver Spring, MD USA 20910 Email: matthew.a.conte.ctr@mail.mil

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WalterReedArmyInstRes ViralDiseaseGenomics

Our group dn the Viral Diseases Branch at Walter Reed Army Institute of Research in Silver Spring, MD is currently searching for a bioinformatics postdoc.

The link to the position is: http://nrc58.nas.edu/RAPLab10/Opportunity/Opportunity.aspx?LabCode=97&ROPCD=971512&RONum=C0430 Anyone interested is free to contact myself and/or Irina who is listed on the page, with any questions.

The position is not limited to U.S. citizens, but non-U.S. citizens must have lived in the US for at least the past three years.

Base Stipend: $70,000.00 USD Travel Allotment: $4,000.00 USD Full Description: Advances in next generation sequencing and bioinformatics have resulted in major developments in the field of infectious disease research and genomic surveillance. With the COVID-19 pandemic, for instance, genomic surveillance has increasingly been used by public health for contact tracing, for determination of virus origins and points of introductions, identification of potential drivers of the evolutionary dynamics, and for surveillance of virus evolution and important mutations that may result in change of virus phenotype. This position will involve research and development of methods for genomic surveillance and virus evolution, including respiratory and FVBI human pathogens of DoD importance. In addition to population-level studies, intra-host pathogen evolution and diversity will be studied, for analyses of transmission, resistance, host adaptation, disease severity and general within-host pathogen evolution, and its correlates to immune responses, infection, therapy response and pathogen spread. This opportunity will involve computational analyses of virus and patient data, as well as development of new methods and tools for further advancement of the field. Familiarity with next generation sequencing technology, advanced bioinformatics tools (including proficiency in R and python), and experience with phylogenetic and phylodynamic modelling is significantly desired.

Keywords: virus; genetics; phylogenetics; bioinformatics; genomic; evolution;

Matthew A. Conte, PhD Principal Investigator, Bioinfor-

YaleU MolecularExperimentalEvolution

TITLE: Postdoctoral Associate in Molecular and Experimental Evolution

AGENCY: Department of Ecology and Evolutionary Biology, Yale University Ogbunu Lab: https://medium.com/geeqslab DESCRIPTION: The Ogbunu Lab at Yale University is recruiting a fully-funded postdoctoral associate to work on a set of projects at the intersection of molecular biology, evolution, ecology, bioengineering, and disease.

TERMS AND SPECIFICS: The expectation is for an in-person position, for laboratory research to take place on site in New Haven, Connecticut, USA. The initial appointment is for one year, renewable upon review. The start date is flexible. Salary is negotiable, but will be based on experience. There is no firm deadline: Interviews will continue until the position is filled.

RESEARCH KEYWORDS: molecular genetics, molecular microbiology, evolutionary biology, infectious diseases, biochemistry, bioengineering

SCIENTIFIC DESCRIPTION: Study systems may include (but are not limited to): proteins, bacteria, bacteriophage, and potentially other systems (e.g. eukaryotic viruses, yeast, tissue culture).

The ideal candidate would have experience with a range of molecular and microbiological techniques, and familiarity with sequencing and analysis methods. Experimental biochemistry, proteomics, and transcriptomics are additional areas of interest, as is tissue culture. Comfort with computational platforms is strongly encouraged, and extra fluency with these tools would be a very strong bonus.

While I am recruiting with several concrete skill sets and projects in mind, I would hire a bright, well-trained, and curious scientist, even if their skills don't exactly fit the description above. We are open to new study systems, provided that we have the facilities to carry

out the proper work.

FORMAL QUALIFICATIONS: Doctor of Philosophy (PhD) or equivalent in one of a number of fields.

PERSONAL CHARACTERISTICS: The ideal candidate would be motivated, organized, and precise. While they should feel comfortable with independence, they should also enjoy being a member of a research program where communication and collaboration are prioritized. While many personality-types are welcome, decency, professionalism, and generosity are absolute requirements. Those driven entirely by competition and self-interest, rather than curiosity, will be a poor fit.

OTHER ASPECTS: Mentoring and professional development are additional aspects of the traineeship: the PI and postdoctoral associate will engage in concrete discussion in these areas. In addition, all members of the Ogbunu Lab are strongly encouraged to participate in outreach, activism, scientific communication, or other activities at the intersection of science and society. Self-care is also a priority.

APPLICATION: 1) A cover letter that outlines your specific interest in the position 2) Curriculum vitae 3) The names and contact information for at least 2, and preferably 3 professional references.

Send questions and application materials to: brandon.ogbunu@yale.edu I can also be reached via social media (Twitter & IG): @big_data_kane

brandon.ogbunu@yale.edu

WorkshopsCourses

cE3c Portugal EvolutionaryBiol Oct25

cE3c Advanced Courses 2021/2022 - List already available

The detailed program of the Advanced Courses organized by cE3c - Centre for Ecology, Evolution and Environmental Changes for the academic year 2021/2022 is already available. There are 21 courses in total, of which three are new.

IMPORTANT NOTE: Most courses are intended to be presential, but if needed (e.g. due to COVID-19 security measures by the time of the course) they may be adapted to be given remotely (online). Courses that will only occur if possible in presential format are noted.

These courses are aimed for students enrolled in Doctoral Programmes in Biology or related areas. They can also be attended by post-graduate students of other Doctoral Programmes or Masters in Biology, or others with basic biology formation (such as BSc in Biology or related areas).

These courses are free for 1st year PhD students of several Doctoral Programmes of the Faculty of Sciences of the University of Lisbon (FCUL) or institutions in partnership with FCUL, counting credits for their formation:

- Biology, Ciências do Mar or other PhD programmes at FCUL;

- Biodiversity, Genetics and Evolution - BIODIV (ULisboa and UPorto);

- Biology and Ecology of Global Changes - BEAG (ULisboa and UAveiro);

- Sustainability Science (ULisboa)

The courses have in general an intensive format, with one week of duration, with 5-6 ECTs recognition for the above mentioned Doctoral Programmes. Some have a shorter format (see details in each course's programme).

We detail below the list of courses, teachers and calendars. More details (including programmes, fees and procedures for applications) can be found at:

https://ce3c.ciencias.ulisboa.pt/training/?cat   Advanced Courses cE3c 2021/2022

October 25th - 29th 2021 - Scientific Writing and Communication (Gabor Lövei). Deadline for applications September 17th 2021. (only occurs if possible in presential format; due to COVID-19, it may be cancelled or re-scheduled).

November 8th - 12th 2021 - Production of Science Communication Activities (Cristina Luís, Filipa Vala & Patrícia Garcia Pereira). Deadline for applications October 15th 2021.

November 15th - 19th 2021 - Stable isotopes in Ecology and Environment: a tool to integrate scales and complexity (Cristina Máguas). Deadline for applications October 15th 2021.

November 15th - 19th 2021 - Natural History Collections and Biodiversity (Maria Judite Alves et al.). Deadline for applications October 15th 2021

November 22nd - 26th 2021 - EvoS-2 - Evolutionary Studies - applying evolutionary thinking outside the biology realm (Filipa Vala). Deadline for applications October 22nd 2021.

January 17th-21st 2022 - Island Biogeography (Ana Margarida Santos et al.). Deadline for applications December 15th 2021. (only occurs if possible in presential format, may be cancelled due to COVID-19)

January 24th - 28th 2022 - Soil ecology and ecosystem services (Teresa Dias & Cristina Cruz). Deadline for applications: December 27th 2021.

February 7th - 11th 2022 - Until death do us apart: living in a symbiotic world (Silvana Munzi, Cristina Cruz & Lourdes Morillas). Deadline for applications January 7th 2021.

February 14th-18th 2022 - Urban Ecology: the green within the city (Pedro Pinho, Julia Bentz,Cristina Branquinho et al.). Deadline for applications January 14th 2022.

March 7th - 11th 2022

Strategies for citizen engagement in science communication (Cristina Luís, Esther Marin et al.). Deadline for applications February 11th 2022.

April 4th - 6th 2022 - Science and the Media: bringing together scientists, journalists and society (Marta Daniela Santos). Deadline for applications March 7th 2022.

May 4th- 6th 2022 - Introduction to R programming and biological data analysis (Inês Fragata & Vitor Sousa). Deadline for applications April 4th 2022.

May 9th - 13th 2022

Advanced R for Ecology and Evolutionary Biology (Inês Fragata & Vitor Sousa). Deadline for applications April 4th 2022.

May 16th- 20th 2022 - Hands on Functional Diversity: from Ecological Indicators to Ecosystem Services (Alice Nunes, Paula Matos, Laura Concostrina-Zubiri et al.). Deadline for applications April 15th 2022.

May 23rd-27th 2022 - Climate Change Adaptation (Silvia Carvalho et al.). Deadline for applications April 1st 2022. (NEW)

May 30th - June 3rd 2022 - Experimental Design and Reproducibility in Science (Inês Fragata, Leonor Rodrigues & Diogo Godinho). Deadline for applications April 29th 2022. (NEW)

June 20th - 24th 2022 - Applied Methods in Community Ecology and Functional Ecology (Paulo Borges & François Rigal). Deadline for applications May 6th 2022.

June 27th - July 1st 2022

Botany in the 21st century: integrating modern molecular methods and classical descriptive taxonomy (Patrícia dos Santos et al.). Deadline

— / —

Online GeneralisedLinearModelsInR Sep6-10

Online training - Generalised Linear Models as a unified framework for data analysis in R

Dates: 6-10 September 2021

Course website: (https://www.physalia-courses.org/courses-workshops/glm-in-r/)

In this course, we will introduce Generalised Linear Models as a unified, coherent, and easily extendable framework for the analysis of many different types of data, including Normal (Gaussian), binary, and discrete (count) responses, and both categorical (factors) and continuous predictors.

The course is aimed at at graduate students and researchers with little statistical knowledge but willing to learn how to extract knowledge from data using statistical models, how to use statistical models to increase our understanding and make predictions about natural phenomena, and acquiring a toolbox to analyse many different types of data (beyond the typical Gaussian responses) using R.

Learning outcomes

Being able to fit, understand, and use statistical models to make predictions and extract knowledge from data

Learn how to analyse data with different statistical distributions, estimating the effects of both categorical (factors) and continuous predictors

Visualise data and fitted models to check assumptions, communicate results, and increase understanding

Practise R programming, particularly applied to data visualisation and analysis (statistical modelling)

Acquire the statistical knowledge required to move on to more complex models (e.g. Generalised Linear Mixed Models, Generalised Additive Models, Bayesian modelling) in the future.

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

Online GWAS Jun21-25

Dear all,

registrations are now open for the 3rd edition of the Physalia course "Introduction to genome-wide association studies (GWAS)" which will be delivered remotely in June (21st-25th)

Limited number of seats available

(https://www.physalia-courses.org/courses-workshops/gwas-2/)

Instructors: 1) Dr. Filippo Biscarini (CNR, Italy); 2) Dr. Oscar González-Recio (INIA, Spain); 3) Dr. Christian Werner (University of Edinburgh, UK)

OVERVIEW

This course will introduce students, researchers and professionals to the steps needed to build an analysis pipeline for Genome-Wide Association Studies (GWAS). The course will describe all the necessary steps involved in a typical GWAS study, which will then be used to build a reusable and reproducible bioinformatics pipeline.

FORMAT

The course is structured in modules over five days. Each day will include introductory lectures with class discussions of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, results will be interpreted and discussed in group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at students, researchers and professionals interested in learning the different steps involved in a GWAS study using them to build a structured pipeline for semi-automated and reproducibile GWAS analyses. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of GWAS and bioinformatics pipeline building, progressively describing all steps and putting there seamlessy together in a general workflow. Attendees should have a background in biology, specifically genetics; previous exposure to GWAS experiments would also be beneficial. There will be a mix of lectures and hands-on practical exercises using R, Linux command line and custom software. Some basic understanding of R programming and Unix will be advantageous. Attendees should also have some basic familiarity with genomic data such as those arising from NGS experiments.

Full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops)

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

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

"info@physalia-courses.org"   <info@physalia-courses.org>

Online IntroToFloraOfAlaska Jun14-Jul14

Dear all,

Are you interested in learning about the Flora of Alaska as well as getting familiar with some unique approaches to delivering a systematic botany course online, this might be the one for you. One of the hallmarks of systematic botany courses is the hands-on learning experience in a laboratory setting. To create a similar lab experience for the online offering, we have carefully chosen technology that will allow students from all over the state (and even outside Alaska) to collect data in their home communities, perform plant dissections and have a hands-on learning experience within the flora's native environment. Instead of traditional course materials like textbooks, students will purchase an inexpensive wide-angle macro lens that connects to their smartphone or tablet. This 2-inch lens lets students take high-resolution, detailed photos of flora on the go with classifying metadata, such as GPS location attached. The technology not only lets students mimic lab spaces in their own natural areas but also expands their digital networks through the submission of images to iNaturalist, enabling them to share and collaborate with enthusiasts around the world and contribute citizen science data to research. Students don't just sit at their computers in this class, they go outside, touch with their hands and share what they discover. The course design includes carefully videotaped lectures using the Learning Glass platform, video dissection demonstrations, virtual biome exploration using a 360$B!k(B camera, and selected interactive reading materials. This course is an exciting intersection of curiosity for wild plants, an exploration of Alaska's plant communities and an accessible introduction to the science of botany.

Class URL: https://introtoflora.community.uaf.edu/ Where: University of Alaska Fairbanks (USA)

Instructor: Dr. Steffi Ickert-Bond (Professor of Botany and Curator of the Herbarium (ALA) at the University of Alaska Fairbanks)

Course goals:

The objective of this class is to introduce you to several aspects of Alaska's unique flora. Class modules and hands-on exercises are designed to familiarize you with the identification, description, and morphology of our local flora. In addition, you will get familiar with dissection of flowers, using technical keys, seeing scientific (Latinized) names, and learn vocabulary that comes with describing and talking about plants, and curate images that you will take of the plants in your immediate surroundings.

Student learning outcomes:

On completion of this class, you will be able to identify and describe several common plant families and species that are native and common to Interior Alaska and be more comfortable with floral dissection and taking photographs of flowering plants that will aid in their identification and classification.

Dates: The 2-credit class will run from 14 June- 14 July and is fully asynchronous.

Registration: You can register at https://ecampus.uaf.edu/register/ and select 51595 BIOLF195. The class costs $468. eCampus courses charge in-state tuition no matter where you reside.

More info: You can read more about the class and watch a video dissection of Brassicaceae at https://news.uaf.edu/online-botany-course-utilizes-student$B!D(B/ Best, Steffi

Steffi Ickert-Bond, Ph.D.

Professor of Botany and Curator of the Herbarium (ALA), UA Museum University of Alaska Fairbanks 1962 Yukon Drive Fairbanks, AK 99775-6960, USA

Phone: 907-474-6277 (office) 907-474-5285 (WRRB lab) Fax: 907-474-5469

Ickert-Bond lab website http://www.frontierbotany.info Herbarium website and Facebook http://www.uaf.edu/museum/collections/herb/ https://www.facebook.com/ALAHerbarium/ Search 270,000 digitized ALA specimens: http://arctos.database.museum/home.cfm Stefanie Ickert-Bond <smickertbond@alaska.edu>

Online MultivariateTraitsEvolution Jun7-11

Dear colleagues,

There are a few places available for the course "Modelling and Analysing Multivariate Traits Evolution using mvMORPH", June 7th-11th, 2021.

Online live sessions from Monday to Friday from 14:00 to 16:30 and 17:00 to 19:00 (Madrid time zone).

Instructor: Dr. Julien Clavel (NNRS, France)

Registration and more info: https://www.transmittingscience.com/courses/evolution/modelling-and-analysing-multivariate-traits-evolution-using-mvmorph/ or write to courses@transmittingscience.com

Course overview:

In this workshop students will be introduced to multivariate phylogenetic comparative methods with the mvMORPH R package.

The mvMORPH package contains tools for modelling the evolution of correlated continuous traits (e.g. morphometric measurement, geometric morphometric datasets, life history traits, gene expression data, etc.) on phylogenetic trees [with either fossil species, extant species or both] as well as statistical tools such as multivariate generalized least squares (GLS) linear models -e.g. multivariate regression, MANOVA, MANCOVA - for studying comparative datasets.

In this course, students will be first introduced to some theory with illustrative examples (both from simulated data as well as students' own datasets) and will learn how to interpret the models, their parameters, as well as how to assess their reliability.

With best regards

Sole

– Soledad De Esteban-Trivigno, PhD. (she/her) Scientific Director www.transmittingscience.com [1]

Twitter: @soledeesteban Instagram: @soledaddeesteban Researchgate: https://www.researchgate.net/profile/Soledad_De_Esteban-Trivigno ORCID: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR),

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Links: —— [1] http://www.transmittingscience.com
Soledad   De   Esteban   Trivigno <soledad.esteban@transmittingscience.com>

Online RNAseqBioconductor Nov1-12

Dear all,

registrations are now open for the 3rd edition of the Physalia course "RNA-seq data analysis in R/Bioconductor": (https://www.physalia-courses.org/courses-workshops/course19/)

ONLINE - November 01-12, 2021

Overview

This course will provide biologists and bioinformaticians with practical statistical analysis skills to perform rigorous analysis of high-throughput genomic data. The course assumes basic familiarity with genomics and with R programming, but does not assume prior statistical training. It covers the statistical concepts necessary to analyze genomic and transcriptomic high-throughput data generated by next-generation sequencing, including: hypothesis testing, data visualization, genomic region analysis, differential expression analysis, and gene set analysis.

Program

** Session 1 'V Introduction (Mon, Nov 01, 3-6 PM, Berlin time)

Introduction to R / RStudio Creating high-quality graphics in R

** Session 2 'V Hypothesis testing (Wed, Nov 03, 3-6 PM, Berlin time)

CDF, p-value, binomial test types of error, t-test, permutation test

** Session 3 - Bioconductor (Fri, Nov 05, 3-6 PM, Berlin time)

Introduction to Bioconductor Working with genomic region data in Bioconductor (GenomicRanges)

** Session 4 - RNA-seq data analysis (Mon, Nov 08, 3-6 PM, Berlin time)

Characteristics of RNA-seq data Storing and analyzing RNA-seq data in Bioconductor (SummarizedExperiment)

** Session 5 - Differential expression analysis (Wed, Nov 03, 3-6 PM, Berlin time)

Multiple hypothesis testing Performing differential expression analysis with DESeq2

** Session 6 - Gene set analysis (Fri, Nov 12, 3-6 PM, Berlin time)

A primer on terminology, existing methods & statistical theory GO/KEGG overrepresentation analysis Functional class scoring & permutation testing

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

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

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR

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Online SeascapeGenomics Oct18-22

Dear all,

registrations are now open for the Physalia course on "Seascape Genomics", which will take place ONLINE from the 18th to the 22nd of October.

Instructors:

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

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

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

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

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

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 Follow us on (https://twitter.com/Physacourses)

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Online Stdpopsim Jun14-17

Online TransposableElementDetection Jun14-18

Stdpopsim is a community-maintained library of standard population genetic simulation models. Stdpopsim is designed to make it easier for researchers to run reproducible, bug-free simulations of genetic datasets from published demographic histories. Under the hood, stdpopsim relies on msprime and SLiM 3 to generate sample datasets in the tree sequence format.

If you are interested in using stdpopsim, but daunted by the command line and Python, we are hosting an open, online workshop in June that will cover both computing skills and using the stdpopsim library for simulating genetic datasets. Topics covered include using Unix Shell, Python, Git, and stdpopsim library. No prior familiarity with this material is required to participate in the workshop.

Signup URL: https://eventbrite.com/e/155644419649 Dates: Mon June 14–Thu Jun 17 Times: 9:00AM–Noon MST (UTC-07:00) each day.

Stdpopsim Docs: https://stdpopsim.readthedocs.io/ This workshop is jointly organized by the NSF-funded Carpentries Initiative at Arizona State University and the Popsim Consortium.

If you have any questions please contact Reed Cartwright <cartwright@asu.edu> and Elise Lauterbur <lauterbur@email.arizona.edu>.

Reed A. Cartwright, PhD Associate Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences and The Biodesign Institute Arizona State University

Address: The Biodesign Institute, PO Box 875301, Tempe, AZ 85287-5301 USA Packages: The Biodesign Institute, 1001 S. McAllister Ave, Tempe, AZ 85287-5301 USA Office: Biodesign B-220C, 1-480-965-9949 Website: http://cartwrig.ht/ "Reed A. Cartwright" <cartwright@asu.edu>

Dear colleagues,

Registration is open for Transmitting Science Online course "Course: Introduction to transposable element detection using sequencing data, June 14th-18th, 2021.

Schedule: Online live sessions from Monday to Friday from 13:00 to 17:00 (GMT+2, Madrid time zone), plus 5 hours of participants working on their own, with tutored exercises.

Instructors: Dr. Anna-Sophie Fiston-Lavier [1] (Institut des Sciences de l'Evolution de Montpellier, France) and Dr. Emmanuelle Lerat [2] (Université Lyon 1, France)

For more information, please check the course webpage: https://www.transmittingscience.com/courses/-genetics-and-genomics/introduction-to-transposable-element-detection-using-sequencing-data/ or write to courses@transmittingscience.com

Program:

* Introduction to the Linux Operating System

* First contact with the shell (Bash Terminal) * Basic command lines * File system (ftp/ssh protocols) * Text editors (emacs, notepad) * Working with text files with commands such as grep, sed , tr and awk

* Introduction on TE biology

* TE discovery * TE classification

* Enforcement to solve common problems in bioinformatics

* Analysis of sequences - Fasta format * Look for particular patterns in TE sequences (LTR, TIR or TSD) * Parsing common annotation files (gff,bed,vcf)Tuesday, June 15th, 2019

* How to detect TE in assembled genomes?

* Annotation of TE families using de novo approaches * Detection and annotation of individual TE insertions

* Application by group: TE annotation in Drosophila

* RepeatMasker presentation and command line * How to interpret the RepeatMasker outputs * How to parse the RepeatMasker output (OneCodeTofindThemAll)

* Each group present their RepeatMasker results

* Introduction to the next-generation sequencing

* Sequencing technologies * Sequencing data - Fastq format

* Discussions : Not all TE insertions are part of the assembly?

* Application by group: TE families detection in Drosophila

* DNAPipeTE presentation and command line * How to interpret the DNAPipeTE outputs

* Each group present their own results

* Sequencing projects - Population genomics projects: case of DGRP

* Presence/absence calls of previously detected TE insertions

* T-lex presentation and command line * How to interpret the T-lex output

* Each group present their own results

* Do not forget the novel TE insertions

* General approach * McClintock presentation and command line * How to interpret the McClintock output

* Application by group: de novo TE detection in Drosophila using DGRP data

* Each group present their own results

* The advantages of the long-read sequencing technology

* Questions

With best regards

Sole

– Soledad De Esteban-Trivigno, PhD. (she/her) Scientific Director www.transmittingscience.com [3]

Twitter: @soledeesteban Instagram: @soledaddeesteban Researchgate: https://www.researchgate.net/profile/Soledad_De_Esteban-Trivigno ORCID: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for

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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 VariantDetection May24-27

The University of Connecticut's Computational Biology Core is offering a workshop on variant detection focused on short read whole genome sequencing data. The workshop will take place over 4 days for three hours each day (3.5 on the first day).

Dates: May 24 - 27 (4 days)

Time: Monday: 8:30am - 12:00pm EDT Tuesday-Thursday: 9:00am - 12:00pm EDT

Location: Online

Cost: UConn affiliates: $350 External: $475

Workshop schedule

Day 1: Introduction to Linux, High performance computing

Day 2-4 : Introduction, reference genome preparation, download and QC of sequence data, sequence alignment, QC and post-processing, variant detection using freebayes, GATK and bcftools, filtering and comparing variant sets, functional annotation, visualization.

Registration

To register, please follow this link: https://forms.gle/RngFkAPZmXiZw12MA Workshop FAQ

Who should attend?

Anyone with keen interest and desire to learn how to detect genetic variation in high throughput sequencing data. Prior course participants have included faculty, post docs, grad students, advanced undergraduates, staff, and industry researchers.

What are the prerequisites?

Prior bioinformatic experience is not required. We have dedicated the first day of workshop to the basics of Linux and high performance computing.

What do I need?

You will need your own laptop to use, have a recent version of R, RStudio installed, and some other applications. We will send you details of software and installation instructions with your registration acknowledgement email.

Can I bring my own data?

We will provide experimental datasets for use during the workshop, as this helps to keep the workshop moving. There will be time, however, to discuss your own datasets and how you might work with them outside of the workshop.

How much does it cost?

The registration fee is $300. It is payable at the time of registration with credit card or KFS (for UConn affiliates).

Where is the workshop?

It will be held on Blackboard-Collaborate platform, and will run from 9:00am (8:30am on day 1) to 12:00pm EDT on the date indicated.

How do I apply?

All registration is "first-come, first-served." There is no application process. Sign up as soon as possible to ensure your place in the workshop.

Questions?

If you have any questions, please don't hesitate to contact us at cbcsupport@uconn.edu

"Reid, Noah" <noah.reid@uconn.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ... plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.