EvolDir

August 1, 2020

Month in Review

Foreword

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

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

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

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Conferences

Conference:Online DiversitySymposium Aug8

Dear EvolDir community, We hope you are well during these unprecedented times! We are a group of paleontology graduate students and early career professionals at Cornell University in charge of organizing the *14th Annual Summer Symposium on Saturday August 8th, 2020 at the Paleontological Research Institution* in Ithaca, NY. This year, due to the effects of COVID-19 we are going *virtual*! Given recent events across the world both outside and within the field of paleontology, we felt the need to facilitate a conversation on diversity, equity, and inclusion with our peers. Consequently, we are dedicating the PRI Summer Symposium to the topic of *Diversity, Equity, and Inclusion in Paleontology* and are inviting speakers to share their experiences and discuss a path forward in our field during several short sessions.

To pre-register, visit our webpage https://www.priweb.org/event/summer-symposium?rq=symposium. A list of speakers will be posted soon, so be sure to check back for updates. We hope to see you there!

"cps257@cornell.edu" <cps257@cornell.edu>

Marseilles 24thEvolutionaryBiology Sep21-24

Dear all ,

The 24th evolutionary biology meeting at Marseilles will take place September : 21-24 2021 web : aeeb.fr https://ebm24.sciencesconf.org/ Here is the philosophy of the EBM. I was talking to a colleague who is interested in the evolution of immune systems, particularly the adaptive immune system in vertebrates. In my opinion, evolution is a universal process and each case can be better understood in a more general context. Let us take the example of the transposome RAG (tranposase RAG, TIR, system of repair ..) and the process of cooption of the tranpososme RAG which allowed my establishment of the system of somatic rearrangement V(D)J of the immunoglobulins and the T cell receptors this cooption process is better understood if we understand the biology of transposomes in general, and if we take into account that this process of co option (DDE transposon that evolves as specific endonulease involved in the programmed developmental rearrangement) is a process that has occurred several times during the evolution of the species : for example, yeast mating type switching and macro / micronucleus transformations in ciliates. This scientific vision is the essence of the Evolutionart Biology Meeting "at" Marseilles In fact, even if the themes presented are different , synergies can occur and the understanding of seemingly different biological systems provides a better understanding of the biological system being studied.

best regards Pierre

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

NewOrleans EvolutionDisease Nov2-5

15thInternational Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases

2-5 November 2021 | Tulane University and Jung Hotel, New Orleans, USA Organized by Elsevier,the15thInternational Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID XV)will include 10 'V 15 plenary lectures, 15 'V 20 two hour-specialized symposia, and several poster sessions. Special emphasis will be given to health problems of specific interest to the present world: COVID-19, the spread of transmissible diseases linked to climate and ecological disorders, tuberculosis, AIDS, malaria, to name a few.

Abstract submission deadline: 4 June 2021

Website: https://www.elsevier.com/events/-conferences/meegid If you would like any further information please let me know.

Best wishes, Sophie

Sophie Hayward Marketing Manager for the 15thInternational Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases

Hayward Marketing The Homestead, Swinbrook Road Shipton-under-Wychwood Chipping Norton Oxfordshire, OX7 6DX Tel: 01993 832633 | Mobile: 07769 313 653

Core working hours: 9.30am - 3pm, Monday, Tuesday, Wednesday and Thursday

Sophie Hayward <sophie.hayward1@btinternet.com>

Online ArthropodGenomics Jul21-23

Dear EvolDir,

Arthropod Genomics Symposium 2020 July 21-23

The symposium focuses on new insights gleaned from analysing arthropod genomes and is designed for scientists interested in genomic studies of arthropods, including model organisms, those of importance to agriculture or health, and those of ecological or evolutionary interest.

The programme will include presentations from speakers covering several major themes with opportunities for online discussions and interactions amongst all participants. AGS has a history of welcoming postdoctoral, graduate, and undergraduate students, who are again particularly encouraged to join.

See the website for further details http://i5k.github.io/-ags2020 Tuesday, July 21 - Arthropod Genomics and Chromosome Genomics Sessions Wednesday, July 22 - China Session and Eco-Evo Genomics I & II Sessions Thursday, July 23 - Vector Genomics and Agricultural Genomics Sessions

Robert Waterhouse

robert.waterhouse@gmail.com

Online COVID19DynamicsEvolution Jul30-31

Please join us July 30/31 2020 for the COVID-19 DYNAMICS & EVOLUTION CONFERENCE! Inspired by the long-running HIV Dynamics & Evolution meeting, this (virtual) event will bring together researchers taking quantitative and computational approaches to studying the SARS-CoV-2/COVID-19 pandemic.

On Thurs July 30th, we are hosting a one-day scientific meeting, featuring a series of talks by experts covering the epidemiology of COVID-19, modeling of viral transmission and control, and phylogenetic analyses of SARS-CoV-2. A program summary is included on our website: https://cpd.ucsd.edu/covid19 On Friday July

31st, we are hosting a two-hour public forum bringing together scientists and journalists to spotlight our current understanding of COVID-19 and discuss knowledge gaps, public health challenges, and science communication.

Registration for either event is available online: https://cpd.ucsd.edu/covid19 In addition, we are already accepting abstracts for our second meeting on Oct 19-20, 2020! https://cpd.ucsd.edu/covid19/101920.html We very much hope to welcome you (remotely!) to "COVID-19 Dynamics & Evolution",

The COVID-19 Dynamics & Evolution Organizing Committee

Chairs: Dr. Emma Hodcroft, University of Basil, co-developer of Nextstrain Dr. Morgane Rolland, Chief of Viral Genetics & Systems Serology, US Military HIV Research Program Dr. Alison L Hill, Research Fellow, Harvard University

"alhill@fas.harvard.edu" <alhill@fas.harvard.edu>

Online EvolEcol Jul29

Dear EvolDir,

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

We will run the seminars one per week, on Wednesdays, throughout July and August.

This coming week:

—

Wed 29 July

Prof. Nyeema Harris (Dept. of Ecology & Evolutionary Biology, University of Michigan, USA)

"Carnivore behavioral ecology in the Anthropocene from cities to national parks"

—

When: 5-6PM BST / 9-10AM PDT, Wednesdays

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

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

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

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

Many thanks,

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

—- Dr. Elizabeth Duxbury

Senior Postdoctoral Research Associate

Prof. Alexei Maklakov Group

School of Biological Sciences

University of East Anglia

Norwich Research Park

UK

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

Online EvolutionEcol Jul22

Dear EvolDir,

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

We will run the seminars one per week, on Wednesdays, throughout July and August.

When: 5-6PM BST / 9-10AM PDT, Wednesdays

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

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (https://twitter.com/EvoEcoSeminars How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg This coming week:

—

Wed 22 July

Prof. Geoff Parker (Institute of Integrative Biology, University of Liverpool, UK)

"Sexual selection and the sexual cascade"

—

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,

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Prof. Alexei Maklakov Group

School of Biological Sciences

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Norwich Research Park

UK

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

Online EvolutionEcology Jul15

Dear EvolDir,

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

We will run the seminars one per week, on Wednesdays, throughout July and August.

When: 5-6PM BST / 9-10AM PDT, Wednesdays

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

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (https://twitter.com/EvoEcoSeminars) How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-ev4fe0io-M7B˜D6p74blV_ZRcDtmAcg This week:

—

Wed 15 July

Prof. Robin Dunbar (Department of Experimental Psychology, University of Oxford, UK)

"Tradeoffs between fertility and predation in the evolution of mammalian social systems"

—

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

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

Many thanks,

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

—- Dr. Elizabeth Duxbury

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

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

Online EvolutionEcolSeminar Jul8

Dear EvolDir,

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

We are now switching to running the seminars one per week, on Wednesdays, throughout July and August.

When: 5-6PM BST / 9-10AM PDT, Wednesdays

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

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

How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-ev4fe0io-M7B˜D6p74blV_ZRcDtmAcg This week:

—

Wed 8 July

Dr. Rob Knell (School of Biological & Chemical Sciences, Queen Mary University of London, UK)

"Sexual selection, adaptation and extinction"

—

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

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

Many thanks,

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

Dr. Elizabeth Duxbury

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School of Biological Sciences

University of East Anglia

Norwich Research Park

UK

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

Online GenesAsEnvironment Nov15-18

AGA2020 President's Symposium - Genes as Environment: Indirect Genetic Effects in Evolution, Agriculture, and Medicine

Indirect genetic effects (IGE) are genetic effects of an individual on the trait values of others in the same species. IGE provides a unifying framework for traditional quantitative genetics, maternal and paternal genetic effects, inclusive fitness, and multilevel selection.

The pandemic is still with us, so the AGA is moving the President's Symposium online. To maximize the number of people who can participate in real time, the meeting will take place over 4 consecutive days from 15:00 -19:00 UTC (11:00 - 15:00 EST, 08:00 -12:00 PST, 16:00-20:00 GMT).

There will be breakout rooms for question-and-answer sessions, and virtual coffee/lunch breaks and happy hours so all participants can interact. Speakers will also have the option to make videos of presentations available for a short time period, to accommodate participants who cannot view talks in real time.

AGA student and postdoc members who submit a "poster" abstract before September 1st will receive free registration and the opportunity for a short presentation. The exact format for "posters" has not been finalized, and we are currently considering several options, including 3-minute lightning talks. President Kim Hughes will select several of the abstracts for 15-minute oral presentations and $50 Presentation Awards.

Register now at https://www.theaga.org/-agatwentytwenty.htm Key Distinguished Lecturer Allen J Moore will open the meeting with his address, *Why we need to understand indirect genetic effects*.

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

theaga@theaga.org

Online GreatLakesEvolutionaryGenomics Jul20-24

The Great Lakes Annual Meeting in Evolutionary Genomics will be held online the week of July 20. GLAM-Evogen is an annual trainee-oriented symposium that brings together faculty and trainees in the Great Lakes region from a range of backgrounds who work at the interface of genomics and evolutionary biology. We have a great set of presentations, starting with keynote speaker Dr. Liz Mandeville from the University of Guelph.

We will have live talks via zoom webinar on -Mon 20 July: 10 am - 12:45 pm EDT -Wed 22 July: 10 am - 12:25 pm EDT -Fri 24 July: 2 - 4:20 pm EDT, followed by a zoom happy hour

Presentation schedule: https://-/docs.google.com/document/d/-1sCvthFSk4OotMJuIh_PHNsNEiuMN4vepRe3CGf8nQPY/-edit?usp=sharing .

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

Registration for the meeting is still open: https://-/forms.gle/CNGs29pnbkNWt5VE8. All participants must register to get zoom and slack information. More information is online at: http://-blogs.rochester.edu/EEB/?page_id=30552 . If you would like to stay updated and receive information about the meeting, you can join the GLAMevogen group here: https://groups.google.com/forum/-#!forum/glamevogen – *Nancy Chen, Ph.D.* Assistant Professor Department of Biology University of Rochester popgenchenlab.github.io/

Pronouns: she/her/hers

"nancy.chen@rochester.edu"
<nancy.chen@rochester.edu>

Online SexualDimorphism Sep14-16

Abstract submission closes on 29 July!

[Molecular Basis and Evolution of Sexual Dimorphism] https://www.embo-embl-symposia.org/-symposia/2020/EES20-09/?_ga=2.238786435.2 053941767.1558936747-2062109751.1554186371

EMBO | EMBL Symposium The Molecular Basis and Evolution of Sexual Dimorphism 14 - 16 September 2020, Virtual

Submit abstract by 29 July

Speakers

Programme

Financial Assistance Females and males display striking patterns of sexual dimorphism in many animals and other organisms. Differences are documented in morphology, physiology and behaviour. In recent years, advances in genomics technologies have facilitated the discovery of genetic mechanisms underlying sex-specific phenotypes, showing that sex-biased expression of hundreds to thousands of genes across the genome contributes to male and female phenotypic differences. The sex-specific evolutionary forces shaping sexual dimorphisms have also begun to be unravelled, including the interactions between 'master' sex determining genes on the sex chromosomes, and other genes during development to control sex-biases of other genes.

This symposium will focus on the molecular basis and evolution of sexual dimorphism across animals and other organisms, including the origins, evolution and biology of sex chromosomes. It will cover topics ranging from the evolution of sex determining systems, sex linkage and sex chromosomes, sex-biased gene expression (on autosomes and sex chromosomes) and X chromosome dosage compensation mechanisms, to the evolution of associated dimorphic phenotypes and the underlying selective pressures.

Session topics:

* The diversity of genetic sex determining regions and sex chromosomes * Evolutionary challenges for sex-linked genome regions: Genetic degeneration and dosage compensation * Adaptive evolution I: Sexual antagonism * Adaptive evolution II: Evolution of sexually dimorphic phenotypes and gene expression * Sexual dimorphism in human disease

The virtual symposium will offer:

* Live-streamed presentations and short talks * Live Q&A sessions * Digital poster presentations * A dedicated discussion platform for knowledge-exchange * Networking sessions built into the programme * Access to recordings of some of the talks after the symposium

Organisers: Doris Bachtrog, University of California, Berkeley, USA Deborah Charlesworth, University of Edinburgh, UK Henrik Kaessmann, Heidelberg University, Germany

CHARLESWORTH Deborah
<Deborah.Charlesworth@ed.ac.uk>

Online SSE-ASN-SSB Jul-Aug Registration

Evolution Community Resources for Early Career Researchers < https://www.evolutionmeetings.org/ > (ECR^2) is a series of online events hosted by the Society for the Study of Evolution (SSE), the American Society of Naturalists (ASN), and the Society of Systematic Biologists (SSB). This series, taking place in July and August 2020, is aimed at re-creating some of the networking and professional development opportunities that are such a valuable part of our in-person Evolution meetings. While this began with a focus on supporting ECRs in a year without an Evolution meeting, we believe that many of the events will prove valuable to our members at any career stage.

The planned events feature a seminar and a variety of workshops, panels and discussion groups, and even feature a virtual edition of the popular small-group networking lunches!

Learn more and register on the ECR^2 website: https:/-/www.evolutionmeetings.org/ –

*Kati Moore*she/her/hers *Communications Manager* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org communications@evolutionsociety.org

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Prague ESEB2021 CallForSymposia DeadlineOct15

CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS FOR ESEB 2021

A defining feature of ESEB congresses is the "bottom-up" approach to determining the scientific content of each meeting. The vast majority of the scientific program is arranged in symposia topics that are suggested by ESEB members, and the symposium organisers then also play a major role in selecting the oral and poster presentations from the submitted abstracts. Symposia topics can be on any theme related to evolutionary biology: specific or broad, emerging or well established. A—symposium normally consists of around 5-12 oral presentations, 1-2 of which are invited, with remaining abstracts in the theme being presented together in the poster sessions. Invited speakers typically have their congress registration covered (but not travel or accommodation), and have extended speaking time.

SYMPOSIUM PROPOSAL

You will be asked to provide:

(1) The names and email addresses of the primary organiser (for all communication) and 1-2 co-organiser(s), who must be committed to attend the whole meeting. (2) Optional - Links to the professional web pages of organisers and short biographies of organisers (maximum 150 words each biography). (3) The proposed symposium title. (4) A—maximum 200 word explanation justifying why you feel your proposed topic warrants a symposium at the conference. (5) The names of two potential invited speakers (please check beforehand whether they are indeed available). You can also submit titles of potential invited talks (optional).

Balance, in terms of gender, nationality and career stage of invited speakers and symposium organisers will be included as one criterion used by the scientific committee when selecting symposia, and successful symposium organisers are expected to do the same when selecting oral presentations. ESEB also supports diversity via conference attendance aid grants.

When organising your symposium at the ESEB conference, we would like you to consider a Target Review paper or Special Issue on the symposium topic to be published in the /Journal of Evolutionary Biology/ (/JEB/), the official journal of the society, soon after the conference or in parallel. /JEB /is particularly interested in publishing summary or synthesis papers of any current evolutionary topic discussed at the ESEB conference.

HOW TO SUBMIT A SYMPOSIUM PROPOSAL

* Please submit your symposium proposal only via the online form that is accessible in the user zone. * Proposals sent by e-mail cannot be considered. * Symposium proposal has to be submitted by a primary organiser of the symposium. * A—primary organiser of the symposium is considered to be a contact person. * At least one of the organisers must be an ESEB member at the time of the "final date for presenters and symposia organisers to register". The organisers will be required to prove member status at a later time, upon registering for the congress.

DEADLINE

The deadline for submission is OCTOBER 15, 2020.

EVALUATION

Proposals will be double-blind evaluated by the Scientific Committee, and the selected list will be communicated in December 2020.

CONTACT

Enquiries can be directed to abstracts.eseb2021@guarant.cz. We will be happy to assist you.

European Society for Evolutionary Biology Email: office@eseb.org Website: eseb.org

ESEB <office@eseb.org>

Roros Norway EvolutionaryDemography Oct6-11

To all evolutionary demographers across the world!

The Centre for Biodiversity Dynamics at the Norwegian University of Science and Technology is excited to invite everyone to the UNESCO's World Heritage Site of Røros, Norway, for the Evolutionary Demography Society's 7th Annual Meeting.

The theme of this year's meeting will be Evolutionary Demography under Global Change, where participants will have the opportunity to present their latest research as well as develop new collaborations, ideas and projects on the interplay between demography and evolutionary biology. To allow a wide audience across the globe in times like these, the meeting will combine physical and virtual attendance.

—Conference: EvoDemo7— What: EvoDemo7, Evolutionary Demography Society's 7th Annual Meeting Where: Røros, Norway When: 6-11 October 2020

—Important deadlines— Early-bird registration: 16 August 2020 Late registration: 15 September 2020

—Financial support— We are also open for applications of financial support. The Centre for Biodiversity Dynamics can offer financial support to physical attendants only. Please find more information here: https://evodemo7.weebly.com/financial-support. Deadline: 16 August 2020.

—Website and social media— The website (https://evodemo7.weebly.com) is updated regularly with the newest information on the scientific program, keynote speakers, registration and much more. Or follow us on Twitter to be the first one to get updates (https://twitter.com/EvoDemo7). Contact us at (evodemo7@bio.ntnu.no) if you have any questions related to the conference.

We are looking forward to seeing you all at the meeting either physically or virtually!

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

GradStudentPositions

Antwerpen CichlidGenomics

Fully funded 4-year PhD position in cichlid fish Evolutionary Genomics available in the Svardal lab at the University of Antwerp

Application deadline: 10 August 2020

The hundreds of closely related but ecologically diverse species of Lake Malawi cichlid fishes provide an exceptional model to study the genomic mechanisms involved in rapid adaptation and diversification.

Cichlid fishes are known for their spectacular adaptive radiations, but some populations are also under recent heavy fishing pressure leading to strong human-induced selection. In this PhD you are going to dissect genomic and phenotypic responses to fisheries-induced and natural evolution.

– You will apply computational genomic approaches to whole-genome sequencing data of 100s of Malawi cichlids to identify genomic adaptations. – Ideally, you will also have an interest in developing your own computational methods in python, R, or C/++ etc. – You will apply ancient DNA methods to sequencing data from museum specimens to track adaptation through time. – Depending on your interest, there will be scope for experiments and field work in Malawi: E.g., measuring growth and maturation traits under controlled conditions in our state-of-the-art fish facilities and (2) using transcriptomes to understand population differences.

Prior knowledge in bioinformatics, data analysis, or statistics is a plus for this position, but also candidates with a different background will be considered, if they can demonstrate strong motivation to develop in this direction.

You can apply for this vacancy through the University of Antwerp's online job application platform until 10 August 2020. Click on the 'Apply' button, complete the online application form and be sure to include the following attachments: a motivation letter (max 2 pages, in English) clarifying specifically why you want to work in our group on this project, your academic CV, your master's grades and percentile in peer group (if available).

https://www.uantwerpen.be/en/jobs/vacancies/-academic-staff/?q=1182&descr=Doctoraatsbursaal-evolutionaire-en-adaptatiegenomica Looking forward to your application. Best wishes,

Hannes Svardal

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

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

Hannes Svardal <Hannes.Svardal@uantwerpen.be>

AustralianNatlU EvolutionaryBiol

Australian National University: International applicants for PhDs in Ecology & Evolution

Are you a high-achieving studentinterested in pursuing a PhD? Do you want to work with top researchers, in a welcoming multinational department, in a liveable, peaceful city, in a beautiful country? Then check out theDivision of Ecology & Evolutionat the Australian National University.

Our Science: We provide an outstanding research environment with a world-class reputation. Our staff include global leaders in molecular ecology, phylogenetics, evolutionary genetics and ecology, behavioural ecology, and macroecology. We research a wide range of topics 'V from orchid interactions with pollinators and mycorrhizae to cuckoo-host arms races; from the evolution of genomes to that of languages. If you are interested in doing a PhD with us check out our Research Groups below, and contact prospective supervisors.

Diverse students: Right now we are home to PhD students from Bangladesh, Brazil, New Zealand, Indonesia, Iran, Sri Lanka, Japan, Mexico, Thailand, Nigeria, China, Taiwan, South Korea, Vietnam, U.S.A., Canada, Northern Ireland, Russia, Italy, and Uzbekistan. We even have a few Aussies!

Our values: We work hard to provide quality supervision and we take pride in creating an atmosphere that values intellectual rigour, inclusivity, mentorship, community, social activities and enjoyment of science. Our PhD students are well supported through internal funding, including for conference travel, and our research facilities are superb. We have a thriving community of PhD students and Postdoctoral Fellows, and our graduates go on to productive careers in many areas of science and beyond. Warning though 'V once you arrive in Australia you won't want to leave!

Location: The ANU is situated in the capital city of Canberra, which is the country'Âs most liveable city. We are surrounded by bushland. There are sometimes kangaroos on campus, and always possums. We are across the street from the beautiful National Botanic Gardens. Due to the many embassies in Canberra there are frequent cultural evenings, art exhibits, film festivals and music events; and the politicians ensure there are countless restaurants and bars to relax in after work.

The Australian National University:We have an international reputation for research excellence. The ANU consistently ranks in the top 50 universities in the world (e.g. 31 on QS World Rankings).

Candidates: Fully funded International PhD scholarships are highly competitive at the ANU. To be a viable candidate you need: (1) excellent undergraduate marks; (2) a Masters by Research with a high mark; or an equivalent large Honours thesis; or (rarely) equivalent proof of research experience. (3) While it is not essential, if you have published papers this is a big bonus.

What do I do?First, contact potential supervisors from the list of staff on the Research Groups above(include your CV and grades). If they are interested in supervising you (conditional on you having funding), then contact theGraduate Program Convenor, Professor Celeste Linde (eeg.hdr.convenor.rsb@anu.edu.au), by 14th August 2020with: a detailed CV, full academic transcripts, the name of your potential supervisor and a brief description of a research project that you and your potential supervisor have discussed. We will then compile a short-list of applicants and invite them to formally apply to the ANU. Our system is designed to avoid discrimination on the basis of which country or institute you studied at. Rich or poor, North or South. As long as it is a reputable, accredited institute you are eligible.

How it works: For now, we are assuming that your personal finances are such that you need an ANU fellowship to do a PhD. We don't want to waste your time, or make you pay an application fee unnecessarily. We will therefore only recommend you apply for a PhD if you have a viable chance of winning an ANU scholarship. Even then it is still a very competitive process (we can make no promises). There is no separate scholarship application. You simply apply for a PhD and tick a scholarship box. Entry to the PhD program is open to applicants with a Bachelor degree and having completed (or in the process of completing) an Honours or Masters research (as opposed to coursework) degree that comprises at least a half year, full time research component and a thesis (5,000-10,000 words). Applicants with significant research experience and publications may be deemed eligible if their achievements can be justified as equivalent to completing an Honours/Masters degree.

Theapplication form is here, along with general information onhow to applyand the details about theDoctor of Philosophy program. But read on now as you need to plan ahead in case you are shortlisted. In brief, your PhD application, due by31 August,requires:

Academic transcripts & graduation/completion certificates from your

— / —

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

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Barcelona EvolutionChordateDevelopment

PhD project: Evolution of chordate development

The role:

We are seeking a highly motivated candidate to join our teams to work on an interdisciplinary project (experimental and computational) involving single-cell genomics and chromatin profiling in different chordate species. The research program for this position focuses on elucidating the origin and evolution of the regulatory programs controlling vertebrate morphogenesis and cell differentiation. To this end, you will apply and analyse advanced functional genomics to characterize cell types and regulatory genome features in vertebrate and non-vertebrate chordate species. Specifically, this involves: (i) scRNAseq to define cell type-specific gene expression across multiple developmental stages, and (ii) bulk ChIP-seq and ATAC-seq to map chromatin states and regulatory element usage. The candidate will spearhead the analysis, integration, and interpretation of these comparative omics datasets.

About the teams:

Our groups study genome regulation from an evolutionary systems perspective. In particular, we are interested in deciphering the evolution of animal cell type developmental programs and the regulatory mechanisms underlying these programs. To this end, we apply advanced single-cell genomics and chromatin experimental methods to molecularly dissect cell types and epigenomic landscapes in phylogenetically diverse organisms. We also develop computational tools to integrate these diverse data sources into models of cell type gene regulatory networks and we use phylogenetic methods to comparatively analyze these models. Our recent work has provided the first whole-organism cell type atlases in different species and mapped key regulatory features underlying both development and cell diversity in non-model invertebrate organisms and the origin of vertebrates. By analysing the development of chordate species at single-cell resolution, we now aim at dissecting the evolution of vertebrate cellular ontogenies and their underlying gene regulatory networks

Details: https://recruitment.crg.eu/content/jobs/-position/phd-student-exploring-evolution-vertebrate-development-using-single-cell Dr. Arnau Sebe-Pedros & Dr. Manuel Irimia Systems Biology Program Centre for Genomic Regulation (CRG) Barcelona Spain

Arnau Sebe Pedros <arnau.sebe@crg.eu>

Belgium EcologicalGenomics

Impact of climate changes on plant-pest interaction: insights from the rosy apple aphid and its apple host in a context of domestication

Amandine Cornille?s group (http://moulon.inra.fr/-index.php/fr/equipes/group-leader-amandine-cornille-young-atip-avenir-team) and Tim Belien?s group (https://be.linkedin.com/in/tim-beli%C3%ABn-4a41164) are recruiting a Master student and a bachelor to investigate the adaptation to climate and plant host of aphid pests.

Lab address?(supervision): PC-Fruit pcfruit vzw Fruittuinweg 1 3800 Sint-Truiden Belgium

Supervisors?: Amandine Cornille (amandine.cornille@inrae.fr), Ammar Alhmedi (Ammar.alhmedi@pcfruit.be) and Tim Belien (tim.belien@pcfruit.be)

Project summary Understanding the extent of local adaptation in natural populations and the mechanisms enabling individuals to adapt to their native environment is a major avenue in evolutionary ecology research. Host-pathogen coevolution is widely seen as a major driver of local adaptation and has therefore been a study model to dissect the evolutionary processes at work during local adaptation. However, the relative contributions of species interactions (i.e. biotic factor) and abiotic factors to local adaptation are still unclear. Addressing these issues is more than a simple academic exercise. Understanding of local adaptation processes in host-parasite interactions will also help tackling pressing issues, such as the ways in which environmental change alters the emergence of pathogens leading to host extinctions, how to promote sustainability of agroecosystems in the face of emerging crop diseases or in guiding for public health practices as more human pathogens and their vectors expand their ranges.

In this project, we investigate whether local adaptation occurred during the recent rapid colonization of cultivated apple by Dysaphis plantaginea, the major aphid pest of cultivated apple orchards, in Europe. We will carry out in April 2020 experimental tests for D. plantaginea fitness differences across environments (i.e. host and climate) to investigate whether the aphid is locally adapted to its host and/or climate. This project will generate original results adding to our understanding of how species interactions and abiotic conditions can shape local adaptation.

Master project The project involves the transplant of Belgian, French and Spanish aphid genotypes on Belgian, French and Spanish apple varieties in three locations (Belgian, France and Spain). The candidate will be involved in the assessment of the adaptive capacities at the ecological level of the rosy apple aphid at the BELGIAN site located at PCFruit (Sint-Truiden, Belgium). The project can last four (Bachelor) to six months (Master), and will consist in participating in aphid infestations and rearing on the field, tree measurement, associated statistical analyses, and final report writing.

1) The candidate will lead the launching of the experiment there during Spring 2021 by transplanting aphids on several apple cultivars and will measure several phenotypic traits. The growth rate of each colony will be measured after 12 days of infestation. Various functional traits which are proxies of the condition of the plant (i.e. chlorophyll content, carbon/nitrogen balance, and flavonol and anthocyanin content measured with the Dualex? pincel) will also be measured.

2) He/She will analyze the dataset that will be generated.

Methodology: Statistical analyses (linear and mixed models, R), ecophysiology, phenotypic measurement, rearing, insect biology, field experiment.

Profile preferred for the candidate: Ideally, the candidate will have skills in ecology and evolution or at least will show strong interest in these fields. He/She will have to be highly motivated about field experiment, as this one will be intense the first two months. He/she will not necessarily be familiar with apple or aphid model.

Deadline for submission: The sooner the better.

Duration : 2 to 6 months, starting date: March 2021, contact Amandine CORNILLE for further discussions.

Supervision?: Amandine CORNILLE - Charg?e de Recherche CNRS CRCN G?n?tique Quantitative et Evolution - Le Moulon Ferme du Moulon 91190, Gif-sur-Yvette, France mail?: amandine.cornille[at]gmail.com Google Scholar profile : https://scholar.google.com/citations?user=EqIE2h8AAAAJ&hl=fr Personal page : http://moulon.inra.fr/index.php/fr/equipes/dygap/355 Group page?:

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EdinburghNapierU EvolutionAquaticSymbiosis

PhD fellowship in 'Developing gregarine apicomplexans as aquatic symbiosis model system' at the School of Applied Sciences at Edinburgh Napier University (ENU), Edinburgh, Scotland.

Application deadline is Wednesday, July 22, 2020 Please quote the project code SAS0068 in any enquiry and your application. Envisioned starting date is October 2020, subject to COVID-19 guidance/recommendations.

About the Project: The Gordon and Betty Moore Foundation's Symbiosis in Aquatic Systems Initiative, seeks to advance the understanding of aquatic symbioses that include microbial partners.

Being part of this initiative we are able to provide a great opportunity for a PhD student to join our international project. This PhD project is based within the School of Applied Sciences at Edinburgh Napier University and is led by Dr Sonja Rueckert (https://www.napier.ac.uk/people/sonja-rueckert) and Dr Anastasios Tsaousis (https://www.kent.ac.uk/biosciences/people/653/tsaousis-anastasios).

Apicomplexans are widely distributed, single-celled organisms that are always described as obligate parasitic. Despite their importance for human health (malaria, toxoplasmosis) and their virulence in animals, there is substantial evidence for mutualistic attributes of some apicomplexans. Gregarine apicomplexans infect almost all invertebrates and are highly abundant across ecosystems. The early diverging gregarines span the whole range of symbiosis from mutualism to parasitism and thus are critical links in the evolution of symbiosis in the apicomplexans. Despite their importance, information on the biology and evolution of these organisms is lacking with e.g. only a handful of transcriptome and genome data available.

In-vitro culturing has not been achieved for any gregarine, thus this PhD project aims to develop gregarines as model system. This model system will enable us to advance the fundamental knowledge on the evolutionary steps of symbiosis in the Apicomplexa, identifying key cellular and molecular transitions in the evolution from free-living relatives to intracellular parasites.

The aim of this project is to develop culturing steps towards an axenic, tissue free system: 1) Develop invertebrate in-vitro culture The student will develop and maintain in-vitro culturing systems for gregarines, using their aquatic invertebrate hosts (e.g. polychaetes, sea squirts, arthropods). The host's microbiome and metagenome will be characterized, and associated metabolic profiles obtained. Gregarine transcriptome, genome and cell biology data for selected systems will be produced to gain a holistic picture of the gregarine-host-microbiome interactions.

2) Develop invertebrate in-vitro tissue culture The PhD student will establish an invertebrate in-vitro 2D tissue culture for gregarine apicomplexans. They will develop invertebrate cell cultures using tissues from the gut of invertebrate hosts employed in step-1. This approach will be assessed by infecting the host cells with the target species and monitor the success of gregarine development and propagation using an in-house automated microscopy system, under controlled atmospheric conditions.

Academic qualifications A first degree (at least a 2.1) ideally in a relevant field such as marine parasitology, protistology, or microbiology, molecular biology with a good fundamental knowledge of microbial eukaryotes, cell biology and laboratory skills.

English language requirement IELTS score must be at least 6.5 (with not less than 6.0 in each of the four components). Other, equivalent qualifications will be accepted. Full details of the University's policy are available online.

Essential attributes: - Experience of fundamental laboratory skills - Competent in aseptic techniques - Knowledge of bioinformatics - Good written and oral communication skills - Strong motivation, with evidence of independent research skills relevant to the project - Good time management

Desirable attributes: - Good fundamental knowledge and strong interest in culturing invertebrates and/or micro-eukaryotes - Laboratory skills including invertebrate dissections, microscopy, parasite isolation and identification, molecular techniques - Competent in data anlysis, phylogenetics and establishing genome and transcriptome data - Image processing

Funding Fully funded position (Home/EU level full-time fees, plus monthly stipend payments at the prevailing rate set by the Research Councils for three academic years).

APPLICATION CHECKLIST: - Application form - CV - 2 academic references, using the Postgraduate Educational Reference Form (Found on the application process page) - A personal research statement (Including a) a brief description of relevant experience/skills, b) an indication of what you would

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IGB Berlin InsectMicrobiotaImmunity

** Doctoral position on host-microbe interactions during metamorphosis. Deadline for applications: 31st July 2020 **

A 4-year doctoral position (TVoD Bund, 65%) is available at the Department of Ecosystem Research of the Leibniz-Institute of Freshwater Ecology and Inland Fisheries to study bacterial resistance evolution towards immune effectors in the metamorphic gut using the waxworm, Galleria mellonella. The project involves manipulation of immune effector expression in the metamorphic gut in order to 1) quantify the rate of bacterial resistance evolution towards combinations of immune effectors; 2) identify the underlying mechanisms of bacterial resistance and quantify their effects on resistance, cross-resistance, and collateral sensitivity; 3) quantify the fitness costs of resistance evolution both in vitro and in vivo and in the presence and absence of the gut microbiota.

The research will be carried out in collaboration with Jens Rolff (Freie Universitaet Berlin) and the Berlin Center for Genomics in Biodiversity Research (BeGenDiv).

Requirements MSc or equivalent in Biology or related discipline. Proficiency in spoken and written English. Strong interest in evolutionary ecology. Laboratory experience with bacteria and/or insects. Experience with experimental evolution is highly desirable.

The position is part of a collaborative Research Unit funded by the Deutsche Forschungsgemeinschaft (DFG) to investigate the tripartite relationships between insect hosts, the microbiota and bacterial infection. The Research Unit will give the opportunity for the candidate to interact with a diverse group of doctoral students, post-docs and PIs, to obtain methodological training, and to collaborate with theoreticians and bioinformaticians. There will be yearly retreats for Research Unit members and access to a graduate training programme.

For informal enquiries, contact Paul Johnston (paul.johnston@igb-berlin.de).

Deadline for applications: 31.07.2020 Apply online: https://karriere-igb.softgarden.io/job/7060700?l=en
"perugolate@zedat.fu-berlin.de" <perugolate@zedat.fu-berlin.de>

JagiellonianU EvolutionaryBiology

Graduate position:Krakow_JagiellonianU.Evolutionary_Biology

PhD position in Evolutonary Biology PhD student position is offered from October 2020 within the Polish National Science Centre grant Environment-dependent balancing selection in a gene involved in sexual conflict in Genomics and Experimental Evolution Group at Jagiellonian University, Institute of Environmental Sciences.

The project The maintenance of genetic variability, enabling populations to adapt to novel environments, is one of the greatest puzzles in evolutionary biology. This is 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 which can take a form of a crossover genotype by environment interaction for fitness in heterogeneous environments. It causes selection to act in environment-dependent manner so that one allele is favored in one environment and the other at another one. 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 6Pgdh polymorphism is maintained by environment-dependent balancing selection, but the exact mechanisms driving this selection are unknown. PhD candidate will investigate ecological factors that determine persistence of the polymorphism.

Scope of work PhD candidate will assess the level of 6Pgdh polymorphism in natural populations and determine environmental factors affecting 6Pgdh allele frequencies in the field. He/she will conduct experimental evolution and will be involved in phenotypic measurements in the lab that will enable direct test of the role of potential factors driving 6Pgdh frequencies. Real-time PCR with TaqMan probes will be used to genotype individuals. PhD candidate may also be involved in other molecular analyses conducted in frames of the project, including transcriptomics.

Place and salary The Student will join a dynamic, cooperative research group at the Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland (www.eko.uj.edu.pl/en_GB). The Institute of Environmental Sciences is one of the most influential and best-recognized research institutions in the fields of Ecology and Evolution in Central Europe located in a beautiful medieval city with rich history and lively cultural life, well connected to other European cities.

The PhD student will receive a tax-free scholarship from doctoral school (ca. 2500 PLN) and/or a tax-free research stipend from the National Science Centre grant (3000 PLN per month).

Requirements

The successful candidate will have a M.Sc. degree in biology or other relevant fields by the start of the studentship. We are looking for a student with good English, strong background in Evolutionary Biology and experience in molecular techniques as well as good skills in data analyses. Excellent communication and organizational skills are also required.

Documents

Please send a CV including contact details for two references and a cover letter to Agata Plesnar-Bielak (agata.plesnar@uj.edu.pl) by August 10. The selected candidate will be assisted with a formal application to the PhD program at Jagiellonian University (the exam will take place between 9th and 14th September 2020)

For more information, please e-mail Agata Plesnar-Bielak.

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

JagiellonianU EvolutionaryPhysiology

PhD position in evolutionary and biomedical physiology at the Jagiellonian University, in a project:

Experimental evolution of the thrifty and spendthrift genotypes, and its consequence for susceptibility to adverse effects of “Western diet”: insights from a selection experiment on bank voles

The project is based on a unique experimental evolution model system, with lines of a common rodent, the bank vole, selected in three distinct directions: http://www.eko.uj.edu.pl/en_GB/zespol-fizjologii-ewolucyjnej/badania. We will answer the question how the selection for high performance under the conditions of unlimited vs restricted energy sources affects vulnerability of animals to adverse effects of the Western diet.

Conditions of employment: A warranted scholarship for 48 months of 5000 PLN / month, equivalent to mean gross income in Poland. Formal requirements

§MSc in life science (biology, biotechnology, ecology, evolution, or related; effective on 5.09.2020),

§admission in the International PhD Biology program at the Jagiellonian University effective on 1.10.2020 (https://science.phd.uj.edu.pl/).

Merit requirements

§Good communication skills, good level of spoken and written English;

§Previous experience in molecular or biochemical laboratory as well as working with terrestrial vertebrates (preferably rodents)

§Achievements such as publications or conference presentations are considered advantageous. Preliminary enquiries: email to the principal investigator - PaweÂ³ Koteja (pawel.koteja@uj.edu.pl)

Detailed information about the enrollment procedure and other formal issues - see here: https://wb.uj.edu.pl/-en_GB/wydzial/aktualnosci/ogloszenia-konkursowe/--/journal_content/56_INSTANCE_NepRLepShInQ/-41643/145578301 The application should be sent by email (pawel.koteja@uj.edu.pl) by 31.07.2020 (the term will be automatically prolonged if needed).

The applications will be considered by the selection committee according to the regulations of the PhD School and the regulations of scientific scholarships in research projects financed by the National Science Centre, Poland (https://www.ncn.gov.pl/sites/default/-files/pliki/2019_09_16_koszty_w_projektach_NCN.pdf).

Contact person: PaweÂ³ Koteja (pawel.koteja@uj.edu.pl)

The Evolutionary Physiology Research Team http://www.eko.uj.edu.pl/en_GB/zespol-fizjologii-ewolucyjnej/badania Institute of Environmental Sciences Jagiellonian University 7 Gronostajowa Street, 30-387 Kraków, Poland e-mail: pawel.koteja@uj.edu.pl office phone: +48 12664 5209 skype: pkoteja ORCID: 0000-0003-0077-4957 ResearcherID: O-4039-2015 Scopus Author ID: 6603751464

PaweÂ³ Koteja <pawel.koteja@uj.edu.pl>

JamesCookU TropicalInvasiveWeeds

Dear colleagues,

I am searching for prospective Australian or international candidates to support their applications to James Cook University's PhD scholarships. Deadline for applications is September 30th, but potential candidates are encouraged to contact much earlier to be able to prepare applications and a research project about the ecology, evolution, and biogeography of tropical invasive plants.

https://www.jcu.edu.au/graduate-research-school/hdr-candidates/postgraduate- research-scholarships

Successful applicants would be granted a 3.5 year scholarship valued at AU$28,092 per annum and will be able to enjoy a tropical lifestyle next to the Great Barrier Reef and the Wet Tropics world heritage areas. https://www.tropicalnorthqueensland.org.au/-where-to-go/cairns-northern-beach es/

Interested candidates can send me an email with their CV and a one page motivation letter.

Please distribute this announcement if you can.

Best wishes, Daniel.

–

Daniel Montesinos

Senior Research Fellow . < https://www.ath.org.au/-australian-tropical-herbarium/daniel-montesinos > Australian Tropical Herbarium | Editor-in-chief . < http:/-/www.web-ecology.net/ > Web Ecology

Invited Professor . < http://cfe.uc.pt/profile/members/-8 > Centre for Functional Ecology | Coordinating Editor . < http://www.nordicjbotany.org/ > Nordic Journal of Botany

Australian Tropical Herbarium . James Cook University . Cairns Campus

Sir Robert Norman Building, E2.204, McGregor Road, Smithfield, QLD 4878, Australia

Tel: +61 (0) 7423 21584 . daniel.montesinos@jcu.edu.au

Twitter: < https://twitter.com/plant_ecology > @plant_ecology | < https://twitter.com/Web_Ecology > @Web_Ecology

I acknowledge the Yirrijandji, Gimuy-Yidinji, and

Djabugay Peoples on whose land I live and work, and pay respect to Elders past and present.

danimontesinos@gmail.com

KielU 2 AncientDNA

2 PhD Positions in Ancient DNA Analysis - Human Immuno-/Population Genomics

The Research Group for Ancient DNA Analysis at the Institute of Clinical Molecular Biology, Kiel University and University Hospital Schleswig-Holstein (UKSH), Kiel, Germany invites applications for two PhD positions in Ancient DNA Analysis. In the framework of the Collaborative Research Centre (CRC) 1266 Scales of Transformation - Human-Environmental Interaction in Prehistoric and Archaic Societies (http://www.sfb1266.uni-kiel.de/en), we are seeking highly motivated PhD students to conduct ancient DNA research in prehistoric human populations using next generation sequencing (NGS). The focus is on the investigation of pathogen and human genomes. Both candidates will be involved in handling human skeletal remains, wet lab work (DNA extraction, NGS library preparation) and data analysis.

PhD position in pathogen evolution and human immunogenetics:

The successful candidate will analyse metagenomic data to detect pathogens, to reconstruct their genomes and to trace the(evolutionary) history of infectious diseases. Additional emphasis will be on human immune genes (in particular HLA) and their pathogen-driven evolution.

PhD position in human immuno- and population genetics:

The successful candidate will analyse genome-wide data to detect pathogen-driven selection signals in human immune genes and to correlate these signals with population genetic markers.

Your profile (for both positions):

* An MSc in a discipline relevant for the project (e.g. bioinformatics, biology, genetics, evolutionary genomics, ancient DNA analysis) is a prerequisite

* Strong interest in working in a very interdisciplinary environment and in archaeological questions is a must

* Expertise in processing both human/non-human genomic data, programming, database curation and ancient DNA data analysis is advantageous

* A strong background in human or evolutionary genomics is desirable

* Very good written and spoken English is required

We offer:

* Exciting projects in the Research Group for Ancient DNA Analysis (https://www.ikmb.uni-kiel.de/-research/junior-research-groups/ancient-dna-research)

* Exceptional infrastructure (Ancient DNA Lab, NGS, bioinformatics) in the Institute of Clinical Molecular Biology (https://www.ikmb.uni-kiel.de/)

* Integration into the interdisciplinary CRC 1266, stimulating collaborations with archaeologists, anthropologists and scientists from the bio- or geosciences

* The contracts run until June 30, 2024 and start as soon as possible. The salary will be according to the German salary scale TV-L (PhD student 65%, German TV-L E13).

Additional Information:

For more information, please contact Prof. Dr. Ben Krause-Kyora (b.krause-kyora@ikmb.uni-kiel.de).

Please submit your documents including a motivation letter, CV (both in English), certificates and contact details of two references as one pdf file (5 Mb max). Please state which of the two offered positions you prefer.

The application deadline is August 16, 2020. Please indicate the reference number on your application.

Please apply online via the following link: https:/-/jobs.uksh.de/job/UKSH-CK-IKMB-2-PhD-Pos_-in-Ancient-DNA-Analysis-%28SFB1266%29-31_07_2020/-610315301/ a.nebel@mucosa.de

KielU EvolutionHumanLongevity

1 PhD Position in Translational Evolution - Genomics of Human Longevity

In the framework of the Research Training Group (RTG) 2501 for Translational Evolutionary Research (TransEvo) (https://transevo.de/) at Kiel University, Germany, we are seeking

a PhD student

to conduct research on the genomic architecture of human longevity (RTG project 6.1) using next generation sequencing (NGS) and genome-wide association studies (GWAS). The successful candidate will perform big-data analysis including bioinformatics and statistics. In particular, the focus will be on analyses of GWAS chip arrays, exome and HLA data to identify new longevity-associated loci, following evolutionary informed approaches.

Your profile:

* An MSc in a discipline relevant for the project (e.g. bioinformatics, genetics, evolutionary genomics, statistical genetics) is a prerequisite

* Background in vertebrate or human genetics/genomics is a must

* Programming skills (ideally in R or python) are required, branching and version control programming with Git is desirable

* Expertise in the analysis of NGS and SNP data (vcf and plink format) is very advantageous

* Strong interest in working in a research environment focusing on evolutionary biology

* Very good written and spoken English is required

We offer:

*Exciting projects in the Human Longevity Group using large-scale data sets already generated from nonagenarians and centenarians

*Exceptional infrastructure (NGS and bioinformatics) in the Institute of Clinical Molecular Biology (https://www.ikmb.uni-kiel.de)

*Integration into the interdisciplinary RTG 2501, stimulating collaborations with scientists from various disciplines, in particular from the Helmholtz Center for Ocean Research Kiel (GEOMAR)

*The contract runs for three years and starts on September 15, 2020. The salary will be according to the German salary scale TV-L (PhD student 65%, German TV-L E13).

Application:

Please submit your documents including a motivation letter, CV (both in English), certificates and contact details of two references as one pdf file (10 Mb max).

*****The application deadline is August 31, 2020.*****

Please apply online via the following link: https://jobs.uksh.de/job/Kiel-Doctoral-Researcher-Position-in-Computational-Genomics-at-IKMB-Schl-24105/612003801/ For more information, please contact Prof. Almut Nebel (a.nebel@mucosa.de), Dr. Guillermo Torres (g.torres@ikmb.uni-kiel.de) or Dr. Janina Dose (j.dose@ikmb.uni-kiel.de).

Almut Nebel, PhD

Institute of Clinical Molecular Biology Kiel University Rosalind-Franklin-Str. 12 24105 Kiel Germany Tel.: +49-431-500-15155

a.nebel@mucosa.de

LeipzigU MadagascarDiversity

Reference Number 142/2020

DOCTORAL RESEARCHER (M/F/D)

ON THE PROJECT “ADAPTIVE EVOLUTION OF PLANT-FRUGIVORE INTERACTIONS ON MADAGASCAR”

Initially limited until 30 September 2021, an extension for further 2-3 years is possible and dependent upon successful renewal of DFG funding for iDiv (evaluation in spring 2021)

65 % of a full-time position

Salary: Entgeltgruppe 13 TV-L

Leipzig University seeks to fill the following position at the German Centre for Integrative Biodiversity Research (iDiv), Flexpool, in Leipzig from 1 October 2020 onwards.

Background

The German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig is a national research centre funded by the German Research Foundation (DFG). It is located in the city of Leipzig and jointly hosted by the Martin Luther University Halle-Wittenberg (MLU), the Friedrich Schiller University Jena (FSU), Leipzig University (UL), and the Helmholtz Centre for Environmental Research (UFZ). For more information please visit: www.idiv.de . The Evolution & Adaptation research group (Dr. Renske Onstein) focuses on the interchange between (macro-) ecology and evolution, to understand the global distribution of genetic, taxonomic and functional diversity. We investigate microevolutionary processes to understand how these play out over macroevolutionary time scales. Understanding these patterns and the processes underlying them is important for predicting how adaptable biodiversity is to current and future global change.

The Project

Madagascar harbours exceptional biodiversity, but this tropical hotspot also faces increasing threat from human activities and climate change. Plants with large, 'megafaunal' fruits are common across the flora of Madagascar, especially within the palm (Arecaceae) family. However, Pleistocene-Holocene extinctions of large-bodied 'megafaunal' fruit- eating and seed-dispersing animals (such as giant lemurs) may have hindered the dispersal of taxa with megafaunal fruits. In this project we aim to investigate the molecular, micro- to macroevolutionary consequences of dispersal limitation in palms, specifically focusing on adaptive evolution of a megafaunal-fruited palm, Hyphaene coriacea, using a comparative framework of Madagascar (all megafauna extinct) and mainland Africa (where H. coriacea is still frequently dispersed by elephants). Specifically, we aim to

(1) identify candidate genes for fruit and seed traits important for plant- frugivore interactions,

(2) pick up genetic traces of selection or adaptation in relation to dispersal by smaller-bodied frugivores, and

(3) evaluate the macroevolution of candidate genes or gene families across the palm family.

This project integrates the fields of plant evolution, molecular evolution and plant-frugivore interaction ecology. It will be in collaboration with researchers from Hohenheim University (Professor Philipp Schlüter) and University of Miami (Professor Mauro Galetti), among others. Besides the salary, there is funding available for field and lab work, conference visits and participation in courses/workshops.

Tasks

- collecting genetic samples from H. coriacea individuals and populations on Madagascar and mainland Africa, and measuring their functional traits (part of these samples has already been collected);

- collecting ecological information about the seed dispersal effectiveness (e.g., using camera traps) and demography of H. coriacea in the study areas;

- using novel genomic and transcriptomic techniques (e.g., RAD-seq, RNA- seq) to infer candidate genes for functional traits and evaluate traces of selection;

- writing and publishing of scientific papers in peer-reviewed journals;

- presentation of results at international conferences;

- doctoral researchers at iDiv benefit from an inter- and transdisciplinary training and support by the graduate school yDiv

Requirements

- M.Sc. or equivalent degree in a project-related field (e.g. molecular biology, genetics, phylogenetics, population genomics, ecology and evolution)

- prior experience using molecular techniques, preferably with transcriptomics or bioinformatics, incl. the basics of scripting/programming for handling and statistically analyzing large genetic/genomic datasets

- prior experience with tropical natural history, fieldwork and basic living conditions is advantageous

- willingness to spend several months in the field (Madagascar/mainland Africa)

- excellent English communication skills (speaking and writing)

- innovative, able to work on his or her own initiative

- team-oriented and strong organizational skills, in order to manage this collaborative research project within an international consortium

- independent mind and the ambition to publish in internationally leading journals

Kindly send your application, quoting the reference number 142/2020,

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MonashU MarineEvolEcol

A PhD project is available with the research groups of Keyne Monro and Kay Hodgins in the School of Biological Sciences at Monash University, Melbourne, Australia.

Climate change is bringing novel environmental conditions that pose new selective challenges and opportunities for biodiversity. Understanding the evolutionary dynamics and extinction risk of populations facing rapid environmental change is critical for managing biodiversity into the future. This project aims to blend quantitative genetics, genomics, and theory to explore the evolution, adaptation and extinction risk of marine populations facing rapid ocean warming in southeast Australia.

We are seeking creative and motivated applicants who wish to pursue research of this kind, with a particular focus on the ecosystem-engineering marine tubeworm, *Galeolaria*. Candidates with interests and experience in evolutionary biology, ecology, genetics, or combinations thereof, along with strong quantitative skills and a good grasp of experimental design, are encouraged to apply.

To apply, please send a CV, academic transcript, and cover letter with a brief outline of research interests and motivation to keyne.monro@monash.edu. Applicants must possess a Bachelor's or equivalent degree with first-class Honours, and/or a distinction in a research Masters degree in a relevant discipline. Short-listed candidates will be contacted for more information and invited to interview. Initial applications should be received before Monday 14th September, 2020.

The PhD stipend is fully-funded for 3 years with the possibility of 6 months extension, and is open to Australian/NZ domestic and international students. The stipend includes all tuition fees, ~$29,000 AUD per annum tax-free, and the cost of compulsory health cover for overseas students. A one-off relocation award is also available to students coming from interstate ($1,000 AUD) or overseas ($1,500 AUD).

Monash University is a member of the Group of Eight, a coalition of top Australian universities recognized for their excellence in research and teaching. The School of Biological Sciences is a dynamic unit with world-class strengths in evolutionary biology, ecology and genetics, and the nexus between these disciplines (http://monash.edu/science/about/schools/biological-sciences/). The University is located in Melbourne, one of the most liveable cities in the world and a cultural and recreational hub.

Keyne Monro

School of Biological Sciences Monash University Victoria 3800, Australia keyne.monro@monash.edu http://monrolab.org/ +61 3 9905-5608

"keyne.monro@monash.edu"
<keyne.monro@monash.edu>

MonashU PlantGenomics

PhD positions available in plant ecological genomics

The Hodgins lab (Monash University, www.hodginslab.com) is currently seeking outstanding PhD candidates interested in studying plant ecological genomics. The project can commence any time during 2021 and will be developed in collaboration with the student. Teaching is not required for the duration of the PhD (3.5 years in Australia). The PhD stipend is fully-funded for 3 years with the possibility of 6 months extension, and is open to Australian/NZ domestic and international students. The stipend includes all tuition fees, ~$29,000 AUD per annum tax-free, and the cost of compulsory health cover for overseas students. A one-off relocation award is also available to students coming from interstate ($1,000AUD) or overseas ($1,500AUD).

There are multiple projects available.

1. Climate change adaptation in an invasive plant In collaboration with Dr. Mike Martin (NTNU) we have re-sequenced whole genome samples from hundreds of herbarium specimens alongside contemporary samples of the global invader common ragweed. The successful candidate will track the signals of climate change adaptation over historic timescales using these data. 2.The role of hybridization during biological invasions

In collaboration with the Cousens lab (The University of Melbourne) and Dr Loren Rieseberg (University of British Columbia) we have sequenced hundreds of whole genomes from two independent replicate hybrid zones formed during invasion by the same two species, Cakile edentula and Cakile maritima. Hybridisation has been thought to aid invasion by introducing genetic novelty, but traditional approaches have been ineffective at evaluating alternative explanations. The PhD candidate will apply new methods on this expansive genomic dataset and develop novel simulations to resolve how hybridisation and colonisation interact to help and potentially hinder biological invasion.

Melbourne is diverse and thriving city with a desirable climate. It is one of the most livable cities in the world and is a cultural and recreational hub. Monash University and The University of Melbourne are members of the Group of Eight, a coalition of top Australian universities recognized for their excellence in teaching and research.

All applicants must have the equivalent of at least six months fulltime independent research experience (e.g., a research based honours or masters) and excellent grades. A publication in an international journal is an asset. Bioinformatics, statistical or computational skills are also an asset. Please send your CV, a transcript, a brief statement of your research interests and the contact details of two referees to kathryn.hodgins@monash.edu. The application deadline is August 15, 2020, but late applications will be considered for other rounds.

Kay Hodgins <yak.hodgins@gmail.com>

yak.hodgins@gmail.com

Munich InsectEvolution

Doctoral position (f/m/d) - Palaeo-Evo-Devo of Insecta

We are seeking a highly motivated PhD student (f/m/d) to take part in the investigation of the evolutionary history of insects, including extant and fossil representatives preserved in amber. The project is funded by the German Research Foundation (DFG).

The project is based on an interdisciplinary approach, in which developmental data of extant and fossil species are incorporated into an evolutionary framework, shortly referred to as palaeo-evo-devo. The major database is provided by morphological investigations of extant and fossil specimens with modern imaging methods. Data are interpreted in a strict phylogenetic framework.

Focus of research is on immature insects and the reconstruction of ontogenetic patterns. The fossil record of immature insects seems quite rich, but is rarely considered in research. Specimens will be provided via scientific collections, fieldwork is not considered.

The prospective PhD student does not necessarily need to have experience with the imaging methods or specific systematic groups, but is expected to gain expertise early in the course of the project. The project includes a distinct amount of traveling to collections in Germany and abroad. The results of the project are expected to be presented regularly at national and international conferences by the prospective PhD student as well as published in peer-reviewed journals.

We are especially seeking for a good team worker being able to cooperate closely with people in the workgroup and national and international colleagues of a wide network.

The successful candidate will be based in the workgroup of Zoomorphology at the campus Martinsried (part of municipality Planegg) south-west of Munich, in close proximity to Munich. Child care facilities as well as schools are nearby.

We offer: DFG-funded PhD position (75%) for 36 months; interdisciplinary research project and working environment; modern imaging equipment (macro- and microscopic)

We expect: MSc (or equivalent) in Biology or Palaeobiology; good English communication skills (oral and written); ability to work in teams; high motivation; keen interest in zoological evolutionary questions

The position is limited to 36 months with a presumed starting date of December 01, 2020.

Applications of women are strongly encouraged. Severely challenged persons will be given preference in case of otherwise equal qualifications.

Please send your application to jhaug@bio.lmu.de until August 31, 2020. The application should include CV, transcript of records, letter of motivation and the names and contact details of two potential referees.

For further information contact: Prof. Dr. Joachim T. Haug, LMU Mu http://www.en.zoomorphologie.bio.lmu.de/people/professoren/jhaug/index.html ; https://www.palaeo-evo-devo.info/ Prof. Dr. Joachim T. Haug - Lichtenberg-Professor - LMU Munich Biocenter - Department of Biology II and GeoBio-Center Großhaderner Str. 2 82152 Planegg-Martinsried Germany Phone 1: +49-89-2180-74132 Phone 2: +49-89-2180-74171 Email: jhaug@bio.lmu.de joachim.haug@palaeo-evo-devo.info

Website of Carolin and Joachim T. Haug: http://www.palaeo-evo-devo.info Joachim Haug <jhaug@biologie.uni-muenchen.de>

SGN Frankfurt MobileDNAEvolution

Job offer ref. # 12-20016

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE-TBG invite applications for a

PhD Position (m/f/d) - Evolutionary genomics of mobile DNA

(part time, 50 %)

Your tasks:

§Comparative genomic analysis of mobile DNA in non-model organisms, with a focus on invertebrates

§Evolutionary inference of mobile DNA to study dynamics, phylogeny, and/or mode of transmission

§Phylogenomic analysis of whole genome data using state of the art methodology

Your profile:

§A master degree in the fields of biology, evolution or bioinformatics

§Preferred experience with genome assemblies, bioinformatics and basic scripting languages (bash, perl and/or python)

§Interest in mobile DNA and its genomic influences

§Experience and exceptional interest in comparative genomics, evolutionary biology research and phylogenomics

§Teamwork oriented and excellent communication skills in written and spoken English, you also work independently and meet deadlines

What is awaiting you?

§Become part of a dynamic team of researchers in an international research group and join the new LOEWE excellence centre with its 20 new research groups.

§Access to unpublished genomes from exotic animal phyla.

§The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics.

Salary and benefits are according to a part time public service position in Germany (TV-H E13, 50%). The contract should start as soon as possible and will initially limited for 36 months. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung. Equally qualified handicapped applicants will be given preference.

Please send your application, mentioning the reference of this job offer (ref. #12-20016) before 10th August, 2020 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your certification to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

For more information please contact Prof. Dr. Axel Janke (axel.janke@senckenberg.de).

– Mit freundlichen Grüßen / Best Regards

Jessica Helm Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß ç 22 BGB) Senckenberganlage 25

60325 Frankfurt am Main

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

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting) - 1564 di-Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1445

Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Karsten Wesche

Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Recruiting <recruiting@senckenberg.de>

StAndrews Southampton Bordeaux EvolComplexAdaptiveSystems

Applications are invited for a fully-funded PhD studentship exploring the evolution of complex forms of adaptive plasticity including learning, culture and adaptive immunity using a novel computational approach. The student will work with Prof Kevin Laland (Biology, St Andrews), Prof Richard Watson (Computer Science, Southampton) and Prof Thomas Pradeu (Immunology, CNRS & Bordeaux) to devise theoretical models of evolution in complex systems. The student must be of UK or French Nationality with a good degree in Computer Science, Computational Biology or related field, and experience of programming. Start date: January 2021, or soon as possible thereafter.

Background: Living organisms must produce suitable responses to highly diverse, complex and constantly changing inputs (e.g. immunological responses to rapidly evolving bacteria and viruses, or learned adjustments to quickly changing situations). Often organisms respond to such challenges through 'exploratory mechanisms', which are complex developmental systems that operate by generating variation (i.e. 'exploring' possibilities), largely at random, testing variants' functionality, and selecting the best solutions for regeneration, in an iterative developmental process. The process of adaptation during development arising from exploratory mechanisms resembles adaptation by natural selection (a.k.a. 'somatic selection'), except that it allows for ontogenetic information gain rather than the acquisition of genetic information. What the genome encodes is the means to explore, not the outcome of the exploration.....

Application deadline Aug 14th 2020.

Please see application details online or feel free to contact me.

https://www.findaphd.com/phds/project/dstl-uk-french-studentship-fully-funded-phd-in-computer-science-computational-biology-evolution-in-complex-adaptive-systems/?p114553 Dr. Richard A. Watson Associate Professor Institute for Life Sciences/Electronics and Computer Science, University of Southampton http://www.ecs.soton.ac.uk/people/raw R.A.Watson@soton.ac.uk

"Richard A. Watson" <R.A.Watson@soton.ac.uk>

TexasAMU MarineEvolution

Position/title

Ph.D. Assistantship 'V Marine Biology (Botany)

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

Responsibilities 'V A PhD assistantship position is available under the advisement of Dr. Barnabas Daru in the direction of Marine Biology. The successful applicant will be working on projects in the Marine Biology program and has a chance to study the use of herbarium plant specimens to explore the distributions and diversity of marine plant microbiomes. The project includes the use of pressed herbarium specimens of marine plants as sources of big data by analyzing the diversity of microbiomes, with the aim of understanding how climate change and urbanization have affected the microbiomes of marine plant species along coasts and estuaries spanning the past 120 years. The student will also get to work with a multidisciplinary and multi-institutional team to explore plant microbiomes in the threatened Arctic biome of North America.

The successful student will obtain Ph.D. degree through the Marine Biology Program, an interdisciplinary degree program.

Qualifications 'V

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

Closing Date

Applications will be considered until candidate is selected

Contact

Send: 1) cover letter, 2) resume, 3) unofficial transcripts and 4) GRE scores to: Dr. Barnabas Daru, through email: barnabas.daru@tamucc.edu

Barnabas Daru (PhD)

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

TrinityCollegeDublin DiseaseClimateChange

A four-year funded PhD position (euro 18,500 per year) starting either October 2020 or January 2021 (Covid-19 allowing) is available at the Zoology Department of Trinity College Dublin, on how climate change affects disease, under supervision of Pepijn Luijckx. This position is only available for citizens of Europe (that is, it does not cover international fees).

Interested candidates should send: 1) a curriculum vitae and 2) a cover letter outlining your research interests and why you would like to do a PhD to: luijckxp@tcd.ie

Project description The health and economic impact of recent epidemics like Zika and Covid-19 underline the urgency of understanding how diseases spread and transmit. Moreover, as disease transmission is sensitive to temperature climate change may alter disease outbreaks. Indeed, there is an increasing number of examples that rising mean temperatures may affect diseases dynamics. However, climate change is not only expected to alter mean temperatures but also the frequency of extreme weather events and temperature variation, which may further affect disease outbreaks. In addition, natural systems experience both diel and seasonal temperature fluctuations which could change disease dynamics. To better understand how temperature variation (that is extreme weather, diurnal fluctuations, greater variance in temperature) affects diseases systems, and develop new theory, the candidate will conduct experiments using the Daphnia-Ordospora host-pathogen system under different temperature regimes. This Daphnia model system is well established and can be used to study both the effect of parasitism and temperature in individual hosts (virulence, fitness) and whole populations (growth rate of the disease Ro, disease dynamics). Experiments could be supplemented with theoretical approaches in collaboration with Andrew Jackson (theoretician in the Zoology Department), genetic approaches to gain better insight in the role of host genetics, or field experiments, depending on the candidates interests and strengths.

Requirements - Undergraduate or Master's degree in ecology, evolution or parasitology (or related field) and a keen interest in host-disease interactions and climate change.

Desirable - Creative, motivated and resilient. - Experience running large laboratory experiments. - Experience with aquatic insects. - Knowledge of experimental design and experience using R. - Willingness to contribute to laboratory maintenance and animal care. - Capable of working both independently and as part of a team. - Proficient in written and spoken English.

Research group

The candidate will be joining PhD candidates Floriane O'Keeffe and Qi Su and Pepijn Luijckx in the sick-waterflea@tcd laboratory at the Zoology Department in Trinity College Dublin. The lab has a keen interest in empirically testing evolutionary and ecological theories pertaining to disease interactions. For example, past work has tested underlying assumptions of theory on host-parasite evolution (Luijckx et al. 2013 Current Biology), the evolutionary maintenance of sexual reproduction (Luijckx et al. 2017 PNAS) and how a warming climate may alter disease outbreaks (Kirk et al 2018). In addition to the sick-waterflea@tcd laboratory the Zoology Department (https://www.tcd.ie/Zoology/) is home to research groups with expertise in statistics and modelling, community ecology, parasitology, and aquatic biology providing ample opportunities for collaborative work.

"LUIJCKXP@tcd.ie" <LUIJCKXP@tcd.ie>

UAkureyri Iceland PtarmiganGenomics

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

We're seeking a highly motivated Ph.D. student to work on a fully funded project on evolutionary genomics and ecology of rock ptarmigan (Lagopus muta) in Iceland. The project is funded for 36 months, starting in autumn 2020.

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

The main supervisor of the Ph.D. student will be Professor Kristinn P. MagnÃo̱sson at the Faculty of Natural Resource Sciences, University of Akureyri (UNAK, www.unak.is), and Icelandic Institute of Natural History (IINH). Other advisors are Professor Jacob Höglund at the Institute of Ecology and Genetics, University of Uppsala, Sweden. Professor SnÃbjörn Pálsson, Faculty of Life and Environmental Sciences, University of Iceland, Dr. Eva Charlotte Halapi, Faculty of Natural Resource Sciences, UNAK, and Professor Jennifer Forbey, Department of Biological Sciences, Boise State University, Boise, USA. The bulk of the work will be carried out at the UNAK/IINH laboratories in Akureyri, but the student will also attend secondments in Uppsala, Sweden, and Idaho, USA.

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

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

Application - Deadline August 15th. 2020 The application should be submitted to the principal investigator for that project, Prof. Kristinn Pétur MagnÃo̱sson, kpm@unak.is. This application should consist of: 1. A cover letter, wherein the applicant states the reasons for their interest in the project, explains how they fulfill the eligibility criteria, and outlines their proposed contribution to the project. 2. A curriculum vitae, listing all relevant qualifications and work experience. 3. A copy of any relevant diplomas and/or transcripts. 4. Contact information of at least two reference persons.

Kristinn Pétur MagnÃo̱sson Prófessor AuÃ°lindadeild ViÃ°skipta- og raunvísindasviÃ° / School of Business and Science Skrifstofa / Office: Borgir rannsóknarhÃo̱s - R414 Sími / Phone: 5900578 Farsími / Mobile: 8918778

Kristinn Pétur MagnÃo̱sson <kpm@unak.is>

UArizon PopulationGenomics

UArizona.BajaGeoGenomics.AnimalAndPlant

A funded PhD Graduate assistantship is available to study Genomics in Baja California using whole genome sequencing and population genomic analyses of rodent, lizard, and plant species, conducted at the University of Arizona and the Desert Laboratory on Tumamoc Hill.

Applications will be accepted until filled.

The project is part of an NSF-funded multidisciplinary GeoGenomics investigation that combines geologic and genomic data to test multiple non-mutually exclusive hypotheses in Baja California peninsula (Mexico). The genomic data will be used to test the effects of marine seaways, glacial refugia, and rainfall timing on the biological diversification through signatures on the genomes of desert reptiles, mammals, and plants. The student will work as part of the larger Baja GeoGenomics consortium composed by a team of geologists and biologists from University of Oregon, Arizona State University, California State University, and the University of Arizona. The position will include field work opportunities

https://bajageogenomics.org/ https://bajageogenomics.org/wp-content/uploads/2019/09/LayAbstractFRES.pdf Eagerness to work in a multidisciplinary setting and team is essential. Strong prior knowledge in bioinformatics is a plus for this position, but candidates will be considered with different backgrounds having demonstrated predisposition to learn these skills. The research project will generate de-novo whole genome sequence, and conduct population genomic analyses to identify genetic variants from low-coverage genome sequence, parametrize Approximate Bayesian Computation models of neutral divergence for multiple species constrained by the geologic evidence, perform landscape genomic analyzes to test concordance with niche modeling hypotheses of expansion-contraction from glacial refugia, correlate present-day ecological niches with spatial signals of natural selection both from genome sequencing and differential RNA-Seq expression, and develop novel bioinformatic approaches for simultaneously integrating geologic, genomic and ecological datasets.

Apply through the University of Arizona Genetics Graduate Interdisciplinary Program. Include a cover letter indicating your background is relevant to this project, your CV, and the names of 2 references.

https://genetics.arizona.edu Copy the cover letter and CV also to:

Ben Wilder (bwilder@email.arizona.edu) Desert Lab on Tumamoc Hill and Adrian Munguia-Vega (airdrian@email.arizona.edu) School of Natural Resources and the Environment. Selected students will work in collaboration with Dr. Melanie Culver's Conservation Genetics Lab in the School of Natural Resources and the Environment

–

Melanie Culver

Assistant Professor, Wildlife Conservation and Management Program Assistant Leader, AZ Cooperative Fish and Wildlife Research Unit, USGS School of Natural Resources and the Environment University of Arizona 314N Environment and Natural Resources Bldg. 2 Tucson, AZ 85721 culver@ag.arizona.edu Office 520-626-3775 Lab 520-626-1636 Fax 520-621-8801

http://www.cals.arizona.edu/research/azfwru/-melanie/ http://www.uawildcatresearch.org/-index.htm http://www.coopunits.org/Arizona/-People/Melanie_Culver/index.html "Culver, Melanie - (mculver)" <Culver@ag.arizona.edu>

UBasel BacterailGenomics

Open position: PhD student in bacterial genomics and metagenomics

The Applied Microbiology Research group, Department of Biomedicine, University of Basel, is looking for a PhD student in bacterial genomics and metagenomics. We are a varied, interdisciplinary and international team, working at the interface of clinical microbiology and genomics research, with access to state-of-the-art facilities. Our group is open and supportive, with close links to the Division of Clinical Bacteriology & Mycology at the University Hospital Basel. With our in-house sequencing platforms (Illumina and Nanopore), we generate microbial sequencing and metagenomic data on a large scale, with the ability to link analyses to clinical data. Recently published projects within the group have involved outbreak analysis of Legionella, Burkholderia and vancomycin-resistant enterococci, descriptions of new bacterial species e.g. Mycobacterium basiliense, influenza immune response, and case studies illustrated with genomic data.

As part of a new Swiss National Science Foundation (SNSF)-funded research project, we aim to explore (i) the within-host evolution of multi-drug resistant bacteria in colonized patients and (ii) the patient's environment in the hospital using a metagenomic approach. In addition, we aim to develop a new standard protocol to rapidly screen for multi-drug resistant bacteria with a high potential for application in routine clinical practice.

Your position. The position as a PhD student in the microbiology research laboratory involves project management, wet lab, and bioinformatics elements. Specifically: processing of samples from the study, DNA and RNA extraction, identification of species (e.g. with MALDI-TOF) and resistance testing (e.g. with E-Test), management of the project's biobank, development of new PCRs, and long-read shotgun metagenomic protocols, and genomic data analysis.

Your profile. We are looking for someone enthusiastic, trained in good microbiology practice and nucleic acid extraction and manipulation. We need someone with hands-on and organizational skills, and prepared to develop new methods. Experience in bioinformatic data analysis, in particular bacterial genomics, is crucial.

We offer you. The opportunity to learn and develop laboratory, project management and bioinformatics techniques in a cutting edge environment, and use these techniques to investigate epidemiology and evolution of bacterial pathogens and communities with a direct link to patients. Access to training from Post-docs and courses is available as required.

Application / Contact. Please send your application by 31st July 2020 including a letter of motivation, CV, certificates, and recommendation letters, in one PDF file to Prof. Adrian Egli and Dr Helena Seth-Smith, Department Biomedicine at the University of Basel (e-mail info@appliedmicrobiologyresearch.net, Subject containing "PhD2020").

Egli Adrian <Adrian.Egli@usb.ch>

UCopenhagen IslandBiogeography

PhD fellowship in Island biogeography of mutualistic networks in the Anthropocene at GLOBE Institute, University of Copenhagen, Denmark We are offering 1 PhD fellowship in island biogeography of mutualistic networks in the Anthropocene commencing 1 January 2021.

Our group and research The successful candidate will be part of the Dalsgaard Group (https://globe.ku.dk/research/cmec/dalsgaard-group/) within the Center for Macroecology, Evolution and Climate (CMEC) at the GLOBE Institute, University of Copenhagen. CMEC is a center of excellence with a cross-disciplinary research program. We offer creative and stimulating working conditions in a dynamic and international research environment addressing fundamental questions on the origin, maintenance, conservation and future of life and biological diversity on Earth. The 40+ researchers at CMEC currently represent 14 different nationalities and the working language is English. The center juxtaposes faculty staff scientists from the fields of macroecology, historical biogeography, oceanography, evolutionary biology, community ecology, population biology, climate change research, conservation biology and environmental economics.

Project description This project is novel in integrating island biogeography theory and theories on how climate and anthropogenic pressures influence mutualistic plant-pollinator and seed-disperser interactions. The project combines field work data collected in the Caribbean with network analysis and biogeographical modelling. The PhD student will work closely together with a postdoc to jointly lead data collection across numerous islands in the Caribbean. The PhD student should be prepared to collect data for approximately 4-5 months in both 2020 and 2021, and s/he is expected to first-author several papers in international peer-reviewed journals. In addition to the PhD-student, we will hire a postdoc and a cohort of MSc students will participate in the project. All project partners will gather once a year to run workshops with the aim of publishing review and synthesis papers. The project is funded by Independent Research Fund Denmark.

Principal supervisor is Associate Professor Bo Dalsgaard, Center for Macroecology, Evolution and Climate, GLOBE Institute, bo.dalsgaard@sund.ku.dk, Direct Phone: +45 42324553. Co-supervisors and project partners are Senior Lecturer Christopher Kaiser-Bunbury and Research Fellow Benno I Simmons (University of Exeter, UK) and Professor Mauro Galetti (University of Miami, USA).

Start: 1 January 2021

Duration: 3 years as a PhD Fellow

Apply here: https://employment.ku.dk/phd/?show=152204 Bo Dalsgaard <bo.dalsgaard@sund.ku.dk>

UMelbourne BehaviourMacroevoluiton

Graduate position:, UMelbourne.BehaviourandMacroevolution

PhD position in behavioural ecology at the School of BioSciences, University of Melbourne, Australia.

We are seeking for a PhD student with interest in avian evolution and behaviour. The proposed project looks into the evolution of avian nests, and involves fieldwork looking for bird nests in different locations in Australia and broad-scale comparative analyses. Specific topics are flexible and you are encouraged to contribute your own ideas. Experience doing fieldwork with birds and experience with R are highly desirable. We are keen to foster a diversity of ideas and perspectives in the lab, so we especially welcome applicants from under-represented groups.

The University of Melbourne offers Scholarships for international and domestic students and we can discuss other funding opportunities. https://biosciences.unimelb.edu.au/study/phd-studies-in-biosciences If interested, please send an e-mail (before Sept 1st) to: iliana.medina@unimelb.edu.au with your CV, a brief statement with your research interests and career path and academic transcripts (these don't need to be official).

Planned start date: May 2021 Deadline official applications: 30th of September (for international applicants), 31st of October for domestic applicants.

https://www.ecomedina.com Iliana Medina Guzman <iliana.medina@unimelb.edu.au>

USouthernMississippi DomesticationGenomics

A graduate assistant position (M.S. or Ph.D) is available in our laboratory to work on domestication and breeding of marine organisms. Potential projects include studies of population structure of wild stocks or studies of the domestication and breeding process of eastern oyster or warmwater fish candidate for marine aquaculture. Typicallab projects employnext generation sequencingto perform genomic studies of wild and/or captive stocks.

The successful applicant will be provided a 12-month full-time Research Assistantship with a tuition waiver. Candidates should possess a Bachelor's degree in a relevant field (e.g. Biology, Ecology& evolutionary biology, Fisheries science) when applying for this position. Bioinformatics skillsand experience with molecular techniques are assets. The position is available starting in spring 2021 with the possibility to work as a research assistant during the fall 2020 semester.

Interested individuals should email a CV, GRE scores if available, and unofficial transcripts to:

Eric Saillant, Ph.D Associate Professor

The University of Southern Mississippi School of Ocean Science and Technology

Thad Cochran Marine Aquaculture Center 103 McIlwain Drive Ocean Springs, MS, 39564 Tel. (1) 228-818-8007 Fax (1) 228-872-4204 E-mail: eric.saillant@usm.edu

Eric Saillant <Eric.Saillant@usm.edu>

UToronto ForestInsectEvolution

Master's and PhD positions in quantitative forest insect ecology

Location: Toronto (UofT) and Montreal (McGill and UQAM)

Start Date: January 2021

Application deadline: August 31, or until suitable candidates are found

We are searching for quantitatively-oriented, enthusiastic, and creative students to tackle problems related to the spatial ecology of forest insect outbreaks. Selected students will have the opportunity to work with a diverse and collaborative research team examining the spatial and temporal dynamics of spruce budworm outbreaks in eastern Canada. Team members include Patrick James (U. Toronto), Dan Kneeshaw (UQAM), Brian Leung (McGIll), Elise Filotas (TELUQ), Mathieu Bouchard (MFFPQ), Deepa Pureswaran (NRCAN-CFS), and Rob Johns (NRCAN-CFS).

The focal subject of this work is the outbreak dynamics of the spruce budworm (Choristoneura fumiferana), a native defoliator that affect millions of hectares of coniferous forest during outbreaks. Despite nearly a century of research, there remain many outstanding mysteries associated with budworm outbreaks and their effects on forests. Developing greater understanding of these underlying population dynamics is essential to improve forecasting and for developing proactive sustainable forest management strategies.

Two projects are available. The general questions associated with these projects are: 1) what determines where, when, and the rate at which populations of spruce budworm increase? 2) How will future climate and forest management regimes affect future outbreak risk and severity?

Both projects will involve leveraging large spatial-temporal databases on forest insect outbreaks to develop predictive statistical, machine learning, and spatially explicit simulation models of outbreak dynamics.

Potential students should have a strong interest in developing skills and expertise in forestry, ecology, scientific computing (e.g., R), GIS, statistics, and modelling. Preexisting expertise in these areas would be an asset.

To apply, please send a short letter of motivation, a current CV, recent transcripts, and the names of two references as a single PDF to Dr. Patrick James at patrick.james@utoronto.ca

We encourage all qualified students to apply. Final selection will however give preference to Canadian citizens and permanent residents given current COVID-19 related uncertainty around international travel.

jwittische@gmail.com

UZurich PlantEvolution

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

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

Biophysical carbon concentrating mechanisms (CCMs) operating at the single-cell level have evolved independently in some eukaryotic algae and a single lineage of land plants, the hornworts. An essential component for an efficient biophysical CCM is a pyrenoid, which represents a specialized compartment inside chloroplasts that mainly comprise the CO2-fixing enzyme RuBisCO. Hornworts with pyrenoids fix significantly more carbon than their relatives without pyrenoids. Given the repeated gains and losses of pyrenoids in hornworts during the last 50 million years, we may assume that their assembly is potentially controlled by a few master regulators of eco-evolutionary relevance. In a joint effort, we will combine comparative -omics with reverse genetics tools to study the genetics, function, and molecular basis of pyrenoid-based CCM in hornwort plastids under different environmental conditions. Guided by ultrastructure-based monitoring of the pyrenoid assembly in hornworts, we aim to identify the genetic toolkit of biophysical CCM in hornworts through two interdependent approaches: First, we aim to predict candidate CCM components in silico though a set of homology searches that compare the hornwort gene set with algal CCM component. Second, we employ an exploratory gene and protein (co)expression profiling of isolated plastids collected under low vs. high CO2 concentrations and under flooding. A strength of our experimental design is that we contrast up to three pairs of pyrenoid bearing and pyrenoid lacking hornwort species. Finally, we will investigate pyrenoid functionality under various environmental conditions. Specifically, we aim to conduct localization and functional validation analyses for a core set of genes discovered in our CCM gene prediction approaches. These experiments are possible through our recent advances to establish Anthoceros agrestis and other hornwort species as a tractable model system. Together, our collaborative project will not only allow a comparison of the mechanisms of pyrenoid assembly between algae and hornworts, but also reveal general principles and species-specific innovations in the evolution of carbon-concentrating plastids. Above that, focusing on and understanding the basis of land plant CCM instead of only the algal form could eventually contribute to efficiently engineer pyrenoid assembly and boost photosynthetic efficiency of crops. Relevant publications: https://www.nature.com/articles/s41477-020-0618-2, https://doi.org/10.1016/j.tplants.2017.02.002 . This project is founded (initially for three years) by the German National Science Foundation (DFG) MadLand (https://madland.science/) program to Peter Szovenyi and Susann Wicke. The project requires collaborative work including frequent visits to Germany and to the USA (Fay-Wei Li‘s lab at Cornell).

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

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

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

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Jobs

AstreaForensics ForensicGenomics

Astrea Forensics www.astreaforensics.com , a sister company of Claret Bio was founded in 2019. We apply ancient DNA techniques, direct genome (Illumina) sequencing, and sophisticated computational methods to forensic casework towards the identification of human remains. Our lab works with highly degraded samples (e.g. rootless hair) that otherwise fail traditional forensic DNA testing, in collaboration with law enforcement and genetic genealogy investigators. Astrea Forensics is a subsidiary of EdenRoc Sciences, working out of the same facility as Claret Bio in Santa Cruz, CA.

The position requires a Masters or higher degree (Ph.D. preferred) in a biological science related field, with at min. 3-5 years of experience in human genomics. Strong organization skills and the ability to manage a genomics wet-lab is a must. Duties include managing a small forensics DNA laboratory that uses next- generation sequencing (NGS) technologies to recover human DNA from degraded samples (e.g. hair, bone, teeth).

The Laboratory Scientist is expected to possess and understand major molecular biology laboratory work skills and genomics research experimental platforms, with experience leading genomics processing such as extractions and sequencing of biomolecules from human tissues. Experience with protocols for degraded DNA, such as previous work in forensics or paleogenomics, is preferred. Familiarity with common NGS analysis tools used for processing genomic datasets (e.g. BWA, SAMtools) and basic bioinformatics skills is a plus.

The Laboratory Scientist is responsible for overseeing the day-to-day functioning of the lab spaces, implementing safety protocols, maintaining active records of forensics cases, drafting case reports, contacting law enforcement agencies, and as we grow, supervising laboratory training of technicians and junior scientists.

Other duties relevant to lab management may be assigned, such as trouble-shooting protocols, lab calendar management, and coordination with and reporting to other laboratory and computational staff. Strong oral and written communication skills are expected. Preferred Qualifications: - Previous supervisory experience - Experience or training in paleogenomics, forensics and/or degraded DNA methods - Familiarity with human skeletal anatomy - Familiarity with forensics QAS/ANAB accreditation requirements - Understanding the application of forensic genetic genealogy (Title of position subject to change based on level of experience)

Submit Cover Letter and CV through: https://edenroc.bamboohr.com/jobs/view.php?id= For additional questions, contact: Kelly Harkins Kincaid, PhD clientservices@astreaforensics.com

Astrea Forensics is an equal opportunity employer. We offer excellent benefits and a generous time off package. We prefer local candidates

Astrea Forensics Client Services <clientservices@astreaforensics.com>

clientservices@astreaforensics.com

DonanaBiologicalStation EvolutionaryBiology

Researcher positions at /Doñana Biological Station:/

The /Doñana Biological Station/ (Estación Biológica de Doñana, EBD; Seville, Spain) is seeking to incorporate top researchers with leadership skills though the EMERGIA program, financed by the Andalusian regional government.

We are looking for researchers that defended their PhD 5-12 years ago and have an excellent track record in evolutionary biology, conservation biology, ecology or global change. This opportunity is open to researchers of all nationalities, and we are particularly interested in cultural diversity. Candidates would lead their own research project and could participate in the lines of work present at the institution: plant-animal interactions, biological invasions, evolutionary ecology, conservation biology, integrative ecology and/or wetland ecology. Proposals are open to those developing theoretical or empirical work or based on analysis of large databases. Multidisciplinary approaches are particularly welcome. Likewise, profiles specialized in the management and conservation of biodiversity, and with direct application to environmental problems will also be eligible. Prospective candidates are strongly encouraged to contact us in advance (direccion.ebd@csic.es).

Deadline for the submission of applications: august 4^th , 2020

Information: http://www.d-andalucia.csic.es/es/noticia/Emergia The Estación Biológica de Doñana is an institute of the Spanish National Research Council (CSIC). EBD has close to 200 employees, including 44 researchers, postdoctoral fellows, PhD students, field and lab technicians, and administrative personnel. EBD has several unique aspects:

-EBD manages two field reserves, one within Doñana National Park (Huelva, Spain) and the other in the Sierra de Cazorla, both devoted to ecological and evolutionary research.

-The field reserve in Doñana National Park is a Singular Scientific-Technical Infrastructure (ICTS-RBD) that offers services and facilities to researchers around the world.

-The institute, located in Seville, is equipped with six laboratories maintained by technical staff, that offer services to all researchers: Molecular Ecology, GIS and Remote Sensing, Chemical Ecology, Aquatic Ecology, Ecophysiology, Stable Isotopes.

-The institute has also an Animal Experimentation Unit and a green house. This includes 11 walk-in climatic chambers and animal care facilities. Our Animal Welfare personnel train and conduct certification courses for our personnel.

-The institute houses the second largest scientific collection in the country which focuses on vertebrates and includes almost 100,000 specimens.

-We actively participate in MSc and PhD programs at the University of Seville and Pablo de Olavide University. We also host PhD students from many other national and international universities as well.

Despite the rich resources available to scientists at EBD, the main advantage of EBD is the quality of the researchers. Several of them are among the most cited researchers in their fields and are internationally recognized. EBD is currently looking to expand the number of investigators and lines of research through the recruitment of young, engaged and brilliant minds. EBD is welcoming researchers from all over the world.

If you need any additional information about the Estación Biológica de Doñana, please check http://www.ebd.csic.es/inicio or contact us at direccion.ebd@csic.es

Carles Vilà Estación Biológica de Doñana-CSIC Avd. Americo Vespucio 26 41092 Seville (Spain) http://www.consevol.org/ carles.vila@ebd.csic.es

EmbarkVeterinaryInc DogGenomics

Research Scientist - Ancestry - Embark Veterinary Inc. Ithaca, NY

About Us

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. Help us end preventable disease in dogs and improve the lives of pets and their people through genomics.

Embark's market-leading dog DNA Test is not only the most comprehensive on the market for breed mix, health, traits, inbreeding, and finding relatives, it is also an engine driving scientific discovery in dogs. Embark uses a 220,000-marker research-grade DNA microarray, enabling us to give our customers the most accurate and comprehensive results on the market. More importantly, it allows Embark to do ongoing research into the genetics of dogs, which are a unique population for genetic study and discovery due to selective breeding over time. Our research focuses on mapping new traits and diseases, improving personalized veterinary medicine, and developing new breeding programs to eliminate preventable diseases.

Interested in joining? We're looking for highly motivated and driven employees who will help us stay on the cutting edge of creativity and innovation in the fast-growing consumer genetics space.

The Role

We are looking to expand our Ancestry team and are accepting applications for Scientists with extensive training and experience in Population Genetics, Genomics and Computational Biology, or Data Science. Talented candidates at all levels of experience are encouraged to apply.

This team is applying a combination of population genetics and data science approaches to improve Embark's core Ancestry products, develop new products such as the next generation of breeding tools, and conduct evolutionary research in dogs, with the goal of accelerating canine genetic science and a long-term vision of ending preventable disease in pets.

The Opportunity

The principal objectives of this role are to continually maintain and improve upon Embark's Breed and Ancestry offerings.

- Contribute to the development of Embark's best-in-class Dog Ancestry products, including the world's only Dog Relative Finder.

- Build population genetic resources to assess and monitor genetic diversity.

- Understand the phenotypic impact of inbreeding and inbreeding depression across dog breeds.

- Work collaboratively across teams to develop and accelerate Embark's resources tailored for dog breeders and professionals.

- Add to a culture of teamwork and continuous learning/teaching.

Requirements

- PhD in Population Genetics, Computational Biology, Bioinformatics, or a related field.

- Comfort with Linux/Unix environments and coding experience including python, R, and SQL.

- Excellent statistical proficiency.

- Excellent oral and written communication skills.

- Experience in applied population genetics preferred.

- Experience with Amazon Web Services preferred.

- A passion for pet health and desire to build products to improve the lives of pets and pet owners.

What We Offer

- Dog friendly office in downtown Ithaca, NY.

- Perks tailored for dog lovers including Trupanion pet insurance and paw-ternity leave.

- Startup perks with big-company benefits.

- Competitive salaries, all-inclusive health care, and equity participation.

- A flexible vacation policy along with paid maternal and paternal leave.

- Fully-stocked office snack bar and regular office events.

- New iMacs and MacBook Pros, or laptops running Linux.

- Continuing education, including attending conferences.

Embark Veterinary Inc. is an equal opportunity employer and values diversity at our company. We do not discriminate on the basis of race, religion, color, national origin, gender, sexual orientation, age, marital status, veteran status, or disability status.

Please apply directly here: https://embarkvet.com/careers/research-scientist-ancestry/ Aaron Sams <asams@embarkvet.com>

Harvard AncientDNA Bioinformatics

Bioinformatics Data Manager,Harvard Medical School Job Code 52391BR (Apply here: https://sjobs.brassring.com/TGnewUI/Search/Home/Home?partnerid%240&siteidS41#jobDetails30332_5341)

Job Summary

We offer an opportunity to support a cutting-edge laboratory that has so far been responsible for producing more than half of the world's ancient DNA data. The successfulcandidate will assume a computational biologist/data scientist position and will work closely with scientists in the lab studying DNA from human remains up to 20,000 years ago.

Under limited supervision, this role is responsible for computational data analysis of the assigned project. Collaborates and consults with researchers and scientists to analyzeproblems, recommend technology-based solutions, and design computational strategies for a project. Contributes to the design, development, implementation, and testing of bio-computing tools. Ability to communicate analyzed data to analysts writing scientific papers

An article on our laboratory ancient DNA work can be found here:https://www.nytimes.com/2018/03/20/science/david-reich-human-migrations.html The John Templeton Foundation "Ancient DNA Atlas of Humanity" initiative that will support this work is described here: https://www.templeton.org/news/john-templeton-foundation-awards-15-5m-for-ancient-dna-atlas-of-humanity This is an ideal opportunity for candidates with several different backgrounds:

- Recent graduates with college or masters degrees in bioinformatics or computer science more generally - Experienced bioinformatician with a background in processing genomic data. - Experienced data scientist who has broad experience working with data and databases

We are looking for candidates intending to stay for an extended period (at least threeyears).

Job-Specific Responsibilities

(1) Processing data through a bioinformatic pipeline and working with its software engineer designers to improve the pipeline:Our laboratory team is constantly producing new genetic data. Each year, we produce trillions of new DNA sequences on more than ten thousand ancient individuals. We need aperson who will take charge of day-to-day computational processing this stream of data, taking the sequences from their raw form (as the data are generated by DNA sequencers)to a processed form that can be used by analysts writing scientific papers based on the data. We have a full-time software engineer who has built a software pipeline that makesthis processing efficient, but the processing needs to be actively supervised, and frequently repeated with new parameter settings or redone depending on the needs of particularanalyses. This is an exciting position that will put the person who fills the position at the heart of the work in our laboratory, and will involve active communication with laboratory-based personnel, with senior software engineers constantly working to improve our data processing capabilities, and with analysts writing scientific papers

(2) Extracting data from published papers, incorporating it into the laboratory's dataset, curating datasets, and harmonizing meta-data:Second major area of responsibility will be to download data published by a variety of scientific groups onto our computers, and reprocess this externally generated to make it ispossible to co-analyze with data generated by our group. Different scientific groups upload data to public databases in a variety of formats, and process their data in a variety ofways, and a key aspect of this position will be to grapple with this variety of formats, reprocess data when necessary, and create a homogeneous combine dataset that can bereliably analyzed. Importantly, the person who fills this position will not only be downloading data but will also need to download meta-data (for example, information on the locationand age of the ancient individuals which needs to be extracted from scientific papers), so that users of the data can have this information available for their analyses

Basic Qualifications - Bachelor's degree in computer science, data science experience preferred

- Fluency in a scripting language (e.g. Python or Perl)

- Linux/Unix proficiency

Additional Qualifications - Some experience in biology or genomics

- SQL database experience
- High-Performance Computing experience (SLURM)
- Interest in anthropology, archaeology or history (need not be professional)
- Excellent written, documentation, and oral communication skills
- Ability to multi-task

Additional Information This is a one-year term position with strong potential for renewal.

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MaxPlanckInst Goettingen CompGenomicsPlanarians

MaxPlanckInst_Goettingen.CompGenomics_Planarians

We offer fully funded postdoc opportunities in comparative genomics of planarian flatworms. Planarians are fascinating animals that can regenerate from tiny pieces, harbor adult pluripotent stem cells, scale their bodies over a wide size range and, as a taxonomic group, display a fascinating spectrum of regenerative abilities, body sizes, reproductive strategies or life expectancies from a few months to seeming immortality. In collaboration with Gene Myers, our group has pioneered planarian high-quality genome assemblies and we have established a large and phenotypically diverse species collection through world-wide field expeditions. Comparative genome mining now promises access to a wealth of intriguing research questions. Current project opportunities include probing of the genomic consequences of asexuality by means of comparisons between the sexually and asexually reproducing strains of S. mediterranea; body size evolution in the giant planarians of Lake Baikal or genomic adaptations to life in the lake's abyssal zone (~ 1600 m depth); intra-organismal population genomics amongst the many independently replicating pluripotent stem cells or the dynamics and functional relevance of the new class of giant planarian retroelements that we discovered. We have a number of fully funded postdoc positions available for talented individuals to pursue these or other questions.

Your Profile

You have a PhD or equivalent degree in a relevant subject area, e.g., biology, computational biology or computer science and extensive hands-on experience with genomic data.

You have a proven track record in one or more of the following: genome assembly, multi-genome alignments; comparative genomics; structural genome variance; transposon mobility; cancer or evolutionary genomics; phylogenetics and or population genomics.

You are passionate about the scientific endeavor and you are not afraid of pursuing your questions beyond the current scientific frontier.

You are self-motivated and independent and enjoy being part of an international and interdisciplinary work environment.

About us

We are a brand-new department at the Max Planck Institute for Biophysical Chemistry in the historic science town of Goettingen. We represent the organismal end of biophysical chemistry at the institute and investigate the mechanistic and evolutionary underpinnings of planarian regeneration. The department hosts a large zoo of planarian species for comparative analyses and we just established a field station at Lake Baikal in Russia, the Galapagos of planarian biodiversity. We are a thoroughly international and interdisciplinary group of people and based at one of Germany's premier research campuses. We enjoy generous funding by the Max Planck Society and the proximity to picturesque Goettingen with its bustling student bars.

Job Add

https://www.mpibpc.mpg.de/17351593/11-20 For Inquiries

Jochen.rink@mpibpc.mpg.de

SangerInst ComputationalBiodiversityGenomics

A permanent Computational Staff Scientist or Senior Staff Scientist (depending on experience) role is available in my group at the Wellcome Sanger Institute to lead on projects in the general area(s) of biodiversity genomics (esp long read population genomics on flying insects), Plasmodium single cell RNAseq, and Anopheles mosquito population genomics using both modern and historic samples.

Each of these three areas already has several active team members producing and analysing data, so I am looking for someone who will be deeply engaged with the whole team and interested in enhancing work already underway while also developing new creative and innovative directions of their own.

Job advert here: https://jobs.sanger.ac.uk/vacancy/-computational-staff-scientist-computational-senior-staff-scientist-420626.html Lab website here: https:/-/www.sanger.ac.uk/group/lawniczak-group/ Any questions, please get in touch.

Thank you. Mara Lawniczak

mara@sanger.ac.uk

UBath MicrobiologyEvolution

Revealing Rewiring Routes to Natural Selection: making predictions on gene regulatory network evolution based on gene co-expression profiles

Come and join the Taylor lab at the University of Bath, UK (https://tiffanybtaylor.wordpress.com/) as a full-time research assistant on a 13-month fixed-term contract funded by a Royal Society 2020 Enhancement Award.

Project description: How are opportunities for rewiring events between gene regulatory networks (GRNs) revealed to selection? Previous work has shown that GRNs are dynamical such that connections are forged and lost frequently across an evolutionary timescale. We predict network activity to be a key factor in revealing opportunities for rewiring events between previously disconnected networks, facilitating novel genetic innovations. With a microbial model system, you will use experimental evolution combined with molecular manipulations to explore the role of environmentally contingent network activity in predicting rewiring between GRNs using motility rescue as a model system. This will inform our understanding of the role the environment plays in shaping GRN arrangement, with the potential for different environments to rewire GRNs differently.

Location: This project will be conducted under the direct supervision of Dr Tiffany B. Taylor, and based within the Department of Biology and Biochemistry at the University of Bath (UK) in the new Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/).

Requirements: We are looking for a biology graduate who has a strong interest in genetics, microbiology and evolution. Some practical experience in microbiology and molecular techniques is highly desired. The successful candidate will be enthusiastic, highly motivated, independent, have experience in microbiology, molecular biology or evolutionary biology (or a combination), and have a relevant degree. The applicant must meet the standard University of Bath English language requirements.

Planned start date: 1 September 2020 (13 months funding)

Contact: For informal enquiries please contact Tiffany Taylor T.B.Taylor@bath.ac.uk. Apply via the University website: https://www.bath.ac.uk/-jobs/Vacancy.aspx?ref=CC7550 Tiffany Taylor <tt515@bath.ac.uk>

UBourgogneFranche BehaviouralEvolution

Ten-month demonstratorship in Behavioural Ecology and Conservation Biology at the University of Bourgogne-Franche Comte, Dijon, France

The master program in Behavioural Ecology and Wildlife Management (more information at www.nature-conservation-ubfc.com/bewm/en/) at the Universite de Bourgogne-Franche Comte in Dijon (eastern France), is seeking a demonstrator to teach a variety of courses in Behavioural Ecology, Conservation Biology, and Biostatistics. In particular, the demonstrator will assist the academic staff in the development of online, online/hybrid and face-to-face courses ensuring student comprehension, retention of knowledge and positive and effective student engagement. Job duties also include some research and service with a strong focus on teaching. We are offering a ten-month tenure-track appointment beginning in Fall 2020.

The applicants are expected to have a PhD and research track record in behavioural ecology, conservation biology or a closely related field, to have a good knowledge of English (the language that is used for instruction), to have competence in the statistical analysis of ecological data, and to be familiar with appropriate methods for delivering content via current e-learning technology.

The net salary will be on the salary scheme for technical staff (at the level "ingenieur de recherche") at French universities, i.e. about 1800 euros per month, depending on the appointee's qualifications and experience. An additional bonus associated with lecturing will be available up to 2000 euros for the whole duration of the position.

Applications should be sent by e-mail to Professor Frank Cezilly (frank.cezilly@u-bourgogne.fr), not later than 15th August. They should consist of a single PDF-file containing a letter with a personal statement outlining your research/teaching interests, how this position fits into your career plan, as well as relevant work experience, a detailed CV including a publication list with journal impact factors, and contact information for two references.

mjperrot@u-bourgogne.fr

UBuffalo MicrobiomeEvolution

The Department of Biological Sciences at the University at Buffalo (SUNY) is seeking outstanding applicants for a prestigious Empire Innovation Professorship studying the broadly defined field of microbiome science. Candidates with research interests in any area of microbiome sciences are encouraged to apply. Work may be focused at the molecular, cellular, systems or organismal level.

Applicants should be at the Associate Professor or full Professor level, and lead a strong, federally funded, interdisciplinary research program focusing on the microbiome. The successful candidate will be expected to participate in graduate and undergraduate teaching. The position will provide a 10-month, state-supported salary plus a competitive startup package.

The University at Buffalo (UB) is the largest and most comprehensive campus in the State University of New York system. UB is the leading research hub in New York State in biological, environmental, and biomedical sciences.

The Department of Biological Sciences is the major focal point for interdisciplinary research and education in life sciences at the University at Buffalo (UB). The department provides a recently expanded and diverse intellectual niche with particular strengths in neuroscience, transcription regulation/signaling, and evolutionary genomics. The department is an interdisciplinary research center with strong connections with multiple schools and departments across the university, including the NYS Center of Excellence in Bioinformatics and Life Sciences, Jacobs School of Medicine, and School of Engineering and Applied sciences. Multiple university-wide initiatives provide excellent institutional support for expanding microbiome research. We expect our new colleague to build upon these diverse intellectual and material resources to build a world-class research program at UB.

To apply, submit electronic versions of a curriculum vitae, cover letter and a 3-page description of current and future research interests to: http://-www.ubjobs.buffalo.edu/postings/24837 . Please include the names and contact information for three colleagues who could be contacted for letters of recommendation. Completed applications will be reviewed beginning September 1, 2020, and will continue until the position is filled. Our plan is to conduct on-site interviews during the fall or winter assuming travel and public health conditions allow.

Please consult our website:http://arts-sciences.buffalo.edu/biological-sciences.htmlfor information about UB, our department and our community.

University at Buffalo is an affirmative action/equal opportunity employer and, in keeping with our commitment, welcomes all to apply including veterans and individuals with disabilities

Omer Gokcumen <gokcumen@gmail.com>

UCalifornia Merced LabTech ComparativePopGenomics

We are looking for a highly competent and organized lab tech / manager to join our lab and the Marine Networks Consortium to conduct lab and field work in support of community genomic analyses of coastal marine species with the goal of providing fundamental insights into spatial patterns of genomic diversity, population connectivity, and responses to abiotic and biotic environmental variation at the level of marine ecosystems.

The project aims to produce an understanding of genomic diversity that scales from individuals to ecosystems. By drawing a new "community genomic" map of coastal California, this project has potential to revitalize our understanding of marine biodiversity and approach to conservation while providing mechanisms for understanding future ecosystem responses.

Your principle role will be fieldwork, lab work, and project organization curating and using multiple samples from throughout California, high mwt DNA extractions, QC, and library prep. A full description of the position and how to apply is available at https://aprecruit.ucmerced.edu/JPF01002 More information on this and related positions is available at the lab's website http://mnd.ucmerced.edu/Info/ON.html This position is a part of the California Conservation Genomics Project < https://sites.lifesci.ucla.edu/eeb-CCGP/ > a state-funded initiative to provide officials with the scientific basis for confronting climate change.

Review of applications will begin Monday, 03 August 2020.—

Enquiries to Mike Dawson at—mdawson@ucmerced.edu

Michael Dawson <mdawson@ucmerced.edu>

UKansas EvolutionNematodes

The Department of Molecular Biosciences, University of Kansas, seeks an assistant researcher with experience and/or interest in molecular biology and genetics of the model organism nematode worm Caenorhabditis elegans, focused on evolutionarily-conserved pathways of nervous system development (e.g. Hox genes). This position is contingent upon funding. The applicant should be motivated, organized, detail-oriented, work well with others, have a willingness to learn, and be able to participate in many different lab activities.

For more details including required and preferred qualifications and directions about how to apply, please visit https://employment.ku.edu/staff/17515BR. The estimated start date is September 7, 2020.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, retaliation, gender identity, gender expression and genetic information in the University's programs and activities. The following persons has been designated to handle inquiries regarding the non-discrimination policies and are the Title IX Coordinators for their respective campuses: Director of the Office of Institutional Opportunity and Access, IOA@ku.edu, Room 1082, Dole Human Development Center, 1000 Sunnyside Avenue, Lawrence, KS, 66045 <webextlink://1000%20Sunnyside%20Avenue,%20Lawrence,%20KS%2066045>, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses; Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

Erik A. Lundquist, Ph.D. University of Kansas he/him/his 785-864-5853 erikl@ku.edu Lab: http://www.people.ku.edu/~erikl/ Professor, Department of Molecular Biosciences 5049 Haworth Hall, 1200 Sunnyside Ave., Lawrence, KS 66045-7534 http://molecularbiosciences.ku.edu/ Associate Vice Chancellor-Office of Research 203 Youngberg Hall, 2385 Irving Hill Road, Lawrence, KS 66045 www.research.ku.edu "To facilitate innovation, creative activity, discovery, and the application and dissemination of knowledge"

erikl@ku.edu

UMelbourne SARS-CoV-2 Phylodynamics

An exciting 2-year fixed term opportunity for a postdoctoral researcher to join the Microbiological Diagnostic Unit public health laboratory, to support COVID-19 surveillance activities within the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL), the Peter Doherty Institute, in particular phylodynamic methods that bridge evolution and epidemiology to infer transmission parameters within outbreak clusters and in the broader community.

MDU PHL is one of Victoria's public health laboratories responsible for providing the highest quality microbiological services, including pathogen genomics to identify, investigate and control protect and improve the public's current and emerging public health threats posed by infectious diseases, antimicrobial resistance and biological agents of security concern.

Remote work is possible. Support for work visa in Australia is possible About you: Minimum Qualifications Required

* PhD degree or equivalent in computational biology or bioinformatics. Skills and Experience required to fulfil the position:

* Experience working with microbial genome data, particularly phylogenetics and molecular evolution. * Familiarity with mathematical methods in evolution and

epidemiology, such as birth-death and coalescent models. * Experience with Bayesian statistics. * Demonstrated experience programming in at least one scripting language (R or Python). * Excellent ability in problem solving, time allocation and maintaining accurate records. * Demonstrated ability to work as a member of a research team and interact in a courteous and effective manner with academic, administrative and support staff.

Excellent oral and written communication skills.

Summary: http://jobs.unimelb.edu.au/caw/en/job/902906/research-officer Full job description: https://secure.dc2.pageuppeople.com/apply/422/gateway/default.aspx?sData=E7tTKDEyyWPyLsAhbioSINLU6eRYsKwHuquo8Zu4OIz7mv4GiqkJnq_vP_h6gO7QFgS9yzvg09Vto_r_pSJw9UZFPKoXf1sykueuqD9UFQHKvstiKlOb7H04QcZWdyfjJ8Y05SnXMIzqtc 3pp9IcTQ ˜ Apply: https://secure.dc2.pageuppeople.com/apply/422/gateway/default.aspx?c=apply&lJobID=902906&lJobSourceTypeID=1090&sLanguage=en

Anders Goncalves da Silva <andersgs@gmail.com>

USFDA Maryland BacterialFoodBioinformatician

USFDA Maryland Foodborne Bacteria Genomics

Description of Work:

The Division of Public Health Informatics and Analytics (DPHIA) within the Center for Food Safety and Applied Nutrition (CFSAN) at the US Food and Drug Administration seeks a creative and enthusiastic research fellow to assist in the analysis of next-generation DNA sequencing data. The primary research focus of the fellow will be on the analysis of the FDA's vast *Listeria monocytogenes, Salmonella enterica, *and *Escherichia coli *genome sequence databases as a means to (1) better quantify the microbial diversity associated with foodborne pathogens and (2) generate scientific criteria for detecting and prioritizing illness outbreaks for follow-up investigations.

The fellow will also support microbiologists in the analysis of data from sequencing projects of bacterial pathogens. The projects using whole genome sequence data from bacterial pathogens include samples collected from foodborne outbreaks, and the research will include the construction of phylogenies from whole genome sequence data, source attribution studies, gene specific analyses, and identification of mobile elements.

The fellow is also encouraged to develop an independent research project that furthers the mission of the FDA and the analytics group within CFSAN. Examples of such a project include the development of novel approaches for analyzing very large genomic datasets in order to identify and monitor foodborne outbreaks, using genome sequence data to predict sources of bacterial pathogens, and the visualization and extraction of information contained in large genomic datasets.

CFSAN and the Biostatics Branch is a vibrant community of specialists from a number of different disciplines (e.g., epidemiologists, chemists, microbiologists, biostatisticians, and bioinformaticians). Applicants should email Dr. Arthur Pightling at arthur.pightling(at)fda.hhs.gov with questions about the position.

Desired Skills: - Educational background (PhD or MS) in microbiology, genetics/genomics, phylogenetics, bioinformatics, statistics and/or computer science - Familiarity with next-generation sequence data (Illumina, PacBio, Oxford NanoPore)

- Fluency with software and algorithms for large-scale clustering of genome sequence data

- Experience with evolutionary analysis of bacterial genome sequences, such as calculating genomic diversity and mutation rates. - Proficient in a computer language such as R, Python, or Perl - Skilled in the management, organization, and querying of large files/databases

Application Materials: - Cover letter describing previous and future research interests - CV/Resume - Contact information for three references - To be mailed as a single pdf to arthur.pightling(at)fda.hhs.gov

Duration: 1 year, with opportunities to renew.

Location: FDA, Center for Food Safety and Applied Nutrition 5100 Paint Branch Parkway College Park, MD 20740-3835 USA

Salary/Benefits: The position is offered by the Oak Ridge Institute for Science and Education. The position does not include funds to offset moving. The position does not include benefits. ORISE offers a benefits plan or the fellow can have her/his own but proof of health insurance is required before beginning the position. Funds are available for travel to conferences/workshops.

Stipend: $7,195/month x 12 months $89,340 per year.

Arthur Pightling <apightling@gmail.com>

USFDA Maryland FoodborneBacteriaGenomicsBioinformatician

USFDA Maryland Foodborne Bacteria Genomics

Description of Work:

The Division of Public Health Informatics and Analytics (DPHIA) within the Center for Food Safety and Applied Nutrition (CFSAN) at the US Food and Drug Administration seeks a creative and enthusiastic research fellow to assist in the analysis of next-generation DNA sequencing data. The primary research focus of the fellow will be on the analysis of the FDA's vast *Listeria monocytogenes, Salmonella enterica, *and *Escherichia coli *genome sequence databases as a means to (1) better quantify the microbial diversity associated with foodborne pathogens and (2) generate scientific criteria for detecting and prioritizing illness outbreaks for follow-up investigations.

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CFSAN and the Biostatistics Branch is a vibrant community of specialists from a number of different disciplines (e.g., epidemiologists, chemists, microbiologists, biostatisticians, and bioinformaticians). Applicants should email Dr. Arthur Pightling at arthur.pightling(at)fda.hhs.gov with questions about the position.

Desired Skills: - Educational background (PhD or MS) in microbiology, genetics/genomics, phylogenetics, bioinformatics, statistics and/or computer science - Familiarity with next-generation sequence data (Illumina, PacBio, Oxford NanoPore)

- Fluency with software and algorithms for large-scale clustering of genome sequence data

- Experience with evolutionary analysis of bacterial genome sequences, such as calculating genomic diversity and mutation rates. - Proficient in a computer language such as R, Python, or Perl - Skilled in the management, organization, and querying of large files/databases

Application Materials: - Cover letter describing previous and future research interests - CV/Resume - Contact information for three references - To be mailed as a single pdf to arthur.pightling(at)fda.hhs.gov

Duration: 1 year, with opportunities to renew.

Location: FDA, Center for Food Safety and Applied Nutrition 5001 Campus Drive College Park, MD 20740-3835 USA

Salary/Benefits: The position is offered by the Oak Ridge Institute for Science and Education. The position does not include funds to offset moving. The position does not include benefits. ORISE offers a benefits plan or the fellow can have her/his own but proof of health insurance is required before beginning the position. Funds are available for travel to conferences/workshops.

Stipend: $7,195/month x 12 months $89,340 per year.

Arthur Pightling <apightling@gmail.com>

UVienna SystematicEvolutionaryBotany

The position of an University Professor of Systematic and Evolutionary Botany

(full time, permanent) is to be filled at the Faculty of Life Sciences of the University of Vienna

Applicants have a strong record in studying processes and mechanisms of plant evolution and systematics with emphasis on genetic, genomic, biogeographic or ecological aspects of diversification at the species level (speciation) and beyond (macroevolution). We expect the successful applicant to develop a competitive research program complementing existing research fields and graduate programs in the Faculty of Life Sciences and to demonstrate strong interest in interdisciplinary research within the Faculty of Life Sciences and beyond. These endeavours are facilitated by excellent research conditions including well-equipped laboratories, an herbarium

(1.4 million sheets), a Botanical Garden (Core Facility of the Faculty; 8ha, with more than 11,000 species), and access to a tropical research station (La Gamba, Costa Rica). The candidate is expected to teach systematic and evolutionary botany at all academic levels.

Further information can be found here: https://personalwesen.univie.ac.at/-jobs-recruiting/professuren/detail-seite/-news/systematic-and-evolutionary-botany/-?no_cache=1&tx_news_pi1%5Bcontroller%5D=-News&tx_news_pi1%5Baction%5D=detail&cHash=-bcfd9c3fdf8822864d2699949b6be486 Applications in English should be submitted as one pdf-file by e-mail to the Dean of the Faculty of Life Sciences of the University of Vienna, Gerhard Ecker, Althanstraße 14, 1090 Vienna (dekanat.lewi@univie.ac.at).

Reference no.: 20/7-2020 The application deadline is 23 September 2020.

Ursula Gerber <ursula.gerber@univie.ac.at>

Other

EvolutionaryEntomology OpportunitiesForStudents

*Entomologists of Color (EOC), *a new initiative, provides paid memberships to various entomological societies, making participation, scientific communication and outreach more inclusive to POC. Thanks to an outpouring of support and contributions, we are pleased to announce the availability of funds for BIPOC of all ages, careers, and backgrounds interested in joining entomological professional societies!

*Why apply for society memberships? *By applying for a *free* *membership,* you gain valuable access to STEM resources, and community activities that help members become lifelong entomology-ophiles. Membership to scientific societies allows participation in networking events, provides access to scientific publications and other member-restricted scientific content, and reduced meeting costs. Whatever your career goal maybe, whether non-profit, teaching, academia, industry, or other career choice, being a member of a society can help you achieve your goals!

*Apply: * Fill out a quick form at www.entopoc.org if you are interested in applying for a free membership (click here to apply < https://www.entopoc.org/-apply.html >)*. *You will be notified by email about your membership once your application is processed. *Before applying we strongly recommend visiting the webpage of the organizations of your interest or visit our website to look up entomological organizations. This list is preliminary, so be sure to keep in mind that many others exist; Feel free to contact us at * *entoPOC@gmail.com** or find us below so we can provide further guidance on selecting a membership that best fits your interests, or any other questions you may have about the path to entomology!*

*Donate: *EOC relies on donations to sustain our mission. If you can please help us by donating here < https://www.entopoc.org/donate.html >.

*Please share widely!**Website: **https://www.entopoc.org *Twitter: **https://twitter.com/EntoPOC* *Facebook: **https://www.facebook.com/entopoc/ *Instagram: *https://www.instagram.com/entomologists_of_color/ *Manpreet Kohli* Postdoctoral Associate Invertebrate Zoology American Museum of Natural History Central Park West at 79th street New York, New York 10024-5192 Ph # : 1- 212-769-5714

Manpreet kohli <manpreetjkohli@gmail.com>

New RoyalSociety Issues

Royal Society Publishing has recently published two special issues from Philosophical Transactions B -Towards the completion of speciation: the evolution of reproductive isolation beyond the first barriers compiled and edited by Jonna Kulmuni, Roger K Butlin, Kay Lucek, Vincent Savolainen and Anja Marie Westram and the articles can be accessed directly at www.bit.ly/PTB1806< http://www.bit.ly/PTB1806 > and Ritual renaissance: new insights into the most human of behaviours compiled and edited by Cristine H Legare and Mark G Nielsen and the articles can be accessed directly at www.bit.ly/PTB1805< http://www.bit.ly/PTB1805 > Both issues are currently FREELY available online!

Felicity Davie Royal Society Publishing

T +44 20 7451 2647 The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG http://royalsocietypublishing.org Registered Charity No 207043

felicity.davie@royalsociety.org

Online EvolCompGen Seminars

Dear colleagues,

ISCB and SMBE are collaborating to organize an online journal club (as part of the ISCBacademy series of webinars) on Evolution and Comparative Genomics.

The next seminar will take place next week, Tuesday July 7, at 11:00AM EDT: Genetic Basis Of De Novo Appearance Of Carotenoid Ornamentation In Bare-Parts Of Canaries presented by Malgorzata Gazda (Universidade do Porto).

Participation is free for any member of ISCB or SMBE, but registration is required. Please follow the link below. https://www.iscb.org/iscbacademy-upcoming#gazda A link to the article: https://doi.org/10.1093/molbev/msaa006 Genetic Basis of De Novo Appearance of Carotenoid Ornamentation in Bare Parts of Canaries < https://doi.org/10.1093/molbev/msaa006 > Abstract. Unlike wild and domestic canaries (Serinus canaria), or any of the three dozen species of finches in genus Serinus, the domestic urucum breed of cana doi.org

The format of webinars is that abstract/papers are presented by their first author to promote presentations by young researchers, and questions and answers are exchanged throughout the presentation to value discussion and attendee input.

If you are interested in presenting, or you want to suggest an article of interest, please send an abstract to webinar@evolcompgen.org with “Abstract for Webinar” as the title of your message.

All the best,

Aida Ouangraoua, on behalf of the organizing committee.

Aida.Ouangraoua@USherbrooke.ca

Online EvolutionEcology Conferences

I’ve started a mailing list for keeping academics up to date with virtual/online conferences.

This weeks edition features an online conference in Systematics and Biogeography https://ecologyseminars.substack.com/p/online-ecology-conferences-e8d Jonathan Clegg

Jonathan Clegg <clegg.jonathan@rocketmail.com>

Software Myriads

Dear evoldir members,

A new version of Myriads (1.2) is available on the website http://myriads.webs.uvigo.es/. This version incorporates new FWER and FDR controlling methods as Hommel and Benjamini & Yekutieli (BY) and the two-stage linear step-up procedure from Benjamini, Krieger & Yekutieli (BKY). The permutation based maxT method has also been implemented for two-sample t-test with equal or unequal variances. Detailed information is available in the program manual.

The Myriads software was developed under the C ++11 language and is available as a binary C++ executable for Windows and Linux-like platforms.

For questions about this software please contact me at myriads@uvigo.es

The method is described in the following paper:

Carvajal-Rodriguez A (2018). Myriads: p-value-based multiple testing correction. Bioinformatics 34 (6): 1043-104

Best wishes,

Antonio

myriads <myriads@uvigo.es>

SSE GlobalMembershipAssistance Program

SSE Global Membership Assistance Program

The Society for the Study of Evolution is working to improve our efforts to support and include the global evolutionary biology community. Our new Global Membership Assistance Program greatly expands the number of countries eligible for free or half-priced SSE membership. This program now offers free or discounted membership to students, researchers, and educators in 140 countries and territories around the world.

Learn more about the program and how to join on our website: http://www.evolutionsociety.org/index.php?module=content&type=user&func=view&pid=8#gma *Kati Moore*she/her/hers *Communications Manager* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org SSE Communications <communications@evolutionsociety.org>

TeachingFellowships Biology International

Dear Colleagues,

We are looking for evolutionary biologists, ecologists, and general biologists who are recent or soon-to-be PhD graduates for a 6 month teaching fellowship.

Science Corps < http://science-corps.org/ > offers fully paid internships to upcoming and recent PhD graduates (up to four years after graduation) to help teach and build science capacity at one of our two host locations a small city on the island of Bohol in the Philippines and a village up in the Indian Himalayas. We are also currently developing new sites in partnership with Pueblo Science < https://puebloscience.org/ >.

Fellows travel to partner institutions to develop science curriculum, teach in secondary school classrooms, train teachers, and build community-based research projects. We are presently interested in recruiting Biologists immediately for both of our sites for fellowships starting within the next year. The deadline for this application round is July 31st, but we still encourage you to contact us if you would like to be considered for a later appointment.

To find out more about us and apply, please go to https://science-corps.org Stephen E. Harris, Ph.D. Assistant Professor of Biology, Purchase College SUNY < https://www.purchase.edu/live/profiles/1759-stephen-harris > Cofounder, Science-Corps < http://www.science-corps.org/ > (614) 915-4686 stephen.harris@purchase.edu

harris917@gmail.com

VoucheringPractics survey

Dear colleagues

I am writing in my capacity as a member of the COVID-19 Task Force, a joint initiative supported by the Consortium of European Taxonomic Facilities (CETAF) and the Distributed System of Scientific Collections (DiSSCo).

In particular, I am involved in the subgroup associated with museum collections, which is tasked with reviewing and recommending guidelines for the preservation of viral evidence. We are especially interested in better connecting the microbiological and museum communities, both personally and through infrastructural changes to the archiving of host specimens (vouchers) in museum collections.

As such, we are seeking the input of ourcolleagues inmicrobiology/virology/pathobiology/parasitology/(veterinary medicine/public healthto assess the strength of current connections to museums and to guide our recommendations moving forward. The survey can be found here:https://bucknell.co1.qualtrics.com/jfe/form/SV_cuc17LGMzwPVC4J We are looking forward to hearing your views on this, and warmly thank you in advance for taking the time to fill out this short survey!

Kindest regards

prof. Maarten Vanhove, PhD Research Group Zoology: Biodiversity & Toxicology Hasselt University(Belgium)

Maarten VANHOVE <maarten.vanhove@uhasselt.be>
Maarten VANHOVE <maarten.vanhove@uhasselt.be>

Webinar BiodiversityRes PeteLowry

Free Webinar: The LEC Presents - Adventures in Biodiversity Research - Dr. Pete Lowry. 1 PM EDT (12 PM CDT) on Tuesday, 4 August 2020.

On Tuesday, 8/4/2020, join the Living Earth Collaborative at 1 PM EDT (12 PM CDT) for a free webinar by Dr. Pete Lowry (https://youtu.be/pD9dy3nDLnQ). Dr. Lowry is a senior curator and Director of the Africa & Madagascar program with the Missouri Botanical Garden, as well as a research associate at the Muséum National d'Histoire in Paris. During this seminar, Dr. Lowry will be discussing his experiences in the field studying the systematics and natural history of the flora of Madagascar and New Caledonia. You'll leave this presentation with new insight into the ways that botanists are able to study and describe the amazing diversity of tropical plants.

The Living Earth Collaborative Presents: Adventures in Biodiversity Research - Dr Pete Lowry. "Tropical botanists still discover new species in the 21st century, and in more ways than you think! Tales from Madagascar, New Caledonia, and Elsewhere." Tuesday, 8/4/2020, at 1PM EDT (12PM CDT). https://youtu.be/pD9dy3nDLnQ The Living Earth Collaborative (LEC) is a biodiversity research and conservation center in St. Louis, Missouri USA (https://livingearthcollaborative.wustl.edu/). By partnering the Missouri Botanical Garden, St. Louis Zoo, and Washington University, the LEC brings researchers and conservationists from around the world together to promote an interdisciplinary understanding of our planet's biodiversity. This summer, the LEC has hosted a seminar series where its Biodiversity Fellows have discussed their travels and experiences carrying out biodiversity research and conservation. To catch up on any of the seminars you may have missed, or to stay up to date on all of the LEC's free content, visit our YouTube channel (https://www.youtube.com/channel/UCfLG3SSfA2BlKqb5mnm8-8Q) and subscribe!

Michael Moore <moore.evo.eco@gmail.com> Michael Moore <moore.evo.eco@gmail.com>

PostDocs

AuburnU EnvironmentalEpigenetics

The Strader Lab < https://mariestrader.weebly.com/ > studies how environmental changes affect marine invertebrates from the level of the epigenomic landscape to an evolutionary ecology viewpoint. The Buckley Lab < https://buckleyscience.com/ > studies immune system evolution from the perspective of echinoderms to uncover fundamental aspects of animal immune response and investigate the origins of vertebrate adaptive immunity. Together, these two labs within the Department of Biological Sciences at Auburn University have recently embarked on an NSF-funded, interdisciplinary project to identify linkages between environmentally-induced epigenetic changes and immune response phenotypes. This research employs the larval stage of the purple sea urchin (*Strongylocentrotus purpuratus*), an experimentally tractable model system with extensive genomic resources that plays a key role in marine ecology.

We are currently recruiting a *Postdoctoral Researcher* to work primarily in the Strader lab in close collaboration with the Buckley Lab. The proposed research integrates aspects of global change biology, whole genome multi-omics analyses (*e.g., *DNA methylation, transcriptomics, Chip-Seq), ecological immunology, experimental marine biology and functional genetics. We expect candidates to have strengths in any one of those subfields and interests in developing skills in any of the others. The postdoc will lead the following (a) analysis of multi-omics epigenetic and microbial data, (b) experimental design and execution of multi-stressor experiments on early stage urchins (c) data interpretation and manuscript writing (d) mentor undergraduate students and contribute to developing outreach activities associated with this project. The PIs will also act as a mentor to the postdoc to aid in their career goals.

Ideal candidates will have:

- A Ph.D. in biology, bioinformatics, or related field and publication record appropriate for career level

- Experience with analyzing and interpreting high throughput sequencing data in non-model systems with a preference for knowledge of marine invertebrate genomics

- Experience profiling microbial community compositions using sequencing data

- Strong skills in bioinformatics and data management

- Strong background in biostatistics, particularly genomic and ecological data

- Excellent written and oral communication skills

- Interest in understanding epigenetics mechanisms regulating gene expression in non-model invertebrates

- Experience mentoring and managing diverse groups of students of various levels

- Dedication to outreach and science communication, especially in promoting BIPOC in STEM.

This position is fully-funded for two years through the National Science Foundation. Applications by members of all underrepresented groups are strongly encouraged. In fact, we would like candidates to address their approach to mentoring and promoting diversity in STEM in their cover letter. To apply or for additional enquiries, please email a cover letter and CV to Drs. Strader and Buckley (mes0192@auburn.edu; kmb0163@auburn.edu). The anticipated start date for this position is January 15, 2021, although this is flexible. Please send materials by October 1, 2020.

Successful applicants will join the Department of Biological Sciences at Auburn University < http://www.auburn.edu/cosam/departments/biology/index.htm >, a welcoming, inclusive environment of 39 research faculty (45% female), and over 100 graduate students. Auburn University is an R1 University and one of the nation'Âs premier land, sea and space grant institutions. Auburn residents enjoy a thriving community that is recognized as one of the "best small towns in America," with moderate climate and easy access to major cities or to beach and mountain recreational facilities.

– Marie Strader, PhD Research Assistant Professor Department of Biological Sciences Auburn University http://mariestrader.weebly.com/ Marie Strader <stradermarie@gmail.com>

CentralStateU Ohio BeeEvolutionaryGenomics

This position is a two-year postdoctoral appointment at the Central State University, near Dayton, OH (the only public Historically Black College University (HBCU) and 1890 land grant institution of Ohio). The candidate will possess advanced genomic and bioinformatic skills for honeybee evolutionary genomics and breeding program. This is a new CSU program that builds upon PI's experience to increase the genetic diversity of honey bees. The candidate should be knowledgeable in the rapidly growing and evolving area in evolutionary/functional genomics, molecular markers, and related field. Potential interests of other research related to bee genomics and genetics are also encouraged.

Essential Duties & Responsibilities: - Perform research for evolutionary genomics and transcriptomic analysis of bee mandibles - Perform research for molecular genetic breeding and selection - Design experiments, perform experiments, data collection, data analysis, bioinformatics analysis, report, write, and publish scientific papers - Facilitate the operation of the lab and assist the faculty/students

Minimum Qualifications - Doctoral degree in entomology, molecular biology, animal science/breeding, ecology/evolution, or other relevant biological sciences

Preferred Qualifications - Knowledge and skills in genomics, genetics, molecular biology, development of insects for at least 2 years - Knowledge and skills in bioinformatics, data science, programming, or computational biology for at least 2 years - Knowledge and skills in honeybee biology for at least 2 years

Any questions and concerns can be sent to Dr. Hongmei Li-Byarlay (hli-byarlay at centralstate dot edu).

Details of the position can be found at https://careers.centralstate.edu/postings/5292 Regards, Hongmei

– Hongmei Li-Byarlay, Ph.D. Assistant Professor Agricultural Research Development Program, Department of Agriculture and Life Science Central State University 362 CENS Building |1400 Brush Row Road | Wilberforce, Ohio 45384 O: 937-376-6424 | Fax: +1-(937)-376-6299

1890 LAND GRANT INSTITUTION

Hongmei Li-Byarlay <hli-byarlay@centralstate.edu>

CNRS Paris EvolutionaryEpidemiology

Postdoc position in infectious diseases evolutionary epidemiology, CNRS Paris (starting Fall 2020, 1 year)

A postdoc position, funded by the Centre National de la Recherche Scientifique ("Momentum" grant), is available to work with François Blanquart in Paris.

The postdoc will join two research groups: one in Quartier Latin in the center of Paris (Centre Interdisciplinaire de Recherche en Biologie, UMR CNRS 7241, Collège de France) specialised in mathematical models to study evolution, the other on the Bichat Medical School campus in the North of Paris (Infection, Antimicrobials, Modelling, Evolution, UMR INSERM 1137) specialised in infectious diseases ecology & evolution. These groups offer opportunities for collaborations with mathematical modellers, bioinformaticians, medical doctors, and biologists.

I am looking for a highly motivated postdoctoral researcher, interested in understanding the evolution of pathogens. One possible project is on the evolution of the commensal bacterial species Escherichia coli in the human population over the last 40 years, and particularly the evolution of antibiotic resistance and virulence. The postdoc will develop mathematical and computational models of evolution and/or analyse epidemiological and genomic data depending on his/her interests. Strong quantitative skills are required for the position, as well as some background or interest in either evolutionary biology, infectious disease epidemiology, or bioinformatics.

The position starts in Fall 2020 (flexible September-December) and is for one year. Salary depends on experience (see table below).

To apply:

If you are interested in this position, please send a CV, a 1-page description of your research interests and motivation, and the contact details of potential references (all in one single pdf) to François Blanquart (francois.blanquart@college-de-france.fr) no later than August 28th 2020.

Feel free to contact me if you have any questions about the position.

François Blanquart

Salary

experience———————————————————————————————— | Net monthly salary

< 2y after PhD———————————————————————————————— |— 2,166.42 euros

between 2 and 7y after PhD ———— ———— ———————— | 3,100.10 euros

â¥7y after PhD | 3,247.97 euros

Further information:

group in Quartier Latin: https://www.lpsm.paris/smile/index.php group in Hôpital Bichat: https://www.iame-research.center/eq1/research-interests/ personal webpage: https://sites.google.com/site/francoisblanquart/ François Blanquart <francois.blanquart@college-de-france.fr> François Blanquart <francois.blanquart@college-de-france.fr>

CornellU MicrobiotaTransmission

Cornell.MicrobiotaTransmission “The Moeller Lab in the Department of Ecology and Evolutionary Biology at Cornell University is seeking applicants for a full-time postdoctoral position.

The successful applicant will have opportunities to pursue a number of projects related to an NIH MIRA to study the modes and genetic bases of microbial transmission in mammals. The successful applicant will also be encouraged to develop their own research directions related to the assembly of microbial communities and evolution of microbial lineages in mammals. More information about our group can be found at https://www.moellerlab.com [1]

A Ph.D. in Evolutionary Biology, Microbiology, Genomics, or a related field is required. Experience with metagenomics, bacterial genome editing, and/or gnotobiotic mouse experiments is preferred. The start date is flexible. Review of applications will begin immediately until the position is filled.

Interested applicants are encouraged to contact Andy Moeller directly at andrew.moeller@cornell.edu. Please include a CV and brief research statement in your introductory email. For more information and to apply please visit https://academicjobsonline.org/ajo/jobs/16527 The Department of Ecology and Evolutionary Biology and the College of Agriculture and Life Sciences at Cornell embrace diversity and seek candidates who will create a climate that attracts persons of all races, ethnicities, and genders. Diversity and Inclusion are central to Cornell University’s heritage and identity. We are a recognized employer and educator valuing AA/EEO, Protected Veterans and Individuals with Disabilities.” –

Andrew H. Moeller Assistant Professor Department of Ecology and Evolutionary Biology E345 Corson Hall Cornell University Ithaca, NY 14853 email: andrew.moeller@cornell.edu website: www.andrewhmoeller.com [2]

Links: —— [1] https://www.moellerlab.com/ [2] http://www.andrewhmoeller.com/ Andrew Moeller <andrew.h.moeller@gmail.com>

CSIRO Australia 4 MuseumCollections

We have four Postdoctoral Fellowship opportunities with National Research Collections Australia at CSIRO:

Computer Vision for Feature Extraction in Biological Specimens http://www.researchcareer.com.au/jobs/5810-csiro/69498 Environmental DNA Metabarcoding of Australian Marine Fishes http://www.researchcareer.com.au/jobs/5810-csiro/69503 Collections Chemical Biodiscovery http://www.researchcareer.com.au/jobs/5810-csiro/69400Linking Indigenous Botanical Knowledge with Western Science http://www.researchcareer.com.au/jobs/5810-csiro/69372 Andrew Young Director, National Research Collections Australia Science Director, National Collections and Marine Infrastructure CSIRO Digital National Facilities and Collections GPO Box 1700, Canberra ACT 2601, Australia P: +61-2-6246-5318 or 61-2-6246-5084 (Ms Cath Reed, EA) F: +61-2-6246-5166 E: Andrew.Young@csiro.au W: https://www.csiro.au/en/Research/Collections Google Scholar: https://scholar.google.com.au/citations?user=8GpWa-YAAAAJ&hl=en Ausmicobiome: https://www.australianmicrobiome.com/ Ten things to know about CSIRO???s biological collections: https://www.csiro.au/en/Research/Collections/TenThingsAboutCollections The RV Investigator: https://www.csiro.au/en/Research/Facilities/Marine-National-Facility/RV-Investigator “Young, Andrew (NCMI, Black Mountain)” <Andrew.Young@csiro.au>

CSIRO NationalCollections GenomicBiodiscovery

Use your skills to develop a high-throughput biodiscovery screening protocol Identify biologically interesting molecules from collection specimens Join CSIRO and kick-start your research career!

CSIRO Early Research Career (CERC) Postdoctoral Fellowships provide opportunities to scientists and engineers who have completed their doctorate and have less than three years of relevant postdoctoral work experience. These fellowships aim to develop the next generation of future leaders of the innovation system. In this position, you will work with a multidisciplinary team from CSIRO and the University of Queensland to develop and apply novel molecular biology and analytical methods for the discovery of valuable molecules using natural history collection specimens. You will develop a high-throughput biodiscovery screening protocol that will involve the use and refinement of genomics, analytical chemistry and bioassay experiments.

Your duties will include:

Carrying out innovative, impactful research of strategic importance to CSIRO that will, where possible, lead to novel and important scientific outcomes. Developing a novel high-throughput pipeline for the discovery of valuable molecules using collections specimens. Adapting protocols for the extraction of invertebrate and plant material for genomics, transcriptomics and metabolomics. Developing or adapting current pipelines for the characterisation of interesting molecules from various omics data. Testing the properties of invertebrate and plant chemical extracts in various bioassays.

Location: Black Mountain, Canberra, ACT Salary: AU$86k 'V AU$94k plus up to 15.4% superannuation Tenure: Specified term of 3 years Reference: 67861

To be considered you will need: A doctorate (or will shortly satisfy the requirements of a PhD) in a relevant discipline area such as molecular biology, chemistry, genetics, or evolution. Please note: To be eligible for this role you must have no more than 3 years (or part-time equivalent) of postdoctoral research experience.

Demonstrated experience with molecular biology laboratory work, including: DNA and/or RNA extraction and Construction of libraries for high-throughput sequencing. Demonstrated experience in bioinformatics for chemical, transcriptomic and/or genomic data analysis. The ability to plan work, manage resources, meet deadlines and deliver project milestones. High-level communication skills including the ability to present research outcomes at national and international conferences. A sound publication record in peer reviewed journals and/or authorship of scientific papers or reports. For full details about this role and to apply go to https://jobs.csiro.au/job/Canberra%2C-ACT-CSIRO-Postdoctoral-Fellowship-in-Collections-Chemical-Biodiscovery/657076200/?locale=en_GB Eligibility The successful applicant will be required to obtain and provide a National Police Check or equivalent. Applicants must be Australian/New Zealand citizens, Australian permanent residents or Australian temporary residents currently residing in Australia and be able to commence in the role by December 2020/January 2021.

Flexible Working Arrangements We work flexibly at CSIRO, offering a range of options for how, when and where you work. Talk to us about how this role could be flexible for you.

Diversity and Inclusion We are working hard to recruit diverse people and ensure that all our people feel supported to do their best work and feel empowered to let their ideas flourish. We are committed to the safety and wellbeing of all children and young people.

About CSIRO At CSIRO, Australia' Âs national science agency, we solve the greatest challenges through innovative science and technology. Join us and start creating tomorrow today!

How to Apply Please apply on-line and provide a cover letter and CV that best demonstrate your motivation and ability to meet the requirements of this role.

Applications Close 30 July 2020, 11:00 pm AEST

"Rodriguez Arrieta, Juanita (NCMI, Black Mountain)" <Juanita.Rodriguez@csiro.au>

CzechAcadSci PhylogenomicsPopulationGenomics

18 month postdoc position: Phylogenomics & population genomics (6 month extension possible)

Laboratory of Molecular Ecology and Evolution (Biology Centre, Czech Academy of Sciences and University of South Bohemia, Czechia) has funding for a Junior Researcher (postdoc) in the fields of phylogenomics & population genomics.

We are reopening a call for a postdoc position (a previously selected candidate could not join the lab due to covid situation in their home country).

We are looking for an independent junior researcher with interest in evolutionary biology and strong background in bioinformatics and analyses of phylogenetic and population genetic data. Knowledge of Linux/unix and experience with scripting & programming languages (Python, R) and phylogenetic inference using WG data is necessary. Experience with population genomic and genome assembly and annotation pipelines is beneficial. A good publication record is important. The applicant should be able to coordinate a team of 2-3 students and have well-developed communication skills.

Job description:

This research position will include (mainly drylab) work on two grant funded projects:

1)Phylogenomics (and species diversity survey) of Dicyemida, an enigmatic group of parasites from cephalopods (60% job time allocation).

2)Population genomics of adaptation in parasites. The project studies interaction between host specificity, genomic differentiation, and adaptation in a freshwater parasite (Ligula intestinalis)(40% job time allocation).

On the 1st project, the postdoc will be responsible for designing the research strategy (amplicon sequencing design for species diversity survey, selection of tools for extracting data from wg datasets) and for analyses of obtained data (transcriptome assemblies, amplicon assemblies, mining and filtering genes into matrices, phylogenetic reconstruction). On the 2nd project, the postdoc will provide assistance with analyses of population level NGS data (whole genome re-sequencing data, RADseq, SNP calling, demographic inference, analysis of selection, etc.).

The postdoc will co-supervise one phd student and will be free to supervise undergrad students if desired (a valuable experience). There is an opportunity to take part in teaching, in field collecting trips, and in other popgen projects running in the laboratory (incl. publication output).

We offer:

We are a relatively young but quickly developing laboratory with interests in evolutionary and ecological interactions between organisms and their environment. We use genetic (increasingly more genomic) data to answer the questions (e.g. https://youtu.be/xvHSjEi0c44?t=7051).

We have advanced computing resources available both in-house (> 300 nodes) and via a connection to the national grid (> 20,000 CPUs). The lab collaborates with institutions/labs abroad (e.g. University of Alabama [Kocot lab], University of Illinois [Catchen lab], University of Saskatchewan & Cornell [J.A.Andres]) and we co-organise the biennial Workshop on Population and Speciation Genomics (http://evomics.org/2020-workshop-on-genomics-cesky-krumlov-czech-republic/).

Biology Centre is a dynamic institution with a strong international community of junior researchers and an "HR Excellence in Research" awarded institution. It is located in the centre of a university campus. English is the working language at the institution. The city of Ceske Budejovice is a charming historical city, has great outdoors nearby, and it is located within easy reach of the capital, Prague, and several cities abroad (Vienna, Linz, Passau).

Funding is guaranteed for 1 year, with extension for another year, based on performance. The salary is approx. 30% above the Czech average income, it is sufficient to cover all necessary living costs with a margin (Czechia is a developed, yet relatively cheap country to live in). Biology Centre offers multiple employee benefits (fully covered health insurance, subsidised lunches, cultural/health programmes, etc.).

In case of questions, enquire using the contact info below.

Applications:

Applications should be prepared as a single pdf containing:

a CV (with publication list)

a detailed statement of research interests

names and contact information for 3 references.

Applications are welcome before August 31, 2020, sent by email to Associate Prof. Jan Âtefka at jan.stefka@gmail.com. Prospective candidates will be interviewed in September.

The position can be filled starting January 1, 2021, but even an earlier or a slightly postponed start is possible.

Jan Âtefka, PhD

Laboratory of Molecular Ecology and Evolution

Institute of Parasitology, Biology Centre, Czech Academy of Sciences

Branisovska 31, Ceske Budejovice, CZECHIA

https://www.paru.cas.cz/en/

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DalhousieU PhylogeneticModeling

Two 3-year funded postdoctoral research positions in statistical phylogenetic modeling are available in the laboratories of Andrew J. Roger and Edward Susko at Dalhousie University. The research project will be to develop, test 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 candidates participate in an international collaborative project (with Dr. Laura Eme in Orsay, France and Dr. Minh Bui in Canberra, Australia) related to the origin of eukaryotic cell by developing novel phylogenetic models and applying them to phylogenomic analyses to resolve key phylogenetic problems. The goals are 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 maximum likelihood framework and their statistical properties will be investigated. Other related topics are also open for investigation.

The ideal candidates should have a Ph.D. in statistics, computational biology or related disciplines. Knowledge and expertise in statistical modeling, theory/implementation of phylogenetic models in a likelihood framework and comparative genomic methods are an asset. Programming experience using scripting languages (e.g. Python), the R statistical package and, ideally, C or C++ would be invaluable.

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 - a cover letter that describes why you are interested in this position and highlights your expertis - a curriculum vitae (CV), and - the names and contact details of 2 or more individuals who have agreed to write reference letters

The applications should be sent by August 10th by email to: Andrew Roger: andrew.roger@dal.ca

Review of complete applications will occur continuously until the search is closed. Please note, 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 qualified individuals from all equity-seeking groups including people who identify as indigenous, African Nova Scotian, 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 J. Roger Ph.D. F.R.S.C. Canada Research Chair Centre for Comparative Genomics and Evolutionary Bioinformatics Dept. of Biochemistry and Molecular Biology Dalhousie University tel: (902) 494 2620 lab website: rogerlab.ca CGEB: cgeb.dal.ca Twitter: @andrewjroger https://scholar.google.ca/citations?user=Dm-pAawAAAAJ&hl=en Andrew Roger <Andrew.Roger@Dal.Ca>

DukeU BacterialEndosymbiontGenomics

Postdoc - Evolutionary Genomics of Bacterial Endosymbionts Duke University, Durham NC

https://academicjobsonline.org/ajo/jobs/16413 The Wernegreen lab seeks a highly motivated postdoctoral researcher to explore the evolutionary genomics of bacterial endosymbionts. This position is part of a collaborative NSF-funded project that, more broadly, explores the phylogenetic history and biogeography of a highly successful ant tribe (Camponotini) and their bacterial associates. The postdoc will focus on whole-genome sequencing for associated endosymbiotic bacteria, particularly the primary nutritional endosymbiont (Blochmannia) that has coevolved with Camponotine ants. Requires research experience in computational biology, development of bioinformatics pipelines, evolutionary/comparative genomics of bacteria, and knowledge of high-throughput sequencing approaches.

Start date: as soon as Jan/Feb 2021. While Covid is an evolving situation, we sincerely hope this position will be in-person (in Durham, NC). To apply, please submit your materials via the website above, including the names and email addresses of 3 references. For additional information, please contact Jen Wernegreen (j.wernegreen@duke.edu).

Jennifer Wernegreen <j.wernegreen@duke.edu>

DukeU ComparativeBiomechanics

Interdisciplinary Postdoctoral Researcher in Comparative Biomechanics

The Patek Lab at Duke University leads a five-university interdisciplinary research team devoted to establishing the principles of extremely fast movement in small systems. Grounded in the extraordinary abilities of animals, plants, and fungi that generate the fastest movements on the planet and exceed current engineering capabilities, this team utilizes multiple approaches to extract fundamental and translatable interdisciplinary principles.

OVERVIEW You will perform comparative biomechanics research on extremely fast, small biological systems with exceptional access to interdisciplinary researchers who work collaboratively to couple these biomechanics analyses with mathematical modeling, materials testing, and engineering analysis and synthesis. You will help lead the team's interchanges and interdisciplinary communication to successfully push the envelope of biological knowledge and translatable physics-based principles.

BENEFITS - Join an exciting, dynamic, and highly functioning interdisciplinary team that has been running for five years. Immediately leverage biological experiments into cutting edge interdisciplinary collaborations and publications. - Access cutting-edge high-speed imaging cameras (Photron Fastcam SA-X and SA-Z models), dynamic materials testing (Electropuls Instron), high resolution light microscopy, confocal microscopy, SEM, ESEM, CLSM, and microCT facilities, multi-material maker facilities, acoustic test chamber, and tropical and temperate saltwater aquarium facilities. - Travel to collaborator labs for an even broader range of high tech capabilities and expertise. - Become part of a diverse and inclusive team, home lab, and university with outstanding job benefits (https://postdoc.duke.edu/resources/-duke-benefits-and-services) in a culturally diverse and affordable geographic region.

REQUIREMENTS Education: Ph.D. in Biology, Physics, Materials Science, or Engineering is required.

Skills: A journal publication record is required to demonstrate existing skills in completing and publishing research projects. You must be comfortable working with live organisms and have previous experience in mechanical analysis including either materials testing or digital image analysis. Experience in evolutionary analysis, including evolutionary biomechanics, is considered a strong asset.

Characteristics: A strong interest in the physical principles of biological movement is essential. Patek Lab postdocs establish and lead their projects - vision and drive for research project leadership is key. A passion for working across disciplines, creativeness, self-sufficiency and motivation in your work and what you can bring to the fast-paced, interdisciplinary team are all important.

RESPONSIBILITIES - Lead a postdoctoral research project on small, fast biological systems. - Integrate biological experimental research with team interdisciplinary themes and efforts. - Communicate research through team meetings, conference presentations, and journal publications. - Participate centrally in team leadership for communicating and guiding interdisciplinary research. - Supervise projects involving undergraduates and graduate students. - Contribute to lab animal care, acquisition, and general lab operations.

APPLY NOW Applications are currently being accepted and will be evaluated on a rolling basis with the goal of hiring as soon as possible. The position is available immediately, although the start date is negotiable. The position is based on current funding for a two year position. The initial appointment will be for 12 months with the possibility for renewal contingent on performance and continuing funding availability for up to 2 years. Salary starts at $52,704. Contact Prof. Patek via email for additional information.

The job application must be submitted to Academic Jobs Online # 16464 using https://academicjobsonline.org/-ajo?joblist—3-16464 (do not email applications to Prof. Patek) and should include: 1. Cover letter including information about specific research interests in this position, how previous research provides a strong foundation for this position, how this research connects to career goals, and aspects of the Patek Lab's research program that are of particular interest. 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, located in Durham, North Carolina, is an Affirmative Action/Equal Opportunity Employer committed to providing employment opportunities without regard to an individual's age, color, disability,

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DukeU EvolutionaryBiomechanics

Postdoctoral Researcher in Evolutionary Biomechanics

The Patek Lab at Duke University seeks the unifying principles that guide, limit and promote the evolutionary diversity of biomechanical systems. Our research yields discoveries of new biological phenomena, original tests of macroevolutionary hypotheses, and new frameworks for understanding the mechanical foundations of biological diversity. We conduct innovative outreach that enhances equity, access, and transparency for diverse participants in research.

OVERVIEW

Movement in biology is most often associated with motor-like mechanisms, such as muscle contractions in animals or hydraulics in plants. However, organisms have another option for generating movement: they can use motor-like mechanisms to load energy into elastic structures, such that pre-loaded elastic structures generate the movement, rather than motors. Latch-mediated spring actuation generates movement largely or exclusively using stored elastic energy and incorporates latches to mediate energy release. You will join a research team to examine how organisms navigate a mass-based transition between movement driven by stored elastic energy versus by direct motor action. Our broader goal is to establish the principles by which biological systems navigate physics-based limits and transitions through developmental and evolutionary processes. You will engage the broader public through a Research Experience for Teachers program and the development and implementation of the open source Muser program which provides a structured process for equitable and transparent access to undergraduate research experience.

BENEFITS

- Join an exciting team of integrative and comparative biologists with interests and expertise including biomechanics, behavior, evolutionary analyses, mathematical modeling, and materials testing.

- Travel to collaborator labs for field work experience and training in physics-based mathematical modeling.

- Build outreach and broader impact skills through working with high school teachers and implementing structural changes in academic research to enhance inclusiveness through Muser.

- Access cutting-edge high-speed imaging cameras (Photron Fastcam SA-X and SA-Z models), dynamic materials testing (Electropuls Instron), high resolution light microscopy, confocal microscopy, SEM, ESEM, CLSM, and microCT facilities, multi-material maker facilities, acoustic test chamber, and tropical and temperate saltwater aquarium facilities.

- Become part of a diverse and inclusive lab and university, with outstanding job benefits in a culturally diverse and affordable geographic region.

REQUIREMENTS

Education: Ph.D. in Biology, Physics, Materials Science, or Engineering is required.

Skills: A journal publication record is required to demonstrate existing skills in completing and publishing research projects. You must be comfortable working with live organisms. You must have previous experience in at least one of the following areas: biomechanical analysis, mathematical modeling, materials testing, digital image analysis, morphological visualization, developmental/scaling analyses, or evolutionary analysis.

Characteristics: A strong interest in the evolutionary or physical principles of biological movement is essential. Patek Lab postdocs establish and lead their projects - creativity, self-sufficiency and motivation in your work are essential. A commitment to building skills for enhancing and engaging broader communities in research is essential.

RESPONSIBILITIES

-Lead a postdoctoral research project focusing on the transitions between motor-driven and spring-driven movement within and across organisms.

-Collaborate with participating labs for marine fieldwork and mathematical modeling aspects of the project.

-Lead outreach and broader impact activities.

-Communicate research through team meetings, conference presentations, and journal publications.

-Supervise projects involving undergraduates and graduate students.

-Contribute to lab animal care, acquisition, and general lab operations.

APPLY NOW

Applications are currently being accepted and will be evaluated on a rolling basis with the goal of hiring as soon as possible. The position is available starting 9/1/2020, although the start date is negotiable and can begin at a later date. The position is based on funding for a three year position. The initial appointment will be for 12 months with the possibility for renewal contingent on performance and continuing funding availability for up to 3 years. Salary starts at $52,704. Contact Prof. Patek via email for additional information.

The job application must be submitted to Academic Jobs Online using this link https://academicjobsonline.org/ajo/jobs/16493 (do not email applications to Prof. Patek) and should include:

Cover letter including information about specific research interests

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EBI Sanger EvolutionaryBiol

The EBI'VSanger Postdoctoral (ESPOD) Programme builds on the collaborative relationship between EMBL-EBI and the Wellcome Sanger Institute, offering projects that combine experimental (wet-lab) and computational (dry-lab) approaches.These are competitive postdoctoral fellowships lasting three years and two fellowships are awarded each year.

This link describes a set of 7 pre-defined projects, including two highlighted below of likely interest to this audience https://www.ebi.ac.uk/research/postdocs/espods Additionally, there is an opportunity to identify a PI at EBI and Sanger and develop your own proposal to work between two groups at these institutes south of Cambridge in England.

Project 2: Mara Lawniczak < https://www.sanger.ac.uk/person/lawniczak-mara-k-n/ > and Ewan Birney < https://www.ebi.ac.uk/research/birney > groups Long reads to investigate within species variation across the Tree of Life https://www.ebi.ac.uk/sites/ebi.ac.uk/files/shared/ESPOD_2020_Birney_Lawniczak.pdf Project 3: Mark Blaxter < https://www.sanger.ac.uk/person/blaxter-mark/ >, Rob Finn < https://www.ebi.ac.uk/research/finn > and Nick Goldman < https://www.ebi.ac.uk/research/goldman > groups Photosymbiosis genomics https://www.ebi.ac.uk/sites/ebi.ac.uk/files/shared/ESPOD_2020_Finn_Goldman_Blaxter.pdf Other projects include

Project 1: David Adams < https://www.sanger.ac.uk/person/adams-david/ > and Alex Bateman < https://www.ebi.ac.uk/research/bateman > groups Deep mutational scanning of the dark proteome

Project 4: John Marioni < https://www.ebi.ac.uk/research/marioni > and Sarah Teichmann < https://www.sanger.ac.uk/group/teichmann-group/ > groups Strategies for integrating spatial data across individuals

Project 5: Ellen McDonagh < https://www.ebi.ac.uk/about/people/ellen-mcdonagh >, Gosia Trynka < https://www.sanger.ac.uk/person/trynka-gosia/ > and Emma Davenport < https://www.sanger.ac.uk/person/davenport-emma/ > groups Investigation of genetic signatures associated with pharmacological outcomes for immune diseases

Project 6: Evangelia Petsalaki < https://www.ebi.ac.uk/research/petsalaki > and Matthew Garnett < https://www.sanger.ac.uk/person/garnett-mathew/ > groups A data-driven framework for uncovering the role of understudied kinases in signalling network adaptation

Project 7: Daniel Zerbino < https://www.ebi.ac.uk/research/zerbino > and Leopold Parts < https://www.sanger.ac.uk/person/parts-leopold/ > groups A unified view of human coding mutation effect

The Wellcome Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

Mara Lawniczak <mara@sanger.ac.uk>

Flagstaff VirusBioinformaticsGenomics

I'm currently recruiting for a bioinformatics-focused postdoctoral fellow to join my lab group at the Pathogen and Microbiome Institute, Northern Arizona University (http://www7.nau.edu/ladnerlab/). This will be a multi-year, NIH-funded position focused on the development and utilization of a novel platform for highly multiplexed antiviral serology, which utilizes high-throughput sequencing technology.

To apply: https://hr.peoplesoft.nau.edu/psp/ph92prta/EMPLOYEE/HRMS/c/HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=-

HRS_APP_JBPST&Action=U&FOCUS=-Applicant&SiteId=1&JobOpeningId=-604999&PostingSeq=1 For more information, feel free to contact me: jason.ladner@nau.edu

Northern Arizona University is located in Flagstaff, AZ, which offers an ideal, scenic environment for living and learning. With a four-season climate, amazing landscapes, and ample sunshine, you'Âll discover outdoor adventures unlike anywhere else in the United States'Xfind out more about NAU and Flagstaff at https://nau.edu/-about/living-in-flagstaff/ . JTL

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Jason Thomas Ladner, Ph.D. Assistant Professor

The Pathogen and Microbiome Institute Northern Arizona University 1395 South Knoles Drive, Building 56 PO Box 4073 Flagstaff, AZ 86011-4073 (Tel) : 928-523-0647

http://scholar.google.com/citations?user=-BERyl5AAAAJ&hl=en https://github.com/jtladner http://www.nau.edu/ladnerlab/ Pronouns: he, him, his

Jason Thomas Ladner <Jason.Ladner@nau.edu>

Hawaii InsectEvolution

My group is seeking an enthusiastic postdoctoral research associate to join us in the investigation of tropical insect pests using genetic, genomic, and bioinformatic techniques at the USDA-ARS Pacific Basin Agricultural Research Center located in Hilo, Hawaii.

The selected candidate will investigate the use of population genetic data with abiotic factors and current geographic distributions with the goal of identifying future invasion hotspots.

The desired candidate will have a strong background in bioinformatic analysis of genomic data and computational biology through a command-line interface and some experience in GIS.

Candidates who have demonstrated strong written and oral communication skills, experience working independently and as part of a group, and strong interpersonal skills are encouraged to apply.

A PhD in biology, genetics, evolution, entomology, bioinformatics, or related disciplines is required at the time of application.

The position will be hired through the Oak Ridge Institute for Science and Education (ORISE) as part of the USDA-ARS research participation program and the candidate selected will serve as a postdoctoral research fellow with an annual stipend of $66,002, health benefits, and a budget for relocation. The position is guaranteed for one year with the possibility of extension contingent on performance and availability of funds.

More information about the position and the application can be found here: https://www.zintellect.com/-Opportunity/Details/USDA-ARS-2020-0145 If interested, please submit a cover letter, CV, and the contact information of three references to: Dr. Sheina Sim, sheina[dot]sim[at]usda[dot]gov.

While the candidate will not be employed in the federal service, it is relevant to note that the US Department of Agriculture, Agricultural Research Service is an equal opportunity/affirmative action employer and all agency services are available without discrimination.

Sheina B. Sim, Ph.D.

Research Biologist

USDA-ARS Daniel K. Inouye US PBARC

64 Nowelo Street

Hilo, HI 96720

Google scholar profile: https://scholar.google.com/-citations?hl=3Den&user=ekWzSzEAAAAJ sheina.sim@usda.gov

Hungary BioinformaticsAntibioticResistance

Dear Evoldir Members,

Please find our job advertisement below:

Open bioinformatician position in the field of evolution of infectious diseases

We are recruiting bioinformaticians at postdoc, PhD student or research assistant level who are eager to pursue groundbreaking biological research in areas such as genomics and evolution of antibiotic resistance genes, genome engineering and phage therapy.

The successful candidate will work together with the labs of Balázs Papp < https://www.google.com/url?q=http://-group.szbk.u-szeged.hu/sysbiol/papp-balazs-lab-index.html&sa=D&ust=1594908932422000&usg=AOvVaw2EAxkXtgDfuzwNTt6ufM63 > (Google Scholar < https://www.google.com/url?q=https://scholar.google.com/citations?user%3D3YzdqwwAAAAJ%26hl%3Den&sa=D&ust=1594908932422000&usg=AOvVaw2cKJuyvtdPF4js2Um27ALS >) and Bálint Kintses < https://www.google.com/url?q=http://group.szbk.u-szeged.hu/sysbiol/kintses-balint-lab-index.html&sa=D&ust=1594908932423000&usg=AOvVaw3JU5dy4Ke7UQL2YK_Q2-JI > (Google Scholar < https://www.google.com/url?q=https://scholar.google.com/citations?user%3Dgax-6nEAAAAJ%26hl%3Den&sa=D&ust=1594908932423000&usg=AOvVaw0bfOGOJ8tlFXyy9NPozroR >). The labs are hosted at the Biological Research Centre < https://www.google.com/url?q=http://www.brc.hu/index.php?change_lang%3Den&sa=D&ust=1594908932423000&usg=AOvVaw36Kac0yI7hu1ldNDiULdyr > (BRC) in Szeged, which is a Centre of Excellence of the European Union. In addition, the candidate will also be affiliated with the Hungarian Centre of Excellence for Molecular Medicine < https://www.google.com/url?q=https://www.hcemm.eu/&sa=D&ust=1594908932424000&usg=AOvVaw0lNVNaV6XY0mECip6Me3J >, a partner institute of EMBL (HCEMM-EMBL). Szeged is a thriving university town with a large community of international students and highly affordable living costs < https://www.google.com/url?q=https://www.numbeo.com/cost-of-living/in/Szeged&sa=D&ust=1594908932424000&usg=AOvVaw0jWkhZOKH-9f58wUEDFBzk >.

What we offer:

- Possibility to work on cutting-edge interdisciplinary research projects connecting biology with medicine and experiments with computation (e.g. see Nature Microbiology 2019 <https://www.google.com/url?q=https://www.nature.com/articles/s41564-018-0313-5&sa=D&ust94908932425000&usg=AOvVaw0QOShxVMLG8RwKYrMalUVw>, Nature Communications 2019 <https://www.google.com/url?q=https://www.nature.com/articles/s41467-019-13618-z&sa=D&ust94908932425000&usg=AOvVaw1mpmhBu5TezMJIqvJ-r94g>) - Opportunities to collaborate with industry (biotech/pharma) - Possibility to earn a PhD. - Training program in project management, scientific writing, visual communication, entrepreneurship, leadership and data science - Competitive salary and travel allowance. The employment contract includes health insurance. - HR department and administrative team offers support with relocation, visa applications, onboarding, family support, etc. - Part-time position and remote work are also feasible.

Whom we are looking for:

- Requirements:

- MSc or PhD in bioinformatics, biology, medical sciences, mathematics, computer science or equivalent. - Research experience in bioinformatics. Relevant publication is a must for postdoc candidates. - Demonstrated experience in programming in at least one scripting language (R or Python) and Linux command line. - Excellent oral and written communication skills in English.

- Experience in the field of statistical methods, phylogenetics, NGS,

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IdahoStateU EcologicalGenomics

Postdoctoral fellow in ecological genomics of wide-ranging taxa as part of the GEM3 Project. Application review will begin date: August 22, 2020 (applications will be accepted until position is filled).

The successful candidate will use ecological genomics to link genome to phenome and help understand the adaptive capacity of widely-distributed taxa in the face of environmental change. The candidate will work with collaborative teams of geneticists, ecologists, and modelers across different academic institutions and governmental agencies. They will be embedded in the collaborative research network of the GEM3 project (https://www.idahogem3.org/)'and potentially work locally with one or more of the labs of Drs. Ernest Keeley, Janet Loxterman, Keith Reinhardt, and Kathryn G. Turner at Idaho State University. Two focal taxa being examined by the research labs are big sagebrush (Artemisia tridentata) and redband/rainbow trout (Oncorhynchus mykiss). The position will provide a unique opportunity to contribute to an interdisciplinary research program that addresses the National Science Foundation's research priority of quantifying the contribution of genetic and environmental factors to phenotypic expression (i.e., linking genome to phenome).

Please see the job ad for more details: https://isu.csod.com/ats/careersite/JobDetails.aspx?id=1070&site=1 Dr. Kathryn G. Turner Dept. Biological Sciences Idaho State University kathryngturner.com

Kathryn Turner <turnkat2@isu.edu>

IllinoisStateU BioinformaticsSexualConflict

Illinois State University School of Biological Sciences

FUNCTIONAL GENOMICS AND BIOINFORMATIC ANALYSIS OF THE ROLE OF NUPTIAL GIFTS IN SEXUAL CONFLICT

Postdoctoral Research Position (1 year) Salary: $43,000 per year

Applications are invited for an NSF-funded Postdoctoral Researcher to join the labs of Scott Sakaluk (biology.illinoisstate.edu/sksakal/Dr._Scott_Sakaluk/) and Ben Sadd (about.illinoisstate.edu/bmsadd/) in the School of Biological Sciences, Illinois State University. The position is part of a project leveraging experimental evolution lines in the decorated cricket Gryllodes sigillatus (see Sakaluk et al. 2019) to understand the evolution of sexual conflict surrounding the provision of nuptial food gifts. We are seeking a Postdoctoral Researcher for a 1-year position to lead the bioinformatic analysis of existing and future gene expression datasets, starting as soon as possible. Renewal of the position may be possible contingent on continued external funding.

Sexual conflict, in which the interests of males and females diverge, is widespread, and males in various insects provide nuptial food gifts at mating that can influence female mating behavior, often against females' own reproductive interests. Prior studies in decorated crickets suggest that the food gift is an agent of sexual conflict. The current research project takes an experimental evolution approach, and evaluates the effects of intensified sexual selection on the chemistry of gifts and their efficacy in evoking female behavioral and physiological responses. Behavioral studies are ongoing, but this position will focus on differential gene expression in females upon nuptial gift feeding and how gifts from different selection line treatments influence female transcriptomic responses. The postdoctoral researcher will set up and analyze the RNAseq data. This includes the analysis of an existing dataset and involvement in design and subsequent analyses of future experiments incorporating the selection lines. Other major responsibilities will be to interact with other project partners in the Sakaluk and Sadd labs, liaise with an external collaborator, interpret, present and work together with the postdoctoral supervisors on publishing project results. We are open to discussion of remote working possibilities.

We are seeking candidates with a strong bioinformatics background, with experience in dealing with large RNAseq datasets from de novo assembly (e.g. Trinity) through to differential gene expression and functional annotation of resulting gene sets. Candidates should have a PhD degree or be in the process of completing one in the relevant areas, with a background in evolution, ecology or animal behavior desired.

In the application process you will need to upload a CV, a cover letter, a statement of your interest in the position and how your skills are concordant with the project's research needs, and a reference list with a minimum of three referees who are familiar with your work. This position is full time and we will consider all applications until a selection of the appropriate candidate is made.

If interested, please apply at https://jobsearch.illinoisstate.edu/cw/en-us/job/509966 For informal inquiries please contact Scott Sakaluk (sksakal@ilstu.edu) or Ben Sadd (bmsadd@ilstu.edu).

Illinois State University is an Equal Opportunity/Affirmative Action Employer

Dr Ben Sadd Pronouns: he, him, his Associate Professor of Infectious Disease Ecology Assistant Director of Graduate Studies School of Biological Sciences Illinois State University Normal, IL 61790-4120

email: bmsadd@ilstu.edu twitter : @Saddlab web: https://about.illinoisstate.edu/bmsadd/ tel: +1 (309) 438 2651 fax: +1 (309) 438 3722

bmsadd@ilstu.edu

IowaStateU PhylogeneticComparativeMethods

Postdoctoral Associate: morphometrics and phylogenetic comparative methods

The Adams laboratory, Department of Ecology, Evolution and Organismal Biology (EEOB) at Iowa State University, is seeking applicants for a fulltime postdoctoral position in geometric morphometrics and phylogenetic comparative methods. This position is for a maximum of two years and is part of an NSF collaborative CIBR project. The postdoctoral associate will contribute to ongoing macroevolutionary studies in vertebrates, will coordinate the development of tutorials and code profiling in geomorph, and will mentor undergraduates in quantitative morphology studies. Successful applicants are encouraged to develop their own independent empirical research in multivariate macroevolution.

Additional details about the position, as well as a link to apply, may be found on the ISU HR website: https://isu.wd1.myworkdayjobs.com/IowaStateJobs/job/Ames-IA/Postdoctoral-Research-Associate—Ecology–Evolution-and-Organismal-Biology_R2794 Questions about the position should be directed to Dean Adams (dcadams@iastate.edu).

Dr. Dean C. Adams Director of Graduate Education, EEB Program Professor Department of Ecology, Evolution, and Organismal Biology Iowa State University https://www.eeob.iastate.edu/faculty/adams/ phone: 515-294-3834

"Adams, Dean [EEOB]" <dcadams@iastate.edu>

Maryland France AnimalsignalDesign

A postdoctoral fellowship is available to study the evolution of animal signal design with Tamra Mendelson at UMBC (www.mendelsonlab.net [1]) and Julien Renoult at CNRS (https://www.eevcom-montpellier.com/julien-renoult.html [2]). The project asks how information theory informs the evolution of pattern preferences and signal design, and the study organism is a lineage of North American freshwater fish called darters, which are beautiful, fun to catch, and fascinating to watch. The postdoc will primarily use AI methods to analyze and manipulate images of fish and habitats, with some behavioral experiments and field collections. We also encourage additional projects suited to the candidate's interests.

The primary geographic location of the research will be in Mendelson's lab at the University of Maryland, Baltimore County (UMBC) in Catonsville, MD, with at least one extended visit to Renoult's lab at the Center for Functional and Evolutionary Ecology (CEFE - CNRS) in Montpellier, France. UMBC is a national model for diversity and inclusive excellence in STEM, and the department of Biological Sciences is research-intensive, with thriving graduate and undergraduate programs (http://biology.umbc.edu [3]). Catonsville is a quiet place to live with easy access to the mountains to the west, ocean to the east, and two major cities, Baltimore and Washington, D.C. The CEFE is the largest French research center in Ecology and Evolutionary Biology. Montpellier, located next to the Mediterranean sea and surrounded by vineyards, hosts the largest community of ecologists in Europe; its university is currently ranked first in Ecology in the global Shanghai ranking.

This is a 3-year NSF-funded position with a starting salary of 54,000 USD per year, increasing 3% per year, plus benefits. Candidates with a doctoral degree focusing on computational biology, animal behavior, and/or evolutionary biology are encouraged to apply. Please send a CV and brief cover letter outlining your interests and experience to tamram@umbc.edu and julien.renoult@cefe.cnrs.fr. We look forward to hearing from you!

Tamra C. Mendelson, Ph.D. Professor and Associate Chair Department of Biological Sciences University of Maryland Baltimore County tamram@umbc.edu - www.mendelsonlab.net [4] Interdisciplinary Consortium for Applied Research in the Environment (ICARE [5])

Links: —— [1] http://www.mendelsonlab.net/ [2] https://www.eevcom-montpellier.com/julien-renoult.html [3] http://biology.umbc.edu/ [4] http://www.mendelsonlab.net [5] http://icare.umbc.edu
Tamra Mendelson <tamram@umbc.edu>

MichiganStateU PopGen

The Bradburd Lab at Michigan State University is looking for two full-time postdocs to join the lab and work on NIH-funded research developing statistical methods in spatial population genetics.

Possible projects include: spatiotemporal models for the analysis of ancient and modern human DNA; two-locus models for the analysis of spatial population structure over genealogical strata; spatial models for identifying adaptive introgression or studying polygenic adaptation; statistical computing approaches for fast and robust analysis of high dimensional data.

Research in the Bradburd Lab combines computational and statistical approaches, with a strong emphasis on empirical data analysis. The positions are ideal for someone with training in statistical, theoretical, or computational population genetics, and/or someone with a strong background in statistical computing and an interest in population genetics.

The positions are available for up to three years (starting at 1 year, with annual review), with a competitive salary and full benefits. Given the uncertainties surrounding the state of the pandemic, the successful candidate may work remotely (i.e. ghostdoc), at least for the first year of the position, and possibly beyond. The positions are available in September 2020, but the start date can be flexible for the right candidate.

The Bradburd lab values diversity and is committed to creating a safe, welcoming, and supportive lab environment. Applications from candidates with related scientific interests who are also passionate about diversity, equity, and inclusion in STEM are strongly encouraged. Michigan State is an excellent place to be a postdoc, with an extraordinarily favorable cost-of-living : salary ratio, as well as many other labs engaged in exciting population genetics and evolutionary research.

Application instructions can be found at http://www.genescape.org/recruitment.html. Applicants will be considered until the positions are filled. Informal inquiries welcome (direct to bradburd[at]msu[dot]edu).

Gideon Bradburd (*he/him*) Dept. Integrative Biology Michigan State University genescape.org

Gideon Bradburd <bradburd@msu.edu>

Montpellier CooperationModelsInCrops

Mathematical models of cooperation in crops

A post-doctoral position is available for 17 months stating this autumn in Montpellier (France), as fuly described here :https://bit.ly/2zPFAFH(https://emploi.cnrs.fr/Offres/CDD/UMR5554-FRAROU-001/Default.aspx?lang=EN for direct access to english version).

This post-doc is part of the ANR-funded SCOOP project (https://umr-agap.cirad.fr/en/recherche/projets-de-recherche/scoop-cooperation-chez-les-plantes-cultivees), led by Hélène Fréville (AGAP, INRAE), which will use a combination of theory and experiments to identify above- and below-ground traits involved in social interactions and their associated cooperative phenotypes in crops (with durum wheat as an experimental model, as well as cooperative alleles. One aim of the project is to provide practical guidelines for breeders and farmers to design selection schemes that promote plant cooperation and optimize crop yield in high-density agrosystems. The post-doc will be supervised by F. Rousset (CNRS, evolution of social behaviour) at the Institut des Sciences de l'Evolution (ISEM), and will benefit from the expertise of different project members, including S Gandon (CNRS, development of kin selection models) and H Fréville (INRAE, experiments on kin selection in crops).

The post-doc will develop models to assess the ability and efficiency of different selection schemes to select for cooperative phenotypes. Previous work by our group (Montazeaud et al 2020) has investigated this question by considering the evolution of plant height in response to competition for light. This theoretical framework will be extended in two directions: (i) we will consider the coevolution between height and shape. This evolution will be constrained by trade-offs with seed production (in the absence of competition there is an optimal height and shape that maximizes yield) but also by potential correlations between these two traits constraining plant architecture. This model will predict the impact of an increase of crop density on these two traits and on yield. We will manipulate relatedness and the level of selection among groups in order to identify practices that maximize yield; (ii) we will account for the change of architecture during growth, and the ability of plants to adjust their development in response to the development of their neighbors. Yield will thus depend on the plastic response in height to the social partners, and the plastic response in shape. Modeling the evolutionary dynamics of the development program of the plant under the influence of neighboring plants will call for methods of optimal control theory.

References

Reference: Fréville H, Roumet P, Rode NO, Rocher A, Latreille M, Muller M-H, David J (2019) Preferential helping to relatives: a potential mechanism responsible for lower yield of crop variety mixtures? Evolutionary Applications 12, 1837-1849. https://doi.org/10.1111/eva.12842 . Montazeaud G., Rousset F., Fort F., Violle C., Fréville H. and Gandon S. Farming plant cooperation in crops. Proc. R. Soc. B http://doi.org/10.1098/rspb.2019.1290 Francois Rousset <francois.rousset@umontpellier.fr>

NewYorkCityC EvolutionaryGenomics

The Blair lab at NYC College of Technology (City Tech/CUNY) focuses on using genomics and sophisticated computational methods to understand evolutionary patterns and elucidate the processes giving rise to such patterns. Specific areas of focus include genomics, molecular phylogenetics, phylogeography, species delimitation, and DNA barcoding. The lab is currently seeking a two year postdoctoral scholar who will work on an NSF funded project that uses multiple species of phrynosomatid lizards to understand the influence of gene flow during the diversification of arid-adapted organisms distributed throughout the major deserts of western North America. A second major goal of the project is to combine genomic data, mtDNA, morphology, and ecology to refine species limits and describe new taxa. Data will be collected from approximately 10 species/species complexes from multiple phrynosomatid genera. This project is a collaborative effort with researchers from multiple institutions with expertise in genomics, phylogenetics, and morphological analysis.

In addition to conducting research to fulfill the objectives of the grant, the scholar will be expected to teach one undergraduate course per semester of his/her choosing. Formal teaching experience can often make postdoctoral scholars more competitive for the job market. City Tech is considered a Hispanic serving institution, with many students being the first in their family to attend college. This postdoctoral position will be particularly attractive to candidates with a dual interest in genomic research and in teaching a large, historically underrepresented population.

Specific duties

Assist in the collection of tissue and voucher samples in the field. Maintain databases pertaining to current tissue holdings. Collect and analyze meristic and morphometric data to aid in species delimitation. Perform standard molecular lab work (e.g. DNA extraction, quantification, PCR, sample prep for next-generation sequencing).

Analyze newly obtained molecular data using recently developed software. Write manuscripts in collaboration with other researchers involved with the project. Assist in supervising undergraduate researchers. Develop a personalized teaching program at the undergraduate level. Present results at national scientific meetings. Meet with PI at least once per week to discuss progress.

Requirements

A PhD degree in a relevant discipline is required prior to the official start date. Candidates should have previous experience with genomics, phylogenetic analysis, population genomics, bioinformatics, and cluster computing. Prior programming experience is not required, but would be beneficial. An interest and background in the biology of reptiles and amphibians would also be helpful, but is not required. Strong written and oral communication skills are required. Candidates should be available for periodic laboratory work. However, many other duties can be done remotely.

Application

Interested candidates should submit a single pdf document containing a cover letter, CV, research statement, and teaching statement to cblair@citytech.cuny.edu. In addition, please include contact information for three professional references. Applications will continue to be screened until a suitable candidate is found. The official start date is somewhat flexible, but will be prior to September 1, 2020. Informal inquires can be submitted prior to a formal application.

Christopher Blair, Ph.D. Associate Professor Department of Biological Sciences New York City College of Technology and Ecology, Evolution and Behavior PhD Program Graduate Center The City University of New York 285 Jay Street Brooklyn, NY 11201 CBlair@citytech.cuny.edu; cblair@gc.cuny.edu Website: https://sites.google.com/site/christopherblairphd/-home Office: Academic Complex 501A; Ph: 718-260-5342 Lab: Academic Complex 401

Christopher Blair <CBlair@citytech.cuny.edu>

NHM London SpongeMicrobeSymbiosis

Dear all,

The Leys, Hill, and Riesgo labs are looking for a motivated postdoc to work on the molecular mechanisms for establishing sponge-microbe symbiosis using Ephydatia muelleri as a model system. If you have skills in molecular biology (especially cloning, vector design, construction and delivery into cells), a publication record, and science communication passion, maybe this is your dream job! The post will be based on Edmonton (Canada) at the Leys lab, in a highly dynamic, diverse, and fun environment, with visits to the Hill lab at the Bates College (Maine, USA), and Riesgo lab (National Museum of Natural Sciences, Madrid, Spain).

You will be part of a great project that aims to understand many different aspects of the establishment of sponge-microbe symbiosis including algal colonization, spatial distribution of microbiome diversity and function, and molecular mechanisms for microbe recognition. If you areinterested and want to see more details, look at the webpage below and send us an email to ephysymbio@gmail.com.

To apply, we needa cover letter, CV, and a brief description of their experience as well as the names and contact information of three references.

Deadline: July 30th.

https://leyslab.weebly.com/newsline/job-post-post-doc-in-sponge-microbe-symbioses-click-her-to-read-more
Cheers, Ana

Ana Riesgo

Research Leader at theInvertebrates Division Department of Life Sciences Natural History Museum of London

Cromwell Road London, SW7 5BD A.Riesgo@nhm.ac.uk anariesgogil@gmail.com http://www.anariesgogil.com/ Ana Riesgo in Researchgate

Ana Riesgo <anariesgogil@gmail.com>

NHM UOslo Norway ComparativeGenomicsPhylogenomics

For the following PostDoc (Jobbnorge ID:190431) please apply at https://www.jobbnorge.no/en/available-jobs/job/190431/postdoc-in-comparative-genomics-phylogenomics The deadline for the deadline is at 16.08.2020.

Job description A 3-year PostDoc position is available at the Natural History Museum (NHM), University of Oslo.

The subject of the PostDoc position will be part of the recently founded RCN-project “InvertOmics - Phylogeny and evolution of lophotrochozoan invertebrates based on genomic data”. The origin and evolution of Bilateria is controversially discussed in several biological disciplines such as systematics or evolutionary developmental biology. In one hypothesis, evolution in Bilateria advances from a simple body organization similar to flatworms towards more complex forms several times independently. In the other one, the evolution progresses in the opposite direction from a complex ancestor more like an annelid to simple organizations by several separate reductions. Support for one or the other depends on the phylogeny and evolution of Lophotrochozoa, one of the major bilaterian taxa, but a robust phylogeny is still lacking despite recent phylogenomic studies. This is due to both low coverage by genomic data and misleading biases in data of lophotrochozoan taxa. In this project, high-quality reference genomes shall be generated and new procedures to both ameliorate negative effects of biases and establish a new support measurement, which is entirely different from all recent support measurements. Due to both the large genomic dataset and these thorough analyses, a robust phylogeny of Lophotrochozoa shall be provided allowing contributions to discussions about the origin and evolution of Bilateria as well as of lophotrochozoan taxa and character traits.

The aim of this PostDoc project is to solve the problems associated with the reconstruction of the phylogeny of Lophotrochozoa. The PostDoc can contribute to both the development a new approach to assess the support for specific phylogenetic hypotheses and the generation of new genomic data in Lophotrochozoa. The new approach shall also determine a priori the best procedure to ameliorate the effect of misleading biases. Therefore, the effects of misleading biases shall be simulated in a phylogenomic setting based on parameter spaces derived from empirical data including confounding effects of reticulate evolution, adaptive radiations and incomplete lineage sorting. Based on these simulated data both a best-practice procedure and new support measurement on how likely a reconstructed relationship is true shall be derived. For the generation of new data, new high-quality genomes for 50 lophotrochozoan species covering all 16 lophotrochozoan phyla shall be determined. Modern genome sequencing strategies combining long and short reads will be employed. In the project, the PostDoc will closely work together and assist in supervision of the already hired PhD student.

The Natural History Museum has a modern DNA laboratory as well as access to the Norwegian Supercomputer facilities. The postdoc will be associated with the research group “Frontiers in Evolutionary Zoology”, specifically Torsten Struck (Professor of Evolutionary Genomics). The starting date for the position shall be no later than January 1st 2021.

Qualification requirements - We seek a person with strong motivation for research in comparative genomics & phylogenomics. - The candidate must be skilled in phylogenetic reconstruction methods and in general molecular laboratory practices. - Experience with next-generation sequencing of genomes, development of new tools for phylogenetics and/or the handling of big datasets is preferable. - Computing skills in either Deep Learning, Neural Networks or Machine Learning Algorithms are advantageous. - Communication skills (including written and spoken English) - A strong academic track record - Team-working and networking skills - A degree equivalent to a Norwegian doctoral degree in biology, bioinformatics or equivalent. For candidates not having finished their doctoral degree the doctoral dissertation must be submitted for evaluation by the closing date of the call. An appointment is dependent on the defense of the doctoral thesis being approved.

We offer - salary NOK 523 200 - 605 500 per annum depending on qualifications in position as Postdoctoral Research Fellow (position code 1352) - challenging research questions and friendly working environment, which is close to both the city center of Oslo, a vibrant and - international city, which is nice to live in, and to nature parks and mountains - full funding of the project research-related activities, including presentation of results at international conferences. - membership in the Norwegian Public Service Pension Fund

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NIH VisionEvolution

We are seeking a postdoctoral fellow with a background in evolutionary biology and bioinformatic expertise to join us in the Neurobiology Neurodegeneration & Repair Laboratory (NNRL) within the National Eye Institute at the National Institutes of Health in Bethesda, MD.

The primary goal of our research in the NNRL is to develop novel therapies for retinal and macular degeneration by identifying the cellular pathways and regulatory networks underlying photoreceptor development, aging, and disease. The postdoc we are looking for will join a nascent group within the NNRL applying an evolutionary framework to a pan-chordata dataset to answer fundamental questions relating to retinal development and function. This is an opportunity to conduct evolutionary analyses in an environment with a wealth of resources.

Applicants should have received a PhD or MD/PhD in genetics, evolution, developmental biology, molecular biology, bioinformatics, or a similar field. Successful candidates will display a strong motivation to conduct scientific research, experience in bioinformatic analysis and use of a high-performance computing cluster, molecular laboratory experience, a solid publication record, and excellent communication and interpersonal skills. The postdoc will be located within the National Eye Institute at the National Institutes of Health. The campus is located in Bethesda, MD'Veasy public transportation access from Washington, DC. The position is for 2-3 years, and includes health benefits. Annual stipend will be commensurate with experience and training. For more information, please visit the NNRL website < https://www.nei.nih.gov/research/research-labs-and-branches/neurobiology-neurodegeneration-repair-laboratory >, as well as the Retinal Development, Genetics and Therapy section website < https://www.nei.nih.gov/research/research-labs-and-branches/neurobiology-neurodegeneration-repair-laboratory/retinal-development-genetics-and-therapy-section> . Interested applicants should submit a cover letter with a description of career goals, cv with publications, and the contact information for 3 references to Dr. Anand Swaroop at swaroopa_at_nei.nih.gov. Questions about the position or lab can be sent to Dr. Noor White at noor.white_at_nih.gov.

– Noor D. White, PhD Postdoctoral Fellow, National Science Foundation Postdoctoral Fellow, National Eye Institute, National Institutes of Health Research Collaborator, National Museum of Natural History, Smithsonian Institution

NNRL < https://nei.nih.gov/research/research-labs-and-branches/neurobiology-neurodegeneration-repair-laboratory >, National Eye Institute < https://nei.nih.gov/ >, NIH < https://www.nih.gov/ > 6 Center Dr. Bethesda, MD 20892 (301) 402-5734 www.noorwhite.com noor.white@nih.gov

SanFranciscoStateU ForensicPopulationGenetics

An NIJ-funded post-doc position available to quantify the accuracy of specialized forensic genetic technologies, particularly

genealogical searching. The postdoc will gain experience in pedigree-based IBD analysis considering population genetic variation. Depending on the interests of the postdoc and practical constraints, these projects may include collaborations with population geneticists Graham Coop at UC Davis, Doc Edge at USC, bioethicist Malia Fullerton at UW, and/or law professor Erin Murphy at NYU. The position is initially for one year, with strong possibility of extension.

While initially the postdoc will work remotely, when on-campus research is feasible, the postdoc will be situated in the joint Pennings-Rohlfs-Roy lab space at San Francisco State University (SFSU). The lab space houses a few postdocs, a few PhD students from other universities, and about 20 SFSU masters students and undergraduates. The postdoc will be well-positioned to mentor some of these students. The position could be permanently remote, so long as the postdoc maintains strong engagement in the lab. The postdoc will also have teaching opportunities, but not requirements. The lab welcomes innovative clear communication, and examination of social justice questions related to our work.

This is an ideal opportunity for a scientist who is looking to do population/statistical genetics research with a social impact, and is interested in working with a diverse population of brilliant, tenacious, and creative students.

Interested scientists can email Rori Rohlfs rrohlfs@sfsu.edu with a 1-2 page cover letter, CV, a paper (or draft) as a scientific writing sample, and names and email addresses for three references.

Rori Rohlfs (she/her) Assistant Professor Department of Biology San Francisco State University Ramaytush Ohlone land

https://rohlfslab.weebly.com/ Rori Rohlfs <rrohlfs@sfsu.edu>

SangerInst SymbiosisGenomics

Postdoctoral fellowship (ESPOD) in Symbiosis Genomics - applications open - European Bioinformatics Institute & Sanger Institute https://tinyurl.com/ESPOD-symbiosis Mark Blaxter (Sanger Institute), Rob Finn (EMBL-EBI) and Nick Goldman (EMBL-EBI) Symbiotic interactions enable high biodiversity in many, otherwise nutrient poor, ecosystems. In the specific case of photosymbiosis, the autotrophic nutrition supplied by these photosymbionts can provide sufficient carbon, fixed nitrogen and energy for holobiont (microbial symbiont and host) metabolism. With advances in sequencing and informatics techniques, we propose to explore the genomes from holobionts at scale. We will analyse the biology of photosymbionts using technologies emerging from metagenomics and systems reconstruction of biochemistry. Using data generated by Darwin Tree of Life and Aquatic Symbiosis Genomics projects (Blaxter) and toolkits developed by the Finn and Goldberg labs you will characterise photosymbiotic relationships from a genomic perspective, developing new approaches to produce high quality, reliable genomes. Through comparative genomic analyses of obligate and facultative symbionts, and closely related non-symbionts, you will elucidate mechanisms that underpin these relationships. These hypotheses will be validated by functional genomic experiments. This work will support understanding of carbon and nitrogen cycles in the oceans and their likely responses to environmental change, of the associations between eukaryotic cells and photosymbionts in lichens that resulted in the first terrestrial biomes, and of the exotic biochemistry behind production of molecules of pharmaceutical and biotechnological interest. Applications are open now; please contact us to discuss ideas. Mark Blaxter <mb35@sanger.ac.uk>, Rob Finn <rdf@ebi.ac.uk>, Nick Goldman <goldman@ebi.ac.uk>

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Sophie Potter PhD Research Administrator Tree of Life Programme

T: +44 (0)1223 496934 W: www.sanger.ac.uk E: sp27@sanger.ac.uk

Wellcome Sanger Institute

Wellcome Genome Campus Hinxton, Cambridge CB10 1SA

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Sophie Potter <sp27@sanger.ac.uk>

SGN Frankfurt Biodiversity

Job announcement ref.#11-20013

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

Senckenberg BiK-F invites applications for a Postdoctoral position in the research project "BEF-Up2: Upscaling exploratories data to understand the drivers of landscape multifunctionality". The project is part of the DFG funded Biodiversity Exploratories project.

Postdoc position in Biodiversity and Ecosystem Services: "Upscaling to understand the drivers of landscape multifunctionality"

(full time position)

We are seeking a quantitative ecologist (m/f/d) to generate new insights into the role of biodiversity in landscape multifunctionality. In this project, which extends the recent BEF-Up project, the successful applicant (m/f/d) will develop quantitative methods and techniques and use the comprehensive data of the Biodiversity Exploratories to construct statistical models that link plot- and landscape-level biodiversity to ecosystem services and solve upscaling problems to produce maps of ecosystem service supply. By combining these maps with existing data on the ecosystem service demands of stakeholders, measures of landscape multifunctionality will then be generated. After establishing this spatial model changes to stakeholder demands, land management and biodiversity will be simulated to evaluate how these affect the supply of multiple ecosystem services.

The project builds on existing synthesis work from the Biodiversity Exploratories project and aims to deliver high-impact publications and robust management recommendations. The work will be conducted in close cooperation with Dr. Peter Manning of Senckenberg BiK-F and many others within the Biodiversity Exploratories research community. For scientific enquiries please contact Dr. Peter Manning: peter.manning@senckenberg.de.

Position requirements

A PhD in Ecology, Ecosystem Services or a related field, and the ability to conduct independent ecological researchExcellent knowledge of at least one of the following: ecological theory, biodiversity, land management, ecosystem servicesFluency in R and an understanding of advanced statistical techniquesCompetency in the use of Geographical Information Systems e.g. Arc GISExcellent written and oral communication skills in English and the capacity to collaborate effectively within a large and diverse team of researchersA strong publication record and the ambition and capacity to publish in high-impact journalsExperience in upscaling and the use of remote sensing data is advantageous

Salary and benefits are according to a public service position in Germany (TV-H E 13, 100%). The position is a full-time position and will be for 2 years, preferably starting in September/October 2020. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants (m/f/d) will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please include the reference to this position (ref.#11-20013) in the subject line and include a letter of motivation to apply, a CV including a full publication list, full credentials and contact details of 2 academic referees. Please submit your application before 21st August 2020 (deadline) via e-mail as a single PDF file to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

E-Mail: recruiting@senckenberg.de

Related Links:

Senckenberg BiK-F https://www.senckenberg.de/en/institutes/sbik-f/

Biodiversity Exploratorieshttp://www.biodiversity-exploratories.de/en/ Peter Manning on Research Gate https://www.researchgate.net/profile/Pete_Manning

Thank you for your attention.

Sincerely,

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung

(Rechtsfähiger Verein gemäß ç 22 BGB)

Senckenberganlage 25

60325 Frankfurt am Main

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

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

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales

- 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting)

- 1564 di-Biase, Maria
- 1478 Gajcevic, Isabel
- 1313 Helm, Jessica

Fax: 0049 (0)69 / 7542-1445

Mail: recruiting@senckenberg.de

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SGN Frankfurt MammalianGenomics

Job Announcement ref. #12-20015

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG), https://tbg.senckenberg.de, is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE-TBG invite applications for a

Postdoc (m/f/d) - Mammalian Genomics: Speciation and Gene Flow

(full time)

Your tasks

§Sequencing, assembly, and annotation of mammalian genomes

§Evolution, gene flow, and population genomic analyses of large multispecies data sets

§Involve classic taxonomy, biogeography and related fields with comparative genomics

§Acquiring third-party funding

Your profile

§PhD in Biology, Genetics, Bioinformatics or related subjects

§Experience with de novo genome assembly and mapping of vertebrate genomes

§Exceptional interest in mammalian evolution

§Experience and solid understanding of comparative genomics or evolutionary biology research

§Teamwork oriented and excellent communication skills with proficiency in written and oral English

What is awaiting you?

§An interesting task in a dynamic team of researchers in an international research group and joining the new LOEWE excellence centre with its 20 new research groups

§The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics

§Flexible working hours - dual career service - leave of absence due to family reasons - parent-child-office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt - leave of 30 days/year

Place of employment: Frankfurt am Main

Working hours: Full time (40 hours/week)

Type of contract: initially limited until 31. December 2021

Salary: according to the German collective agreement TV-H(pay grade E 13)

Salary and benefits are according to a full time public service position in Germany (TV-H E13). The contract should start on as soon as possible and will initially be limited to the end of phase one of LOEWE-TBG in December 2021. Subject to further funding and extension of the project, an extension of the employment is envisaged.

The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The employer is the Senckenberg Gesellschaft für Naturforschung.

How to apply

Please send your application, mentioning the reference of this job offer (ref. #12-20015) until August 2nd, 2020 by e-mail (attachment in a single pdf document) and include a cover letter detailing your research interests and experience, a detailed CV, a list of publications and copies of your certificates, transcripts and grades to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt a.M.

E-Mail: recruiting@senckenberg.de

For scientific information please contact Prof. Axel Janke (axel.janke@senckenberg.de), see also “Comparative Genomics” at https://tbg.senckenberg.de . – Mit freundlichen Grüßen / Best Regards

Jessica Helm Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß ç 22 BGB) Senckenberganlage 25

60325 Frankfurt am Main

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

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting) - 1564 di-Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1445

Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Karsten Wesche

Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Recruiting <recruiting@senckenberg.de>

Smithsonian BiodiversityGenomics

Please spread the news - we are looking for a postdoctoral fellow in biodiversity genomics. Info is here: https://datascience.si.edu/opportunities/-biodiversity-genomics-postdoctoral-fellowship The Smithsonian Institution Data Science Lab (datascience.si.edu), housed within the Office of the Chief Information Officer, is looking to fill a postdoctoral fellowship in the area of biodiversity genomics.

The Data Science Lab was formed in response to the dramatic increase in all forms of digital data across the Smithsonian (19 museums, 9 research centers, and zoo). We seek to build collaborations both across Smithsonian units, as well as universities and other institutions. Members of our group work on a variety of data-intensive research topics including biodiversity genomics and machine learning applications of digitized museum collections. See a list of our recent publications here: https:/-/datascience.si.edu/data-science-lab-publications The successful applicant may design their own project or choose to build off of our current projects and collaborations. They will have the opportunity to become a certified Carpentries instructor and teach genomics and data science skills as part of our training program for Smithsonian staff, fellows, and interns (https://-datascience.si.edu/carpentries) if desired.

Qualifications: Applicants should possess a Ph.D. in a biological or computational discipline, demonstrate a strong publication record and ability to conduct independent research. Proficiency in genome assembly, annotation, and phylogenomic methods as well as a standard programming language such as Python, and experience using a High Performance Computing Cluster is desired.

Appointment is initially for one year, and renewable for a second year based on performance. Due to COVID-19 restrictions, the Data Science Lab is working remotely for the foreseeable future. Applicants are not required to relocate to the Washington, DC area. Stipend: $60,000 per year, with an additional $5,000 health insurance offset and $5,000 research budget. Start date is flexible.

To apply, submit a curriculum vitae, a 1-page statement of research interests, and contact details for 2-3 academic references to Rebecca Dikow (DikowR@si.edu). Review of applications will begin July 27th, 2020 and continue until the position is filled.

-Rebecca

Rebecca B. Dikow Research Data Scientist Data Science Lab Office of the CIO Smithsonian Institution

https://datascience.si.edu 'X Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu http://invertebrates.si.edu/osborn/- http://orcid.org/0000-0002-4226-9257 SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY Facebook < https://www.facebook.com/-nmnh.fanpage/ > | Twitter < https://twitter.com/-NMNH > | Instagram < https://www.instagram.com/-smithsoniannmnh/ >

Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

To: OsbornK@si.edu

Spain PlantPhenotypicPlasticity

The Andalusian regional government have launched the EMERGIA program to finance top researchers with leadership skills (Please, visit http://www.d-andalucia.csic.es/es/noticia/Emergia). The purpose of this call is to facilitate the incorporation of top researchers of any nationality into the universities and research institutions of Andalusia. Candidates must hold a PhD degree obtained not earlier than 5 nor later than 12 years before the date of publication of this call in the Official Gazette. Please, check the aforementioned webpage for information on salary, research costs, profiles and research lines. Deadline for the submission of applications is 04/08/2020. Our lab (www.evoflor.org) at the Estación Experimental de Zonas Ãridas (http://-www.eeza.csic.es) is offering the following two complementary research lines:

(1) Phenotypic plasticity in floral signalling and rewards and its effects on pollinator networks.

Phenotypic plasticity (PP) is a pervasive feature of life. Although it has been profusely studied in plants, and many traits are already known to be plastic, how PP in key floral traits influences ecological networks remains largely unexplored. Our lab works with Moricandia (Brassicaceae), an arid plant that exhibits within-individual floral plasticity fostering a significant shift in pollination niche. During the mild spring, it produces large, cross-shaped, UV-reflecting lilac flowers attracting mostly long-tongued large bees. During the hot and dry summer it produces small, rounded, UV-absorbing white flowers attracting many generalist pollinators. Here, we offer a postdoctoral position to explore the occurrence of PP in some floral signalling and rewards critical to understand these observed changes in the interaction with pollinators. Specifically, the goal of this position is to study the within-individual PP in nectar and pollen production as well as in floral volatile emissions, and to quantify how these plastic changes modify the visitation rate, behaviour, and effectiveness of main pollinators. This information will be fundamental to understand how PP reshapes pollinator networks and help plants to cope with changing environments.

(2) Phenotypic plasticity in photosynthetic metabolism in arid plants: its role to cope with climate change.

Phenotypic plasticity (PP) is a pervasive feature of life, pivotal to understand the ecology and evolution of most organisms. Although PP has been profusely studied in plants, and many traits are already known to be plastic, one important aspect remaining largely unexplored is the PP in photosynthetic metabolism. And this happens despites it could shed light on how plants cope with global change. Our lab works with Moricandia (Brassicaceae), an arid plant group with a peculiar C3-C4 photosynthetic pathway that faces two contrasting climatic conditions, mild during spring and dry and hot during summer. Because of this strong change in environmental conditions, the plants exhibit within-individual PP for several floral and vegetative traits. But little is known about how the photosynthetic metabolism respond to this change in conditions, although it is probably key to understand how plants may keep active during the harsh summer. Here, we offer a postdoctoral position to explore this phenomenon. Specifically, the position will be focused on disentangling the physiological, anatomical and genetic mechanisms underlying the seasonal change in photosynthetic metabolism. This research will be crucial to understand how plants can face harsh environments and respond to present-day anthropogenic perturbations and future climate change scenarios.

For further information on this research: Gomez et al (2020) Within-individual phenotypic plasticity in flowers fosters pollination niche shift. Nature Communications, in press.

The potential candidates should have a track record in evolutionary biology, experimental ecology, ecophysiology, ecology of interactions, plant physiology, or plant genetics, and should have interest and knowledge in the interactions between plant and pollinators and on plant signalling and rewarding traits (line 1) or in the comparative study of C4, C3-C4 and C3 photosynthesis from one of these general approaches: the physiological, molecular and evolutionary one (line 2).

Prospective candidates may contact Jose Maria Gómez (jmgreyes@eeza.csic.es) and Cristina Armas (cris@eeza.csic.es).

Dr José M. Gómez Estación Experimental de Zonas Aridas (EEZA-CSIC) Ctra Sacramento s/n La Cañada de San Urbano 04120 Almería, Spain

Tel.: +34 634 531859 Web: www.evoflor.org Web EEZA-CSIC: www.eeza.csic.es Luis Navarro <lnavarro@uvigo.es>

SQuID Norway StatisticalBiodiversity

The international working group SQuID (Statistical Quantification of Individual Differences; https://github.com/hallegue/squid) and the Center for Biodiversity Dynamics at the Norwegian University of Science and Technology (https://www.ntnu.edu/cbd) is seeking to hire a POSTDOCTORAL SCHOLAR to join us for 19 months in augmenting three SQuID activities: 1. Developing new biological understanding by blending the statistics of linear mixed models with simulations of biological processes affecting real data; 2. Refining in-person workshops focused on teaching applications of linear mixed models; and 3. Expanding remote or on-line educational materials.

Please read more here on position and how to apply:

http://www.behavioural-ecology.bio.lmu.de/news/index.html

Best wishes,

Anne Charmantier for the members of SQuID:

Hassen Allegue: UQAM, Montreal, Canada Yimen Araya-Ajoy: NTNU, Trondheim, Norway Anne Charmantier: CNRS, Montpellier, France Barbara Class: USC, Sunshine Coast, Australia Eduardo da Silva dose Santos: USP, Sao Paulo, Brazil Niels Dingemanse: LMU, Munich, Germany Ned Dochtermann: NDSU, Fargo, ND, USA Laszlo Garamszegi: IEB, Budapest, Hungary Kate Laskowski: UC-Davis, Davis, CA, USA Shinichi Nakagawa: UNSW, Sydney, Australia Denis Reale: UQAM, Montreal, Canada Holger Schielzeth: University of Jena, Germany Celine Teplitsky: CNRS, Montpellier, France David Westneat: UKY, Lexington, KY, USA Jon Wright: NTNU, Trondheim, Norway

Anne.CHARMANTIER@cefe.cnrs.fr

TUGraz RegulatoryGenomics

The Institute of Biomedical Informatics at TU Graz (https://www.tugraz.at/institute/bioinfo/) is inviting applications for a 6-year postdoctoral position.

We are looking for a highly motivated molecular biologist experienced with Oxford Nanopore Technologies (https://nanoporetech.com/) to work in the field of regulatory genomics.

To be eligible to apply for this position, candidates should have: - Completed doctoral studies or equivalent in molecular biology, genetics, biochemistry, biotechnology, or a similar field. - Practical laboratory experience sequencing with Oxford Nanopore Technologies. - Profound knowledge and practical laboratory experience in the field of molecular genetics (DNA extraction and amplification, library preparation, cloning, qRT-PCR, etc.).

The successful candidate will develop, engineer, and re-design biological nanopores to identify and characterize regulatory elements as well as detect epigenetic modifications in eukaryotic genomes.

For details, please see:

https://www.tugraz.at/institute/bioinfo/news/vacancies/ “Taher, Leila” <leila.taher@tugraz.at>

TulaneU MimulusEvolution

Postdoctoral Scholar, Ecology & Evolutionary Biology

Tulane University: Ecology Evolutionary Biology

Location

New Orleans, LA.

Start Date

September 1st, 2020 or Flexible

Description

A post-doctoral scholar position is available immediately in the Ferris Lab to work on NIH funded work related to the genetic and phenotypic basis of adaptation and speciation in Monkeyflowers (Mimulus). The Ferris Lab, located in the Department of Ecology and Evolutionary Biology at Tulane University, values diversity in all forms and is committed to fostering a supportive, inclusive, and welcoming work environment. Applications from candidates passionate about diversity, equity, and inclusion with overlapping scientific interests are encouraged to apply.

Possible projects include (1) a long-term field study in the Sierra Nevada, CA to examine spatially and temporally varying phenotypic and genomic selection, (2) mapping the genetic basis of parallel evolution within and between species, (3) examining the genomic basis of local adaptation and phenotypic plasticity, and (4) investigating the genetic and phenotypic basis of adaptation and reproductive isolation with gene flow in sympatric species. Applicants with a background in some of the following are especially encouraged to apply: evolutionary biology, genomics, quantitative or population genetics, and ecological field research.

The earliest start date is September 1st, 2020, but this is flexible given the current pandemic and a remote "ghost-doc" start could be worked out. The position would be for three years (contingent upon annual review at year 1) with the possibility of further extension. The starting salary is $50,004/year + full benefits.

The Department of Ecology and Evolutionary Biology at Tulane is a diverse and welcoming community of scientists with excellent scholarship across a wide range of ecological and evolutionary topics. Tulane is a private, research one university and a member of the 63 prestigious Association of American Universities. Tulane is a collegial, collaborative, and stimulating environment for learning and research and is ranked among the top 40 universities by US News Report. New Orleans is a beautiful, vibrant, multicultural, and truly unique city in which to work and live.

Qualifications

Required:

PhD in one of these fields: Ecology and Evolutionary Biology, Plant Biology, or Genetics/Genomics.

Preferred:

Experience working with genomic data, a strong conceptual background in evolutionary biology, especially relating to population and/or quantitative genetics, experience with field work.

Application Instructions

To Apply Submit the below to kferris@tulane.edu:

- One page Cover Letter
- C.V.
- A relevant publication or manuscript in preparation
- Contact information for 2 References

Applications will be considered until the position is filled.

Informal inquiries about the position are encouraged: kferris@tulane.edu

Katie Ferris <kferris@tulane.edu>

UAberdeen ClimateAdaptation

A team led by Lesley Lancaster (Aberdeen, UK), Greta Bocedi (Aberdeen, UK),Rachael Dudaniec (Macquarie, Australia), Maren Wellenreuther (Plant and Food Research, New Zealand), Bengt Hansson (Lund, Sweden), and Erik Svensson (Lund, Sweden) is seeking to host a Marie Curie postdoctoral fellow in Aberdeen to studyparallel adaptation to climate during range expansion. The post requires backround in population genetics. We have already drafted a preliminary proposal, which will require minimal editing before submission,and we are looking for a motivated candidate to take the work forward in their own way. We, as a team, are prepared to offer suitable candidates full support and collaboration in adapting the draft proposal for the MSCA fellowship application format, with a deadline of **September 9, 2020**. Please contact Lesley Lancaster at lesleytherese@gmail.com for more details on the project and to express interest in this exciting research opportunity. See also the associated hosting offer on Euraxess:https://euraxess.ec.europa.eu/jobs/-hosting/marie-sklodowska-curie-individual-fellowships-if-parallel-adaptation-climate-during A justification and summary of the proposal is as follows:

"The poleward movement of generalist species in the Anthropocene is a major cause for concern, and indeed represents one of the outstanding ecological problems to address in the 21stcentury. This accelerating phenomenon, originally documented in the 20thcentury, has now been described repeatedly from diverse taxa, across latitudinal gradients and in nearly every type of ecosystem. Poleward-moving species often replace native biodiversity, resulting in large scale biotic homogenisation of the world's ecoregions, and also result in novel pests and disease vectors at higher latitudes, posing risk to food security and human health. Range shifting species are particularly problematic for freshwater ecosystems, which are among the most threatened globally, with many endemic, high latitude species currently facing new patterns of competition from range-expanding generalists (including our selected model species, the damselflyIschnura elegans,with its highly competitive, predatory aquatic larval stage). Why do poleward-moving species often possess generalist phenotypes that allow them to outcompete natives and destabilising ecosystems? The traditional, although largely empirically unsupported, assumption is that expanding species have always been generalists in their native range, and generalists are simply more likely than specialists to undergo range shifts. However, a wealth of previous studies have failed to find that niche breadth at any particular location in the native range reliably predicts successful range shifts. Moreover, it is already well-documented that niche traits often rapidly evolve during colonisation. Our previous pioneering work suggests that the rise of range-expanding generalists observed across ecosystems today has resulted from changes in niche breadth and plasticity which evolve during the process of colonisation. However, the underpinning mechanisms remain to be elucidated. * The time is now ripe to understand how iterative evolutionary processes during colonisation drive the evolution of generalist syndromes during species range shifts.* Enabled by our extensive resources and data, this project will tackle major outstanding questions about evolution of the climate niche during range shifts: 1) How repeatable are genomic responses to novel thermal environments during colonization? 2) What is the role of standing genetic variation vs. new mutations in this process? 3) How do gene interactions and developmental plasticity underpin changes in niche breadth evolve in colonizing populations? 4) Do patterns of neutral or adaptive genetic variation generated at the range front enable future adaptive evolution, and which process dominates? 5) What are the genetic mechanisms underpinning greater evolvability and plasticity of cold tolerance during range shifts, in contrast to heat tolerance? 6) What underpins greater evolvability of heat tolerance, in comparison to cold tolerance? We are uniquely enabled by our past research and extensive genomic and phenotypicdatasets to disentangle these mechanisms across replicate spatial expansion gradients and replicate temporal sampling times, and thus will be able to generate rigorously validated answers to these important questions. Using a robust, parallel design, we propose to elucidate the genetic processes underlying adaptive evolution of climate tolerances during species' range shifts to higher latitudes. This research will lead to a step change in our understanding of how niche traits evolve under non-equilibrium conditions (i.e., during colonisation), and provide detailed, empirically

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UArizona EvolutionaryBiol

Postdoc ad in evolutionary biology

The Michod lab in the Department of Ecology and Evolutionary Biology at the University of Arizona invites applications for an NSF-supported Postdoctoral Fellow position anticipated to begin this Fall (depending on COVID-19 and the University of Arizona re-entry plan). The general topic of the project is the evolutionary transition from unicellular to multicellular life. Evolution by natural selection requires heritable variation in fitness at the individual level. During evolutionary transitions in individuality, such as the transition from unicellular to multicellular organisms, fitness must be remapped from the cell level to the level of the multicellular group. The general goal of the project is to determine how a new genotype-phenotype map arises at the cell-group level, when initially the map is present only at the cell level. The methods used in our work involve lab experiments with volvocine green algae, comparative phenomics and genomics, molecular biology, mathematical models, computer models and philosophical analysis. More information about our work can be found at http://michodlab.arizona.edu/ or https://www.researchgate.net/profile/Richard_Michod . We are especially interested in candidates with molecular biology skills, such as gene expression, gene knockout and CRISPR, to investigate the genetic basis for group formation and somatic cell development in the volvocine green algae. We encourage applications from candidates who have recently completed, or will soon complete, their PhD.

Yearly renewal of the position is possible. Yearly salary will likely be in the $45,000 range, depending on experience and availability of funds.

To apply, email the following to Rick Michod (michod@arizona.edu) with the subject line "NSF Postdoc application: [Your full name]:" (i) A letter briefly explaining what interests you about this project. (ii) A curriculum vitae, including a full list of publication. Pre-print articles can be included. (iii) A one-page research statement describing your research experience and future research interests. (iv) Contact information for three references.

Please contact Rick Michod (michod@arizona.edu) for any questions. Informal inquiries are welcome.

At the University of Arizona, we value our inclusive climate because we know that diversity in experiences and perspectives is vital to advancing innovation, critical thinking, solving complex problems, and creating an inclusive academic community. As a Hispanic-serving institution, we translate these values into action by seeking individuals who have experience and expertise working with diverse students, colleagues, and constituencies. Because we seek a workforce with a wide range of perspectives and experiences, we provide equal employment opportunities to applicants and employees without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, protected veteran status, or disability. As an Employer of National Service, we also welcome alumni of AmeriCorps, Peace Corps, and other national service programs and others who will help us advance our Inclusive Excellence initiative aimed at creating a university that values student, staff and faculty engagement in addressing issues of diversity and inclusiveness.

"Michod, Rick - (michod)" <michod@arizona.edu>

UBritishColumbia EvolutionaryBiology

The Mank lab at the University of British Columbia is looking for a new post-doctoral fellow to join our group of evolutionary biologists! The exact topic is open and will be determined by the interests of the successful candidate. We are looking for someone who brings new skills and perspectives into the group, but who also has research interests that align with current work in the lab (https://www.zoology.ubc.ca/mank-lab/research/). Potential approaches could include molecular evolution, recombination, genetic knockouts, field work, or pretty much anything else of relevance to the evolution of sex chromosomes, sex-biased gene expression or sexual dimorphism. Informal questions can be emailed to Judith (mank@zoology.ubc.ca). If you wish to apply, please send a cover letter describing your career goals and research philosophy, CV, a statement of your interests and the contact details of three references as a single PDF to Jacelyn Shu (jacelyn@zoology.ubc.ca). The post is funded through a Canada 150 Research Chair, and the initial appointment is for one year with possibility of extension. Start date is negotiable, and remote work is possible initially in the event of travel restrictions. The review of applications will begin on August 17 2020, and will continue until the position is filled.

The lab is a diverse, highly interactive group, and we value a constructive and collaborative environment. We have recently finished installing a brand new, state-of-the-art molecular lab, including the capability for single-cell RNA-Seq. We also have new fish labs with high-density flow-through racks for pedigrees and selection experiments. We have stocks of several Poeciliid species available, although work on them is not a requirement of the job! The UBC Biodiversity Centre (https://biodiversity.ubc.ca/) and Department of Zoology (https://www.zoology.ubc.ca/) form an outstanding community of evolutionary biologists and ecologists, and Vancouver is a beautiful and welcoming city with a multitude of outdoor and cultural opportunities.

Judith Mank Professor of Evolutionary Genomics Department of Zoology and Biodiversity Research Centre University of British Columbia

http://www.zoology.ubc.ca/mank-lab/
mank@zoology.ubc.ca

UCalifornia Davis EcologicalGenomics

Postdoctoral researcher in ecological genomics of marine invertebrates Application review begin date: August 20, 2020 (applications will be accepted until position is filled)

SUMMARY: We are seeking a postdoctoral researcher with expertise in ecological genomics, population genetics, and/or marine evolution and ecology for a collaborative project with Professors Rachael Bay, Rick Grosberg, and Eric Sanford in the Department of Evolution and Ecology at UC Davis.

The postdoctoral researcher will work on an NSF-funded project investigating the evolutionary and ecological dynamics of range expansion in owl limpets (Lottia gigantea). During the recent marine heatwaves along the Pacific coast of North America, populations at the northern range limit of L. gigantea in northern California have expanded, with ongoing reproduction even after subsidence of the heatwave events. We plan to integrate individual tracking data we have been collecting in northern populations with range-wide genomic data and experimental phenotyping of larvae and juveniles to understand patterns of selection and gene flow that facilitate or impede geographic range expansions.

The postdoc would work closely with a team of faculty, graduate students and undergraduates. The postdoc would be based on the UC Davis campus, but the position could also involve field and/or laboratory work at the Bodega Marine Lab and along the coast of California. The postdoc will be encouraged to develop their own research project that furthers our understanding of ecological genomics in marine systems. The postdoc will be part of a broader community of ecologists, evolutionary biologists, and marine scientists within the Department of Evolution and Ecology, the Center for Population Biology, and the Coastal and Marine Sciences Institute.

QUALIFICATIONS: - A Ph.D. in Evolution, Ecology, or a closely related field - Experience using bioinformatic pipelines to analyze genetic or genomic data - Demonstrated ability to follow through on project deliverables and communicate findings in high quality peer-reviewed journals - Strong statistical skills and demonstrated proficiency with R or another statistical program - Attention to detail, as evidenced by prior research - Preferred experience with marine organisms

SALARY: Salary and benefits are consistent with UC Davis policy and applicant experience. See link for current salary scale: https://grad.ucdavis.edu/-sites/default/files/upload/files/facstaff/salary_19-20_march_1_2020.pdf TO APPLY: Interested candidates should submit (1) a CV, (2) the names and contact information for three potential references, and (3) a cover letter explaining the candidate's interest in the position and how their past research and future research goals fit within the position. All materials should be submitted in PDF format by email to rbay@ucdavis.edu, with the subject header "Ecological Genomics Postdoc." Applications received by August 20 will receive full consideration, but the position is open until filled. The position is available immediately, but flexibility in this start date is possible for the ideal candidate. Questions about the position should be directed to Rachael Bay <rbay@ucdavis.edu>. The University of California is an affirmative action/equal opportunity employer with a strong institutional commitment to the development of a climate that supports equality of opportunity and respect for differences.

Rachael Bay <rachaelbay@gmail.com>

UCalifornia Merced ComparativePopGenomics

We are looking for a highly motivated Postdoctoral Scholar to join our lab to lead multi-species 'community genomic' analyses across a dozen coastal marine taxa with the goal of understanding variation in susceptibilities to environmental change, species interactions, and the extent to which (and why) the historical demographies of interacting species in key habitats have been individualistic or concerted.——

As the project postdoc, you will play a central role in our multi-institutional marine networks (MariNet) consortium that brings together a collaborative of investigators from across California to produce an understanding of genomic diversity that scales from individuals to ecosystems.

Your principle role will be in bioinformatics curating and using multiple reference quality genomes and wgs population genomics datasets to understand between and within species differences that drive community-level responses and undertaking synthetic analyses with the marine consortium.——

The project contributes to the $10 million California Conservation Genomics Project < https://sites.lifesci.ucla.edu/eeb-CCGP/ > a state-funded initiative to provide officials with the scientific basis for confronting climate change.

More information on this and related positions is available at the lab's website http://mnd.ucmerced.edu/Info/ON.html A full description of the position and how to apply is available at https://aprecruit.ucmerced.edu/JPF01003 Review of applications will begin Monday, 03 August 2020.—

Enquiries to Mike Dawson at—mdawson@ucmerced.edu

mdawson@ucmerced.edu

UCalifornia SanDiego HostMicrobeEcoEvo

A post-doctoral position is available in the Jackrel Lab at UC San Diego. Start date is flexible. The position is available for one year, and renewable for up to three years dependent on progress. Our lab studies how ecological interactions and ecosystem functions are affected by intraspecific variation, including plasticity, genetic variation, and variation imparted by host-associated microbes. Multiple research topics falling within this theme are available and dependent on the interests and expertise of the applicant. Review of applications will begin immediately until the position is filled.

Please see the job ad for more details: https://biology.ucsd.edu/jobs/postdoc.html#How-ecological-interactions-and "sjackrel@UCSD.EDU" <sjackrel@UCSD.EDU>

UConnecticut ComputationalGenomics

Postdoctoral Scholar - Computational Genomics - Deep Learning for Genome Annotation

The Plant Computational Genomics laboratory at the University of Connecticut (Storrs, CT) has an opening for a Postdoctoral Scholar. This individual will take a lead role in the development of EASEL (Efficient, Accurate, Scalable Eukaryotic modeLs), an integrated and accessible deep learning framework to improve the annotation of eukaryotic genomes. This software will provide an efficient and flexible approach, encompassing the full workflow from repeat identification through gene model annotation. EASEL will improve the accuracy of evidence-based and ab initio-derived gene models for organisms with limited or extensive external genomic evidence. The final product will be implemented as stand-alone software, within open-source community platforms, and compatible with HPC systems. We are committed to developing mechanisms for cross-platform data/application sharing that builds on existing efforts with Galaxy (usegalaxy.org), the Tripal platform (tripal.info < http://www.tripal.info/ >), and cloud-based HPC.

The successful candidate will work as part of an interdisciplinary team. They will also work closely with existing genome assembly and annotation projects that represent tremendous organismal diversity. EASEL will be integrated into large-scale international efforts to annotate genomes. As such, the scholar will provide high quality genome annotations for a large network of collaborators through the development cycle. The candidate should have experience with genomic/transcriptomic data, machine learning, and software development. Experience with genome annotation is ideal. The successful candidate will also be involved in training end users and leading publications.

The qualified applicant will have a PhD degree in Bioinformatics, Evolutionary Biology, Computational Biology, Genetics, or a related field. Biology/Bioinformatics experience is essential and previous experience with software development is desired. The applicant should have experience with Linux/Unix, scripting languages (Python), R, and machine learning. The position is renewable after the first year, for up to three years. As a result of the pandemic, the successful candidate can start work remotely.

The Plant Computational Genomics Lab (http://plantcompgenomics.com/) is part of the Department of Ecology and Evolutionary Biology and is closely linked with the Institute for Systems Genomics. Our lab is highly collaborative, multi-disciplinary, and inclusive. Diversity, creativity, integrity, and ambition are values we affirm. We are committed to open and inclusive science. This includes transparency in data acquisition, analysis, and code.

Interested applicants, Please send the following THREE documents: cover letter, research statement, and CV to: Jill Wegrzyn at jill.wegrzyn@uconn.edu

Applications will be accepted until the position is filled. Location: University of Connecticut, Storrs, CT, USA Start Date: ASAP Duration: Full-time

jill.wegrzyn@uconn.edu

UCopenhagen AncientDNA

Postdoc in computational ancient environmental DNA at the Globe Institute, University of Copenhagen We are offering a Postdoc position in computational ancient environmental DNA commencing 15 October 2020 or as soon as possible hereafter.

The successful candidate will be part of the Copenhagen group of the ERC Synergy project, Seachange, in which a cross-disciplinary approach is adopted to assess the impact of major cultural transitions on marine ecosystem functioning and biodiversity. Apart from ancient environmental DNA analyses, the overall project includes classical zooarchaeology, isotope analyses, dating methods, marine historical ecology and ecosystem modeling. You will play an active role in the overall Seachange project. In the Copenhagen group, you will work alongside and train a PhD student, specifically on metabarcoding and shotgun sequencing of environmental DNA time-series in midden, bulk-bone and/or marine sediment core samples from Australia, Antarctica and/or Iceland. The main focus will be on creating bioinformatic workflows for sequence data processing and on ecological analyses of the generated environmental DNA time series data in relation to cultural transitions at one or more sites. You will also work on modelling and simulating eDNA time-series data and exploring the use of such data in population genomic studies. Another major task in the project would be to develop methods, and use current methods, to integrate the data from the different disciplines in the overall Seachange project. Ideally, you will take some part in field work and data generation. Within this overall framework, you will have some freedom to design your own project in consultation with the advisors.

Further details: https://employment.ku.dk/all-vacancies/?show=3D152132 Best wishes,

Kristine < kbohmann@sund.ku.dk >

kbohmann@sund.ku.dk

UCopenhagen MutualisticNetworks

Postdoc in Island biogeography of mutualistic networks in the Anthropocene at GLOBE Institute, University of Copenhagen, Denmark We are looking for a highly-motivated and dynamic researcher for a 3 year postdoc position, commencing 1 January 2021.

Our group and research The successful candidate will be part of the Dalsgaard Group (https://globe.ku.dk/-research/cmec/dalsgaard-group/) within the Center for Macroecology, Evolution and Climate (CMEC) at the GLOBE Institute. CMEC is a center of excellence with a cross-disciplinary research program. We offer creative and stimulating working conditions in a dynamic and international research environment addressing fundamental questions on the origin, maintenance, conservation and future of life and biological diversity on Earth. The 40+ researchers at CMEC currently represent 14 different nationalities and the working language is English. The center juxtaposes faculty staff scientists from the fields of macroecology, historical biogeography, oceanography, evolutionary biology, community ecology, population biology, climate change research, conservation biology and environmental economics.

Project description and your job This project is novel in integrating island biogeography theory and theories on how climate and anthropogenic pressures influence mutualistic plant-pollinator and seed-disperser interactions. The project combines field work data collected in the Caribbean with network analysis and biogeographical modelling. Your tasks would be to work closely together with a PhD-student to jointly lead data collection across numerous islands in the Caribbean. You should be prepared to collect data for approximately 4-5 months in both 2020 and 2021. You would be expected to first-author several papers in international peer-reviewed journals. In addition to the postdoc position, we will hire a PhD-student and a cohort of MSc students will participate in the project. All project partners will gather once a year to run workshops with the aim of publishing review and synthesis papers. You would also be expected to assist in teaching and supervise MSc student thesis projects. The project is funded by Independent Research Fund Denmark.

Principal supervisor is Associate Professor Bo Dalsgaard, Center for Macroecology, Evolution and Climate, GLOBE Institute, bo.dalsgaard@sund.ku.dk, Direct Phone: +45 42324553. Co-supervisors and project partners are Senior Lecturer Christopher Kaiser-Bunbury and Research Fellow Benno I Simmons (University of Exeter, UK) and Professor Mauro Galetti (University of Miami, USA).

Start: 1 January 2021

Duration: 3 years

Apply here: https://employment.ku.dk/faculty/?show=152203 Bo Dalsgaard <bo.dalsgaard@sund.ku.dk>

UExeterCornwall VirusHostShifts

Apply and full info https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=045735TDF4&WVID=3817591jNg&LANG=USA Postdoctoral Research Fellow to conduct research on host-pathogen interactions working with Wellcome Trust Sir Henry Dale research fellow Dr Ben Longdon, at the University of Exeter, Penryn campus.

This full time post is available on a two year fixed term contract, with the possibility of extension.

About the role

Host-parasite interactions offer fascinating opportunities to study coevolution, local adaptation and rapid evolutionary change. Our work uses a unique experimental system of up to 50 species of Drosophila and naturally occurring RNA viruses to ask fundamental questions about pathogen host shifts 'V where a pathogen jumps from one host species to another. Host shifts are a major source of emerging infectious diseases, with HIV, Ebola virus and SARS coronavirus having all jumped into humans from other host species. By taking a comparative approach, with a strong set of hypotheses from ecological and evolutionary theory, we can provide insights into the factors underlying host shifts that will be generally applicable to any group of hosts or viruses.

Understanding pathogen host shifts is critical, especially in light of environmental change. Our model system has provided key insights into host shifts, namely the importance of genetic similarity between hosts. Based on work in Drosophila melanogaster, we know the interactions between host antiviral immunity and the ability of the virus to supress this immune response, can play a role in explaining differences in susceptibility. The initial aim of the postdoc is to examine why viruses can infect some hosts and not others by looking at how the viral suppressor of immunity functions in different host species, and how this influences patterns of susceptibility across the host phylogeny, but there are many opportunities to develop new projects to explore the ecology and evolution of pathogen host shifts.

Applicants will possess a relevant PhD or equivalent qualification/experience in a related field of study.

The successful applicant will be responsible for leading experimental work, data collection and analysis, working closely with the PI and collaborators. The post will be based at the University of Exeter in the internationally excellent Centre for Conservation and Ecology https://www.exeter.ac.uk/cornwall/research/facilitiesandcentres/cec/. The centre has a huge number of researchers working in ecology and evolution, including a large group of researchers working on host-parasite interactions (including Prof Angus Buckling, Prof Camille Bonneaud, Prof Edze Westra, Prof Robbie McDonald, Dr Alex Hayward and Dr Stineke Van Houte) and provides an exciting and stimulating research environment.

To view the job description, please refer to the attached document above.

Please highlight in your cover letter why you would like to work in our group (www.benlongdon.com), why you are interested in this project, and how your skillset/experience is relevant. If you think you might be a great fit for this position but are unsure on whether you have relevant experience, please get in touch.

“Longdon, Ben” <B.Longdon2@exeter.ac.uk>

UGlasgow GenomicsReproductiveMode

We have a research opportunity open at the University of Glasgow’s Institute of Biodiversity, Animal Health & Comparative Medicine (IBAHCM) working in the Evolutionary Analysis Group and the research team of Kathryn Elmer (http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kathrynelmer/) in collaboration with Oscar Gaggiotti at University of St Andrews (https://risweb.st-andrews.ac.uk/portal/en/persons/oscar-eduardo-gaggiotti(43985656-390b-478e-b9a7-05fe88181e46) The project is primarily based at Glasgow with research periods based at St Andrews supported.

We are seeking a motivated, creative and enthusiastic postdoctoral researcher for a project on the genomic basis of oviparous and viviparous reproductive modes, funded by The Leverhulme Trust. This project will apply advanced statistical analyses to population-wide whole genome sequences to identify regions of the genome that show signals of response to selection, the molecular targets of that selection (genes, gene functions, and biological pathways), and genetic units fundamental to egg-laying vs live-bearing. The research model is the common lizard, which is a fascinating and unusual species because it is reproductively bimodal.

A strong track record of genetic and evolutionary research is necessary, and on vertebrates is a benefit. Bioinformatic experience with NGS data is required and expertise in whole genome analysis is preferred. Skills in quantitative trait mapping, comparative genomics, ecological and/or population genomics, statistics, and phylogenetics are also valuable. Lab work and fieldwork skills are not strictly required but would be advantageous. Team working and positive attitude are a must. Candidates must have completed their PhD by the start of contract. International applicants will be eligible for a UK work visa. We strive to be a supportive environment and welcome a diversity of applicants!

The position is for 3 years, with start date reasonably flexible. The position is open at grade 6 (early career postdoc) or grade 7 (more experienced postdoc).

IBAHCM is a stimulating and interactive research environment with a wealth of opportunities for discussion, collaboration and cutting edge research in evolution, ecology, and disease. The University of Glasgow ranks in the world's top 100 universities. The University and IBAHCM are both recognised with Athena SWAN awards. The city of Glasgow is lively and cultural, and sits on the doorstep of the great outdoors of the Scottish Highlands, islands, and coast.

The official job description and application requirements are available on the University of Glasgow homepage under current vacancies; http://www.gla.ac.uk/about/-jobs/vacancies/ at job reference 039224

The advertisement closes 7 August 2020.

Informal inquiries in advance are very welcome: kathryn.elmer@glasgow.ac.uk

Kathryn Elmer <Kathryn.Elmer@glasgow.ac.uk>

UGOE Germany BioinformaticsEvoDevo

PostDoc Position (1 year) in Bioinformatics at the Department of Developmental Biology of the Georg-August-University of Göttingen starting from November 1, 2020

Closing date for applications: August 23, 2020. For further information visit our website (https://www.posnien-lab.net/) or contact me via Email (nposnie@gwdg.de).

Background and aim of the project:

We study the evolution of Drosophila head shape and compound eye size (e.g. see doi: 10.1371/journal.pone.0037346) to contribute to a better understanding of the molecular basis of the morphological diversity. The PostDoc project will focus on interspecific differences in head development between D. americana and D. novamexicana and it builds on prior phenotypic and genetic data. The major aim of the project is revealing interspecific differences in developmental gene expression and chromatin accessibility using an already available extensive RNAseq and ATACseq dataset. Expression and accessibility data will be integrated with genome wide association mapping (GWAS) data (see doi: 10.1101/2020.03.24.005413) to link variation in gene regulation to phenotypic differences. Additionally, the impact of various inversions that are present between D. americana and D. novamexicana (see doi: 10.1093/gbe/evy239) on gene regulation and phenotypic differences will be tested.

Your profile:

- PhD in Biology, Bioinformatics or related fields
- Experience with Next Generation Sequencing (NGS) data is expected
- Background in Bioinformatics, Statistics and strong analytical skills is expected
- Experience with molecular biology (cloning, PCR) and/or Drosophila genetics is advantageous

What we offer:

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

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Nico Posnien

Georg-August-University Göttingen

Johann-Friedrich-Blumenbach Institute for Zoology and Anthropology

Department of Developmental Biology

Ernst-Caspari-Haus (GZMB)

Justus-von-Liebig-Weg 11

37077 Göttingen

Germany

NEW Phone: +49 (0) 55139 28662

E-mail: nposnie@gwdg.de

Website: < http://www.posnien-lab.net/ > http://www.posnien-lab.net

Twitter: @PosnienLab

nico.posnien@gmail.com

UGothenburg PlantPopulationGenomics

Postdoc in plant population genomics (Amazonia and/or Arctic)

https://www.gu.se/english/about_the_university/-job-opportunities/vacancies-details/?id=6238 Project description

Understanding which factors determine how a species responds to environmental change allows us to anticipate future shifts in community composition. Populations that experience severe stress, such as in the face of climate change, may avoid extinction through adaptation by natural selection. This process is known as evolutionary rescue and can provide a means for species conservation. Our objectives are to leverage plant genomic diversity to 1) infer population structure and genetic diversity, 2) determine adaptive potential to future predicted climate change, and 3) model the future spread of allelic variation and adaptive genotypes. Through a combination of existing common garden experiments and sampling from natural populations, together with genomics and ecological niche models, we aim to identify adaptive potential to climate change across scales and over time. Linking information about intraspecific genomic responses to climate will allow us to better predict population and species persistence under different future climate change scenarios. The project will likely involve a combination of field work at one or more Amazonian and/or Arctic locations, development of target sequence capture data, leverage of existing full genome data, and data synthesis using public databases.

The researcher will be hosted in the Department of Biological and Environmental Sciences under the supervision of Dr. Christine D. Bacon. There will be ample opportunity for collaboration with other scientists in the Biological & Environmental Sciences at the University of Gothenburg, as well as at Lund University. The project is linked to the strategic research area BECC (Biodiversity and Ecosystem services in a Changing Climate; http://www.becc.lu.se/). Job assignments

This employment includes the following tasks:

- conducting independent and collaborative research - responsibility for managing own workload - production of scientific articles - effective communication across the team and beyond - including in seminars and conferences, amongst others.

Eligibility

The applicant must hold a PhD degree in an area relevant for the tasks at hand e.g., genomics, biodiversity research, computational biology, or conservation. The exam must be finished before the closing date for this announcement. Assessments

We are seeking a highly motivated person to take a leading role in this project. The following skills are crucial for this employment:

- expert skills in programming languages such as R, Python, Bash - excellent communication skills in English, written and spoken

We will consider the following selection criteria for the applicant:

- previous scientific production (scientific publications and software, if applicable) - specialist skills (genomic informatics and analysis) - soft skills (communication, ability to collaborate, independence etc)

The application must be written in English and include:

- A cover letter briefly stating why you are applying for this position and why you would be a suitable candidate. Consider the selection criteria listed above for the applicant - A full list of qualifications (CV) including contact information to 2-3 potential referees - Certificate of PhD exam and other educations of relevance - Complete list of publications, including submitted and accepted manuscripts - Employments certificates and other documents deemed important by the applicant

The top ranked candidates will be selected for an interview, which will be held in English and could also be performed over Skype or Zoom.

– Christine D. Bacon

Senior Lecturer in Biodiversity University of Gothenburg Gothenburg, Sweden

Gothenburg Global Biodiversity Centre Box 461, SE 405-30 Göteborg, Sweden

Associate Researcher Universidad CES Medellin, Colombia

Christine Bacon <christinedbacon@gmail.com>

UIdaho QuantitativeGeneticModeling

Quantitative Genetics Modeling Idaho NSF-EPSCoR GEM3

A Postdoctoral Research Associate position is available at the University of Idaho in the NSF-EPSCoR GEM3 program. The successful candidate will be co-supervised by faculty Paul Hohenlohe and Adam Jones in the Department of Biological Sciences and interact closely with a state-wide team of interdisciplinary researchers.

The GEM3 program seeks to understand how genetic diversity and phenotypic plasticity affect species responses to environmental change, focusing on two taxa: redband trout and sagebrush. These taxa are integral to ecosystems in the American West and central to land-use management decisions that drive the regional economy. The selected candidate will build quantitative genetics models of the genetic and plastic basis of phenotypic traits in these taxa and their role in adaptive capacity and population responses to changing environmental conditions.

The position is part of an interdisciplinary cohort of postdoctoral researchers and Ph.D. students working at scales from genomics and physiology to landscape-scale mapping and monitoring of social-ecological systems. The quantitative genetics models will be informed by empirical data on trout and sagebrush being collected by other GEM3 researchers in common-garden experiments, genome-wide association studies, and other projects. The position will have substantial opportunity for project development and collaboration across the GEM3 program, with potential opportunities for teaching, mentoring graduate and undergraduate research, and engagement with stakeholders.

This is planned as a three-year position, with the second and third years contingent on performance and availability of funding. The successful candidate will interact closely with members of the Institute for Modeling Collaboration and Innovation (IMCI; https://www.imciuidaho.org/) and the Institute for Bioinformatics and Evolutionary Studies (IBEST; https://www.ibest.uidaho.edu), as well as GEM3 faculty, postdocs and students at the University of Idaho, Idaho State University and Boise State University. The University of Idaho is located in Moscow, a friendly mid-sized town on the rolling hills of the Palouse, with great parks, bike paths, restaurants, farmer's market and fantastic opportunities for recreation in the adjacent mountains and rivers. It is only eight miles from Washington State University in Pullman, Washington, providing an academically and culturally rich community. For more information about the community and university, go to https://visitmoscowid.com/ . Minimum qualifications include: a Ph.D. in biological sciences, mathematical biology, or a related discipline; experience with population genetics or quantitative genetics demonstrated by publications in the field; ability to work as part of a multi-disciplinary team; evidence of strong written and oral communication skills. Experience with mathematical modeling or computer programing are desirable.

Our research program is collaborative, supportive, and open to all. We strongly encourage members of underrepresented groups to apply for this position, and please contact us for more information.

Apply at: https://uidaho.peopleadmin.com/postings/29101 Review of application will begin August 3.

The University of Idaho is an equal opportunity/Affirmative Action/equal access employer.

GEM3 program < https://www.idahogem3.org/ > Paul Hohenlohe < http://hohenlohelab.github.io/ > Adam Jones < https://pipefishguysite.wordpress.com/ > Department of Biological Sciences < https://www.uidaho.edu/sci/biology >

Paul Hohenlohe Associate Professor University of Idaho http://hohenlohelab.github.io "Hohenlohe, Paul (hohenlohe@uidaho.edu)" <hohenlohe@uidaho.edu>

UIllinois UC FishPopGenomics

Postdoctoral Research Associate Population Genomics of Big River Fishes Illinois Natural History Survey Prairie Research Institute University of Illinois at Urbana-Champaign

Description

The Illinois Natural History Survey is seeking a Postdoctoral Research Associate to assist with a population genomics assessment of big river fishes in the Upper Mississippi River. The two-year position will primarily be laboratory based, though with occasional opportunities for field work. The project is a component of the Upper Mississippi River Restoration Program Long Term Research Monitoring, and the objective is to combine population genomics, otolith microchemistry, and vital rate estimation to inform restoration and management of fish populations in the Upper Mississippi River System. Specifically, the successful applicant for this position will generate, analyze, and interpret population genomic data for over 2000 specimens across 8 big river fish species. Further, the post-doc will lead the dissemination of this research via technical reports, peer-reviewed manuscripts, and presentations at regional and national scientific meetings.

The associate will work under the direction of Mark Davis, work closely with INHS scientists Jim Lamer and Milton Tan, and collaborate with researchers working in the Collaborative Ecological Genetics Laboratory. The position is based in Champaign, Illinois, on the University of Illinois Urbana-Champaign campus, where the successful applicant will join an interdisciplinary community of researchers, graduate students, and technicians. Funding for the position is guaranteed for two years.

Major Duties and Responsibilities:

- Coordinate with project collaborators on sample transfer, and assist with inventorying, databasing, and managing incoming samples - Lead the extraction and quantification of DNA, and preparing libraries of population genomic data via Restriction-site Associated DNA sequencing (RADseq) - Work closely and coordinate efforts between state, federal, and University partners associated with the project. - Analyze data, synthesize results, write annual technical reports, and lead the preparation of multiple manuscripts for submission to peer-reviewed scientific journals. - Assist in training and mentorship of graduate and undergraduate student partners. - Disseminate research findings to management agencies, the scientific community, and general public through presentations at professional meetings, written reports, and public outreach activities - Ensure the safety of staff and equipment. - Respond to requests for scientific/technical information and communicate effectively with collaborators. - Participate in community outreach and service events, and mentor hourly staff - Keep abreast of developments in this discipline - Perform other duties as needed in order to further the mission and goals of the Survey, PRI, and the University of Illinois

Qualifications

Applicants should have a Ph.D. (within the last 10 years or by the start date) with extensive experience in population genomic data generation and analyses with particular expertise in RADseq data analytics. Alternate degree fields in ecology or natural sciences will be considered depending on the nature and depth of the experience at it relates to this position. Applicant should possess strong analytical skills and proficiency with R, command line, python, and modern bioinformatics pipelines for RADseq data. Applicants with experience fish population genomics are preferred.

Experience

A minimum of three years conducting population genomics research on fish and/or wildlife. Must be able to write clearly and scientifically as demonstrated through prior publications. Must possess excellent organizational, interpersonal, oral and written communication skills. Ability to apply analytical/scientific thinking to define and solve problems. Ability to work independently, collect and analyze population genomic data, and coherently communicate findings (verbally and in writing) to granting agencies and to scientific and public communities. Experience managing and analyzing "Big Data" sets is a preferred. Skills in effective communication, personal relations, collaboration, organization, teamwork, and leadership are required. Demonstrated ability to perform effectively in a diverse and fast-paced work environment under stringent deadlines with minimal supervision. Attention to detail, sound judgment, and strong conflict resolution skills are required. Must have valid driver's license.

Salary and Appointment

Funding for the position is guaranteed for two years, with a salary of $48,000 plus benefits.

Application

For full consideration, applications should be received by September 1,

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UKentucky HostEndosymbiontEvolution

The project ’V Many arthropods are infected with bacterial endosymbionts that confer a variety of phenotypic effects on their hosts. We are seeking a postdoctoral scholar to conduct research on symbiont interactions in a species of Linyphiid spider, Mermessus fradeorum. This spider is infected by up to 5 different strains of inherited symbiont, which result in different reproductive anomalies for the host depending on which combination of symbionts are present. A newly funded, 4-year research project will explore the interface between symbiont interactions within a host, and interactions among differentially infected spiders in the population. This project is a collaboration among Dr. Jen White < https://entomology.ca.uky.edu/person/jennifer-white > and Dr. Jeremy Van Cleve < http://vancleve.theoretical.bio > at the University of Kentucky, as well as Dr. Yuval Gottlieb-Dror < http://ksvm.agri.huji.ac.il/staff/gottliebdror_yuval.htm > at the Hebrew University of Jerusalem.

The postdoctoral researcher ’V They will be primarily responsible for designing, executing, and analyzing long-term laboratory population and selection experiments, supervising associated laboratory personnel, and acting as lead author on resulting manuscripts. Additional avenues of inquiry include development of computational or mathematical evolutionary models, characterization of bacterial genomes, or exploration of novel symbiont-induced phenotypes, depending on candidate’Âs interests. Development of novel research avenues based on the applicant’Âs complementary areas of expertise will be welcome and encouraged. The position is available for 2+ years, with annual renewals based on performance. *Starting salary will be $47,476/yr, and the position includes health care benefits*.

Requisite qualifications include 1) has a PhD in Ecology, Entomology, Microbiology or related field and 2) experience designing/conducting/analyzing/publishing research. Additional selection criteria will include 3) demonstrated organizational/management skills, 4) experience with basic molecular techniques such as PCR and gel electrophoresis, 5) experience rearing arthropods, 6) experience with computational modeling and 7) experience/interest in mentoring undergraduate researchers. International travel between the US and Israel is likely, once COVID-19-related travel restrictions are no longer in effect.

The location: We are at the University of Kentucky, in Lexington, Kentucky. Lexington is a mid-sized city of ~300,000 people, within a 1.5 hr drive from both Cincinnati, OH and Louisville, KY. We are also less than an hour from great hiking, camping, and climbing in the Red River Gorge.

The process: Please contact Dr. Jen White at jenwhite.uk@gmail.com or jenawhite@uky.edu for more information and include a letter of interest, CV and contact information for three references.

The White, Van Cleve, and Gottlieb-Dror labs are committed to maintaining an inclusive, equitable, and diverse environment and we enthusiastically encourage applications from BIPOC and other underrepresented groups. – Jeremy Van Cleve

Assistant Professor Department of Biology University of Kentucky E-mail: jvancleve@uky.edu Webpage: http://vancleve.theoretical.bio Phone: (859) 218-3020

Jeremy Van Cleve <jvancleve@uky.edu>

ULille PopulationGenomics

Postdoc position in population genomics, Lille (starting Fall 2020, 18 months) at the Ãvo-Ãco-Paléo laboratory.

A postdoc position, funded by the iSite Université Lille Nord-Europe is available to work with Camille Roux in Lille and Jonathan Romiguier in Montpellier.

We are looking for a postdoctoral researcher interested in a population genomics project about the evolution of social hybridogenesis in Messor ants.

The position starts in Fall 2020 (flexible September-December) and is for 18 months.

To apply:

If you are interested in this position, please send a CV and the contact details of potential references (all in one single pdf) to both Camille Roux camille.roux@univ-lille.fr) and Jonathan Romiguier (jonathan.romiguier@umontpellier.fr), no later than August 20th 2020.

Please, feel free to contact me if you have any questions about the position or wish to have more details about the project.

Camille and Jonathan

Further information: Our team in Lille: https://eep.intranet.univ-lille.fr/en/research/group_CR
Camille Roux <camille.roux@univ-lille.fr>

camille.roux@univ-lille.fr

ULiverpool UK RobustConservation

3 year Postdoctoral Research Associate position in Spatial Ecology modelling

Department of Evolution, Ecology, and Behaviour, University of Liverpool, UK

Application deadline 13th August 2020 23:30

A postdoctoral research associate is needed to work in the group of Dr Jenny Hodgson, bringing together insights from multiple disciplines to improve conservation planning worldwide. Given the global challenge of climate change, conservation planning needs a new foundation of methods, able to cope with rapidly changing environments and species, and to make robust recommendations under high uncertainty. This project offers a unique opportunity for a quantitative scientist to apply their existing skills in a new context, as well as receiving intensive training in the methods used by Dr Hodgson and her international collaborators.

We seek a pro-active team member who will become increasingly independent over time. The ideal candidate will stand out for their quantitative skills and the insight to build an efficient model to address a scientific question. These skills may have been developed in any scientific field. It would also be a great advantage to have experience in analysing satellite imagery, as well as a strong interest in and aptitude for ecology. You should have (or be about to obtain) a PhD in a relevant, quantative discipline including biological, geographical or environmental sciences. You will work in a friendly department with Athena Swan Gold award, benefiting from bespoke training in collaborators' groups.

For more details, and information in how to apply, see https://bit.ly/UniLivJob020450 or search for job reference 020450 on the University of Liverpool jobs listing page.

"Cornell, Stephen" <Stephen.Cornell@liverpool.ac.uk>

UMadrid BiodiversityEcolEvolution

The Complutense University of Madrid (UCM) will launch the first call for the postdoctoral recruitment programme UNA4CAREER on 13 July within the framework of its research internationalisation strategy. Deadline for applications closes 13 September 2020.

UNA4CAREER is a programme that involves hiring experienced researchers to develop research, training and knowledge transfer projects, with a total budget of 7.4 million euros, and which is co-financed by the UCM and the European Union through the COFUND call for Marie SkÂ³odowska Curie Actions in Horizon 2020.

Through this first call, the Complutense University of Madrid hopes to hire up to 20 postdoctoral researchers to join one of the University's 94 research groups classified as "excellent", according to the external evaluation carried out by the Spanish State Research Agency.

The main objective of UNA4CAREER is to allow participating researchers to broaden their scientific and non-academic competencies and improve their employability, as well as to access career development opportunities with a European dimension.

To guarantee this objective, the essential elements of the funded projects must be interdisciplinary, intersectoral and international. In this sense, UNA4CAREER is structured on the Una Europa - University Alliance, of which the UCM is a member.

Universities participating in Una Europa (https://www.una4career.eu/una-europa/) will ensure that the funded projects fulfil this priority by collaborating with a wide range of research groups and non-academic entities associated with them that will welcome researchers for long-term research stays.

Additional information: https://www.una4career.eu/
The Evolution and Conservation Biology Group (https://www.ucm.es/bcveng) is eligible to host candidates with a background in Zoology or Physical Anthropology and broad interest in ecological or evolutionary questions. A

summary of our expression of interest for the programme is available at:

https://www.una4career.eu/listing/group-of-evolution-and-conservation-biology/ Please visit the group's website (https://www.ucm.es/bcveng) to find and contact the best PI to support your application, or help us spread the word!

Javier Pérez-Tris –

Javier Pérez-Tris Departamento de Biodiversidad, Ecología y Evolución Universidad Complutense de Madrid Tel.: (+34) 91 394 4949 E-mail: jperez@bio.ucm.es Web: http://www.ucm.es/perez-tris

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

UMemphis InsectBioinformatics

A postdoctoral fellowship in bioinformatics (insect genomics and evolution) is available in the laboratory of Dr. Duane McKenna (http://www.duanemckenna.com) at the University of Memphis.

Position Summary: The successful applicant will be primarily responsible for data analysis associated with a variety of comparative genomic, phylogenomic, and evolutionary studies of insects (especially beetles) and will work closely with Dr. McKenna, his collaborators, and other members of the McKenna lab. All researchers with relevant background will be considered, regardless of the organism(s) previously studied. Exceptional skills in bioinformatics, a strong interest in organismal biology and evolution, and strong communication and interpersonal skills, are critical for success in this position. The position offers opportunities for mentoring students and for being mentored, building new collaborations, writing grants and high-impact scientific papers, learning/developing/implementing cutting-edge analytical methods/pipelines/tools, and pursuing one'Âs own research interests.

The position offers a competitive salary plus benefits. The initial appointment is for one year, and is renewable for at least 3 additional years, contingent upon outstanding annual performance evaluations and availability of funding. Applications must be submitted online at https://workforum.memphis.edu/ and include a cover letter, CV, two representative publications (ideally, showcasing your bioinformatics skills), and contact information (not letters) for at least three professional references.

Required Qualifications: - Ph.D. in bioinformatics, computational biology, genetics, genomics, phylogenomics, systematic biology, or similar. - A strong record of scientific publication in peer-reviewed journals. - Experience with analyzing various kinds of genomic/molecular data. - Strong communication and interpersonal skills, including a proven ability to work both independently and as part of a team.

Desired Qualifications (Ideal applicant; applicants without these skills will be considered): - Proficiency in computer programming.

The McKenna Lab: Lab members study insect systematics, genomics, evolution and diversity. Focal areas of study include the phylogeny and evolution of beetles (order Coleoptera) and other insects, the evolution and genomic basis of plant-feeding in beetles, and interactions between insects and plants on ecological and evolutionary time scales. 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'Xa leading metropolitan research and teaching institution in Memphis, TN, U.S.A.

Start date: On or after August 3, 2020. Application deadline: The position is open until filled, but we will begin reviewing applications on Friday, July 24, 2020. For more info. and to apply, visit: http:/-/workforum.memphis.edu/postings/25665 Contact for questions: Duane McKenna (dmckenna@memphis.edu)

Duane McKenna PhD William Hill Professor of Biology Director, Center for Biodiversity Research Director, Agriculture & Food Technologies Research Cluster, FedEx Institute of Technology University of Memphis Memphis, TN 38152 dmckenna@memphis.edu http:/-/duanemckenna.com www.umbiodiversity.org "Duane McKenna (dmckenna)" <dmckenna@memphis.edu>

UNeuchatel HostParasiteInteractions

A postdoctoral position on the resource ecology of parasite-host interactions is available in Jacob Koella's research group at the University of Neuchatel. The postdoc will join a team working on various aspects of the evolutionary epidemiology of host-parasite interactions, focusing on the interactions between malaria, microsporidians and mosquitoes.The postdoc's research can be tailored to her or his interests, but should be within the broad framework of an SNF-funded project, which deals with the effects of resources on the dynamics of a parasite within its host. Since a central part of the project is the role of oxidative stress as a mediator of trade-offs between resource availability, immune functions and life histories of mosquitoes and their microsporidian parasites, I am ideally seeking someone with experience with phase to phase extractions and analytical methods for physiological markers (e.g. mass spectroscopy, spectroscopy, enzymatic essays, etc).

The Institute of Biology has a broad range of interactive research groups. Although the University of Neuchatel is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University of Neuchatel has four faculties and approximately 4'200 students. It is situated on a beautiful campus on the shores of Lake Neuchatel, near Zurich, Geneva and Bern, and is close to the Swiss Alps.

The position is envisaged at 80% for an initial period of 18 months, with a possible renewal of up to 18 months, depending on funding. Most of the postdoc's time will be dedicated to research, but some teaching is expected, including the possibility of supervising master students. The starting date is flexible; funding is available immediately. Informal enquiries and formal applications should be sent to Jacob Koella (jacob.koella@unine.ch). The applications must be a single pdf that includes a cover letter detailing your research interests, experience and motivation for applying, a CV, and the names of two or three referees.

The University of Neuchatel promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

Jacob Koella

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

jkoella@gmail.com

UNorthCarolina PopulationGenomics

The Schrider Lab (https://www.schriderlab.org/) in the Department of Genetics at the University of North Carolina at Chapel Hill is hiring a postdoctoral research associate. The successful candidate will perform computational research addressing problems in population and evolutionary genomics which may include but are not limited to the following:

1) Inferring populations' selective and demographic histories (including gene flow/introgression between closely related species) 2) Investigating the evolutionary consequences of genomic structural variation (e.g. duplications, deletions, inversions) 3) Estimating recombination rates from population genetic data 4) The application

of machine learning tools to these and other problems in population genetics and/or phylogenetics

This a multidisciplinary position and candidates from a variety of backgrounds will be considered and receive training to address deficits as needed. A PhD in Evolution, Genetics, Bioinformatics, Computer Science, or a related field must be completed prior to the postdoc's hire.

Those interested should email Dan Schrider (drs@unc.edu) and include their CV as an attachment.

The University of North Carolina at Chapel Hill is an equal opportunity and affirmative action employer. All qualified applicants will receive consideration for employment without regard to age, color, disability, gender, gender expression, gender identity, genetic information, race, national origin, religion, sex, sexual orientation, or status as a protected veteran.

– Dan Schrider Assistant Professor Department of Genetics University of North Carolina at Chapel Hill email: drs@unc.edu phone: (919) 966-1764 website: https://www.schriderlab.org/ Dan Schrider <drs@unc.edu>

UPadova HumanPopGenetics

Hello,

please find here https://tinyurl.com/PadovaPostdoc a call for a 16 months Postdoctoral position at the University of Padova, Italy, to improve calculation of Polygenic Scores in recently admixed individuals (PI: Luca Pagani - https://scholar.google.co.uk/citations?user=-2TYX99YAAAAJ&hl=en).

The candidate is expected to further expand the Marnetto et al. 2020 method developed by the PI's research group (https://www.nature.com/articles/s41467-020-15464-w) with the help of the local research team and in collaboration with the Institute of Genomics of the University of Tartu, Estonia.

Computational experience on human whole genome data and programming skills are mandatory. Deadline for the application is 5th August 2020. Starting date: 1st September 2020. Salary after taxes: ~1850 EUR/month. Most of the work can be carried out remotely or in presence.

The position is part of the PI's ASPERA Project: ttps://www.biologia.unipd.it/news/leggi/news/grant-and-awards-series-starsunipd-luca-pagani/?tx_news_pi1%5Bcontroller%5D=News&tx_news_pi1%5Baction%5DÃta
Please circulate to potential candidates and encourage them to get in touch for further info. Email: lp.lucapagani@gmail.com or luca.pagani@unipd.i

Best and thank you, Luca Pagani

Associate Professor, Department of Biology, University of Padova Via Ugo Bassi 58/B, 35131 Padova, Italy

Luca Pagani <lp.lucapagani@gmail.com>

UPadova HumanPopulationGenetics

Hello,

please find here https://tinyurl.com/PadovaPostdoc a call for a 16 months Postdoctoral position at the University of Padova, Italy, to improve calculation of Polygenic Scores in recently admixed individuals (PI: Luca Pagani - https://scholar.google.co.uk/citations?user=-2TYX99YAAAAJ&hl=en).

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The position is part of the PI's ASPERA Project: https://www.biologia.unipd.it/news/leggi/news/grant-and-awards-series-starsunipd-luca-pagani/?tx_news_pi1%5Bcontroller%5D=News&tx_news_pi1%5Baction%5D=detail&cHash=704d4d96999ee73de8e8166496388dab Please circulate to potential candidates and encourage them to get in touch for further info. Email: lp.lucapagani@gmail.com or luca.pagani@unipd.it

Best and thank you, Luca Pagani

Associate Professor, Department of Biology, University of Padova Via Ugo Bassi 58/B, 35131 Padova, Italy

Luca Pagani <lp.lucapagani@gmail.com>

UPennsylvania HumanGenomics

GLOBAL GENOMICS POSTDOCTORAL HEALTH EQUITY FELLOWSHIPS The Penn Center for Global Genomics & Health Equity in the Perelman School of Medicine at the University of Pennsylvania (https://-globalgenomics.med.upenn.edu/index.html) is seeking candidates for postdoctoral fellowships. With funding from Genentech, a member of the Roche Group, this fellowship aims to help train basic and translational research scientist from groups which are traditionally under-represented in biomedical research as outlined by the National Institutes of health < https://extramural-diversity.nih.gov/diversity-matters >. The goal of this fellowship is to facilitate training in biomedical research that aims to elucidate genomic and environmental risk factors contributing to health disparities and development of diagnostics and therapeutics to translate this research into the clinic and help reduce the burden of health disparities across the globe.

The University of Pennsylvania does not discriminate based on race, religion, gender, gender expression and/or identity, age, national origin, disability, marital status, sexual orientation, military status, or any other protected status.

Application Due Date: Applications will be reviewed on rolling basis until positions are filled.

HOW TO APPLY Before applying, applicants must first identify a Penn Perelman School of Medicine based faculty mentor whose research aligns well with the candidate's research interest. With the consent of the faculty member, prepare a 1-page personal statement and a 2-page research proposal to be submitted with the application package.

Fellowship Qualifications / Eligibility

* Open to all nationalities (No US Citizenship or permanent residency required) * Candidate must complete their requirement for Ph.D. and/or MD degree by the fellowship start date.

* Candidate must have completed their PhD and/or MD within the last five years.

* Record of research productivity and appropriate skills * Proposed research must focus on genetics/genomics research of diseases that show health disparities and/or genomic studies of groups traditionally under-represented in human genetic studies (e.g. see Sirugo, G., Williams, S.M., Tishkoff, S.A., The Missing Diversity in Human Genetic Studies, Cell 2019 <https://pubmed.ncbi.nlm.nih.gov/30901543-the-missing-diversity- in-human-genetic-studies/>).

* Candidate must be from a group under-represented in the biomedical sciences.

* Research fit with selected training faculty.

Please contact Sarah Tishkoff (tishkoff@pennmedicine.upenn.edu) or Dorothy Hammond (Dorothy.Hammond@Pennmedicine.upenn.edu) if you have questions.

Sarah Tishkoff, Ph.D.

David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670 tishkoff@pennmedicine.upenn.edu http://www.med.upenn.edu/tishkoff/ Director, Center for Global Genomics & Health Equity https:/-/globalgenomics.med.upenn.edu/index.html "Keep strong and carry on!"

tishkoff@pennmedicine.upenn.edu

UReading 2 HomininEvolution

Postdoctoral Research Assistant / Research Assistant (depending on qualifications) in Hominin Morphology and Evolution at the Department of Biological Science, University of Reading, UK. Starting 1 January 2021 or as soon as possible thereafter - contract length three years fixed term.

We are seeking an enthusiastic candidate to join our group as a part of the work funded by the grant 'The evolutionary and biogeographical routes to hominin diversity' awarded by the Leverhulme Trust (RL-2019-012). The project seeks to bring innovative phylogenetic methods to the study of hominin evolution and biogeography.

The successful candidate will work with Chris Venditti and other members of the Evolutionary Biology Group at the University of Reading to collect and curate an extensive specimen-level morphological trait database from the primary literature surrounding fossil hominins and hominids.

The main responsibility will to collect and curate morphological and geographical data from primary literature on primates with particular emphasis on Hominins. The successful candidate will contribute to empirical projects, publications and running statistical and phylogenetic analyses.

To be eligible, the candidate needs to have a Master's or a doctoral (PhD) degree in a relevant discipline; the ability to work as a part of a team; in depth knowledge of primate or hominin cranial and postcranial morphology; and experience in collecting and curating large morphological datasets. Importantly, the candidate should have a strong interest in evolutionary and phylogenetic studies.

Please see the following link for more details: https://jobs.reading.ac.uk/displayjob.aspx?jobidg79 Please contact Chris Venditti (c.d.venditti@reading.ac.uk) with any informal enquires.

Postdoctoral Research Assistant / Research Assistant (depending on qualifications) in Climate and Hominin Evolution at the Department of Biological Science, University of Reading, UK. Starting 1 January 2021 or as soon as possible thereafter - contract length three years fixed term.

We are seeking an enthusiastic candidate to join our group as a part of the work funded by the grant 'The evolutionary and biogeographical routes to hominin diversity' awarded by the Leverhulme Trust (RL-2019-012). The project seeks to bring innovative phylogenetic methods to the study of hominin evolution and biogeography.

The successful candidate will work with Chris Venditti and other members of the Evolutionary Biology Group at the University of Reading to collect, curate and synthesize long-term global and regional climate proxy records from the literature for the duration of fossil hominins and hominids.

The main duties of the post will be to collect and synthesize long-term global and regional climate proxy records from the literature to produce a dataset of spatially resolved global climate proxies that covers at least the last 7 million years of hominin evolution. The successful candidate will contribute to empirical projects, publications and running statistical and phylogenetic analyses.

To be eligible, the candidate needs to have a Master's or a doctoral (PhD) degree in a relevant discipline; the ability to work as a part of a team; in depth knowledge of climate proxy data and/or climate modelling; and experience in collecting and curating large datasets. Importantly, the candidate should have a strong interest in evolutionary studies.

Please see the following link for more details: https://jobs.reading.ac.uk/displayjob.aspx?jobid=6778 Please contact Chris Venditti (c.d.venditti@reading.ac.uk) with any informal enquires.

Chris Venditti <c.d.venditti@reading.ac.uk>

URhodeIsland PhylogenomicMethods

The Schwartz Lab in the College of the Life Sciences and the Environment at the University of Rhode Island is hiring a Postdoctoral Researcher for a project funded by the National Science Foundation. The researcher will use computational tools, including machine learning, to examine phylogenetic datasets. The postdoc will be expected to lead data analysis, apply for additional funding, collaborate with graduate students and undergraduates, and publish results. Prior experience with genetic data, phylogenetics, and scripting is expected. No prior experience with machine learning is necessary, but a willingness to learn is required. The position will be for one year with the expectation of renewal on successful performance.

Required skills and expectations:

**Special note: if you have any questions about whether your skill sets meet the criteria below feel free to contact me. If you are interested in the research it's best to apply and allow me to judge whether you're qualified rather than removing yourself from the applicant pool.

- PhD by the time of hire in a biological or computational field with work relevant to bioinformatics and evolutionary biology - Record of academic success, including at least one published paper - Background in phylogenetics and evolution - Experience with genome sequence data including building phylogenies in RAxML, IQTree, or similar - Experience coding in R, Python, or another language - Commitment to supporting diverse students and an inclusive lab environment

Preferred skills:

- Experience working in an HPC environment - Experience developing software (e.g. R packages) - Experience with machine learning tools (e.g. Scikit-learn) - Interest in open-access and reproducible research

I recognize that many people will not be in a position to relocate immediately. The position may begin remotely, although the postdoc will be expected to relocate by summer 2021.

Salary: $50,000 plus family medical benefits. A limited moving subsidy and necessary computing equipment will be provided.

Location: URI is located in the southern part of Rhode Island, approximately a 40 minute drive from Providence and a 10 minute drive to multiple beaches. The Schwartz Lab is housed on the main URI campus in Kingston in the new Center for Biotechnology and the Life Sciences.

The Schwartz Lab is a collegial and supportive environment that provides holistic training for students and postdocs to continue on in both academic and nonacademic jobs.

To apply, please submit the following applications materials:

Cover letter CV Names of three academic/professional references Submit application materials and any questions about this position to Rachel Schwartz, rsschwartz@uri.edu. Application review will begin on August 1 with an expected start date between January 1 and June 30, 2021.

Rachel Schwartz, PhD Assistant Professor Department of Biological Sciences College of the Environment and Life Sciences The University of Rhode Island Kingston, RI 02881 https://schwartzlaburi.github.io/ "rsschwartz@uri.edu" <rsschwartz@uri.edu>

UToronto PopulationGenetics

Postdoc position - University of Toronto Consequences of population outbreaks on genetic structure and demographic inference

An opportunity is available in the James Lab at the University of Toronto for a creative and enthusiastic researcher interested in the consequences of cyclic irruptive population dynamics on spatio-temporal patterns of genetic variation. This project will use demo-genetic simulation models to better understand how spatially synchronous outbreaks of forest insect pests affect the development of spatial genetic structure and our ability to make inference regarding underlying demographic and evolutionary processes. Location: The position is based in the Graduate Department of Forestry at the University of Toronto (St. George Campus) and is for two years starting in January 2021 (or sooner if possible). Salary will be commensurate with experience. Project: The postdoc will develop and implement spatial simulation models to explore the effects of outbreak frequency, dispersal capacity, range expansion, landscape heterogeneity, and effective population size on population genetic inference. The post doc will be expected to contribute to the functioning of the lab, assist in supervising students, publish results in peer-reviewed journals, and to participate in scientific conferences.

Requirements: Applicants must have completed their PhD by the start date (which is somewhat flexible) and should have a strong record of scholarly publications and scientific presentations. In terms of technical qualifications, I am looking for someone with experience in population dynamics, population genetics, landscape genetics/genomics, statistical modelling, and an interest in using demo-genetic simulations to ask fundamental questions in population and landscape genetics. Competencies in scientific programming (e.g., R, Python), data wrangling, and effective communication are also required. Work environment: The Graduate Department of Forestry is a tight-knit community of forestry-oriented researchers and students with strong connections to the other departments across the U of T. The departmentÃ' euro s interdisciplinary nature facilitates strong relationships with industry, multiple levels of government, and environmental non-profits. The University of Toronto is a world-class academic institution based in is one of the most multicultural cities in the world. The James Lab is an energetic and rapidly growing team of ecologists interested in spatial and temporal dynamics in forest systems. More information about the lab can be found here: www.jameslab.ca How to apply: Applicants should send a cover letter, CV, and the names and contact information of three references as a single .pdf document to Patrick James (patrick.james@utoronto.ca). The posting will remain open until the position is filled. We encourage all qualified students to apply. Final selection will however give preference to Canadian citizens and permanent residents given current COVID-19 related uncertainty around international travel.

Julian Wittische <jwittische@gmail.com>

UWashington Seattle BatDiversification

A postdoctoral position is available in the Santana Lab at the Department of Biology and Burke Museum of Natural History and Culture (University of Washington, Seattle, USA; https://tinyurl.com/santanalab). The postdoc will be part of the NSF-funded collaborative project "Understanding the role of developmental bias in the morphological diversification of bat molars". This project investigates how the modular structure of developmental gene regulatory networks (GRN) underlies the diversity in molar morphologies across the adaptive radiation of noctilionoid bats. The project will combine CT-scanning, morphometric, transcriptomic, developmental, and functional studies to test hypotheses about the links between molar GRN and morphological diversity. Data from the project will also be used to build new computational models of tooth development and evolution.

The postdoc will help lead research, including (a) the collection of morphological data from adult and embryonic specimens through micro-CT scanning and 3D reconstruction of bat molars, (b) development of morphometric and phylogenetic analyses, (c) data interpretation, and (d) manuscript writing. The postdoc will also help mentor undergraduate interns and contribute to developing outreach activities associated with this project.

The ideal candidate will have a strong background in relevant methods. Proficiency with CT scanning, mammal dental morphology, R, phylogenetic comparative methods and multivariate statistics will be highly regarded. Familiarity with bat diversity and taxonomy, and museum research experience will also be viewed favorably. We seek a highly motivated candidate who is able to work both collaboratively and independently. We particularly welcome applications from women and people from backgrounds underrepresented in science. The position will be filled as soon as possible, with September 1st being the desired start date.

Applicants must have a Ph.D.; exceptional candidates completing their Ph.D. within the next few months will also be considered. Applicants should prepare: 1. A cover letter describing research experience, interests and goals, and their relevance to the project. 2. A full CV, including a list of publications, and 3. The names and contact information for three individuals willing to serve as references.

Please submit all application materials as a single PDF file to ssantana@uw.edu with "Postdoctoral application" as the subject line. The same materials should be loaded to Interfolio: http://apply.interfolio.com/77333 Funding is available for three years contingent upon positive annual reviews. Review of applications will begin on July 20th, and continue until the position is filled.

The postdoc will join a center of excellence in ecology, evolutionary and organismal biology at UW (http://www.biology.washington.edu), s/he will have constant interaction with the rest of the project's collaborative team (Sears lab at UCLA), and will have ample opportunities for career development in research, teaching and outreach at the Department of Biology and the Burke Museum of Natural History and Culture.

Sharlene Santana <sharlene.santana@gmail.com>

UWashington Seattle EvolutionBatTeeth

A postdoctoral position is available in the Santana Lab at the Department of Biology and Burke Museum of Natural History and Culture (University of Washington, Seattle, USA; https://tinyurl.com/santanalab). The postdoc will be part of the NSF-funded collaborative project "Understanding the role of developmental bias in the morphological diversification of bat molars". This project investigates how the modular structure of developmental gene regulatory networks (GRN) underlies the diversity in molar morphologies across the adaptive radiation of noctilionoid bats. The project will combine CT-scanning, morphometric, transcriptomic, developmental, and functional studies to test hypotheses about the links between molar GRN and morphological diversity. Data from the project will also be used to build new computational models of tooth development and evolution.

The postdoc will help lead research, including (a) the collection of morphological data from adult and embryonic specimens through micro-CT scanning and 3D reconstruction of bat molars, (b) development of morphometric and phylogenetic analyses, (c) data interpretation, and (d) manuscript writing. The postdoc will also help mentor undergraduate interns and contribute to developing outreach activities associated with this project.

The ideal candidate will have a strong background in relevant methods. Proficiency with CT scanning, mammal dental morphology, R, phylogenetic comparative methods and multivariate statistics will be highly regarded. Familiarity with bat diversity and taxonomy, and museum research experience will also be viewed favorably. We seek a highly motivated candidate who is able to work both collaboratively and independently. We particularly welcome applications from women and people from backgrounds underrepresented in science. The position will be filled as soon as possible, with September 1st being the desired start date.

Applicants must have a Ph.D.; exceptional candidates completing their Ph.D. within the next few months will also be considered. Applicants should submit: 1. A cover letter describing research experience, interests and goals, and their relevance to the project. 2. A full CV, including a list of publications, and 3. The names and contact information for three individuals willing to serve as references.

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sharlene.santana@gmail.com

UYork 6 EvolutionaryBiology

Post-Doctoral Research Associate in Ecosystem Service Changes https://www.york.ac.uk/professorial-jobs/lcab/#vac6 Available full-time for 3 years to lead research into ecosystem service changes that have taken place over time and in different places. The postholder will be mentored by Jasper Kenter (Environment & Geography), Lindsay Stringer (Environment & Geography) and Chris Thomas (Biology) in collaboration with others.

We are looking for a person with knowledge and skills that span the social and natural sciences. They will be critical to the Centre's endeavours to understand how the benefits and harms that people obtain directly and indirectly from nature have changed during the Anthropocene, and thus contribute to the development of research programmes of the Centre. This research will focus on the capacity of humans to increase ecosystem services as much as on our capacity to reduce them. They will also contribute to the development of research priorities within the Centre. The postholder will be a member of LCAB and will work with colleagues across disciplines, as well as being a member of a University Department most appropriate to their project.

This role will provide an assessment of the extent to which humanity has increased the carrying capacity of the Earth for humans. Whilst there has been a great deal of recent research on how people benefit from nature (ecosystem goods and services, also referred to as nature's contributions to people), research is required to enumerate those benefits which are a consequence of humans having intentionally and unintentionally changed the world's biological systems (human niche creation).

1) You will develop projects to assess the extent to which global and regional (typically national) ecosystem service values can be regarded as directly co-produced (e.g., from sown crops), indirectly 'co-produced' (e.g., through increased carbon uptake by ecosystems) or 'original' (e.g., harvests of wild species). This will encompass positive and negative effects, and include diverse economic, shared, social and cultural values. The work will also identify benefits that are derived from the exploitation of immigrant species and from species that have evolved alongside humans by both natural and artificial selection (including new genetic technologies). We anticipate that this research will occupy about 60% of the

researcher's time. 2) You will collaborate with other LCAB researchers to enhance your own core projects and theirs, for example exploring conflicts, trade-offs and synergies between different services and beneficiaries in different locations over different time frames. 3) You will jointly develop, coordinate and engage in cross-cutting themes within the Centre (e.g., considering inequalities and cultural attitudes to ecosystem and biodiversity change), bringing together its researchers in programmes of work and collaboration designed to build transdisciplinary understanding of novel biodiversity. 4) You will play an active role in LCAB's general intellectual life, contributing to and developing the range of research interactions and discussions, and offering expert guidance and contributions to the other strands of the Centre's research.

Closing date: 3 August 2020

– Leverhulme Centre for Anthropocene Biodiversity University of York York YO10 5DD

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Post-Doctoral Research Associate in the History of Power, People and Nature https://www.york.ac.uk/professorial-jobs/lcab/#vac4 Available full-time for 3 years to lead research into the extent to which individual and common rights, accessibility and land ownership have influenced the creation of modern landscapes, and the consequences for biodiversity. The postholder will be mentored by Jonathan Finch (Archaeology) and Kate Pickett (Health Sciences) in collaboration with others.

We are looking for a person with a humanities or a social and political sciences perspective, who has an interest in developing an interdisciplinary project. They will be critical to the Centre's endeavours to understand reciprocity between human social development and biodiversity change. The research will focus on identifying potential synergies between access/exclusion and landscape character, biodiversity, and ecosystem services. They will also contribute to the development of research priorities within the Centre. The postholder will be a member of LCAB and will work with colleagues across disciplines, as well as being a member of a University Department most appropriate to their project.

Transitions in rights and ownership have transformed landscapes across the world on multiple occasions, leading to changes in human condition and biodiversity. This role will develop knowledge of the interrelationships between human social change, biodiversity change

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UYork AccumulationOfBiodiversity

Post-Doctoral Research Associate in the Accumulation of Biodiversity in Anthropocene Environments https://www.york.ac.uk/professorial-jobs/lcab/#vac1 Available full-time for 3 years to conduct research on ecological diversification associated with ecosystem changes. The postholder will be mentored by Chris Thomas at York, and in collaboration with Maria Dornelas at St. Andrews, Mark Vellend at Sherbrooke and Phil Platts at York.

We are looking for a person with advanced analytical skills, including high levels of competency in statistical modelling, meta-analysis, spatial statistics, and the ability to obtain and manipulate species, phylogenetic, ecosystem, taxonomic and diversity data. The post will use global and national databases, statistical modelling, and meta-analysis approaches primarily to assess population and community, landscape-scale, and regional biodiversity changes associated with land use change, biological invasions, and other human-associated causes of change. They will collaborate with social scientists, evolutionary biologists, modellers and others to understand human-associated and biological drivers of biodiversity accumulation in novel and perturbed environments.

This role will develop knowledge of biological change in response to human perturbation of the Earth system. It will quantify and identify why some places are gaining species, higher taxa and ecosystem types, while other places are losing them.

1) You will identify the biological, geographic and societal predictors of positive changes in different aspects of biodiversity, including community assembly and ecosystem diversity, and beta diversity, and hence identify circumstances under which particular elements of biodiversity are increasing. You will develop analytical and statistical approaches and use existing data to estimate the different temporal and spatial scales, regions, and human-environmental conditions under which trends are negative or positive. In a world experiencing multiple drivers of dynamic changes to biodiversity, is it possible to recognise opportunities for humanity to increase biodiversity deliberately? We anticipate that this research will occupy about 60% of the researcher's time.

2) You will collaborate with other LCAB researchers to

enhance your own core projects and theirs. In particular, you will jointly develop an overall framework for ecological and evolutionary changes in the Anthropocene, to which the above project will contribute, ranging from the consideration of human motivation to bring about change through to the mathematics of ecological and evolutionary diversification. This will take up approximately 20% of the researcher's time.

3) You will jointly develop, coordinate and engage in cross-cutting themes within the Centre, bringing together its researchers in programmes of work and collaboration designed to build transdisciplinary understanding of novel biodiversity.

4) You will play an active role in LCAB's general intellectual life, contributing to and developing the range of research interactions and discussions, and offering expert guidance and contributions to the other strands of the Centre's research.

Closing date: 3 August 2020

Leverhulme Centre for Anthropocene Biodiversity University of York York YO10 5DD

Leverhulme Centre for Anthropocene Biodiversity <lcab-enquiries@york.ac.uk>

VanderbiltU MicrobiomeEvolution

Postdoctoral or technician positions are offered to join the Bordenstein Lab in the Department of Biological Sciences and Vanderbilt Microbiome Initiative in Nashville, TN. The candidates will join one of two projects with demonstrated curiosity, training, independence, and passion in the scholarship.

The first project seeks applicants with interests, experience, and skill sets in the evolution and function of phage genes underpinning selfish drive systems including cytoplasmic incompatibility and male killing. The project will involve nucleotide and amino acid sequence analyses, fluorescence microscopy, antibody development, and high throughput sequence analytics.

The second project seeks applicants with interests and skill sets in precision, multi-omic analyses (genome, microbiome, metabolome, metagenome, proteome, etc.) to investigate the consequences of genetics and environmental factors on microbiome variation in humans or animal models. The candidate will take a training and leadership role in experimental design and analytics for the community affiliated with the trans-institutional Vanderbilt Microbiome Initiative (vu.edu/microbiome). Demonstrated expertise in team building, communication, data analysis, and data visualization are required.

More information about the lab, topics, and systems can be found at the lab and initiative websites: lab.vanderbilt.edu/bordenstein and vu.edu/microbiome

If interested, contact Seth Bordenstein (s.bordenstein@vanderbilt.edu) with informal inquiries or a single, compiled pdf including: (i) earliest start date (ii) a full curriculum vitae with at least three references (iii) a statement of intent, career goal, research experience, and your areas of growth and (iv) two example publications or other writings.

The Vanderbilt University campus is a National Arboretum located in the heart of Nashville, the capital of Tennessee, known internationally as "Music City USA", Nashville is also home to Nashville Hot Chicken or Tempeh (a lab favorite), professional sports teams, the Nashville Symphony, the Frist Center for the Visual Arts, and numerous activities for outdoor enthusiasts.

Education required: * Degree(s) in symbiosis, genetics, evolutionary biology or closely related fields

Desirable Qualifications: * Experience in evolutionary genetics, multi-omic profiling and integrative analyses, fly transgenics, fluorescent microscopy, gene expression, and/or gene knockdown technology * Strong background in team leadership, community organizing, scientific independence, writing, and teaching.

Preferred Starting date: as soon as possible

Application Deadline: until position is filled

"Bordenstein, Seth R" <s.bordenstein@Vanderbilt.Edu>

WashingtonStateU TasmanianDevilGenomics

POSTDOCTORAL RESEARCHER

Washington State University

School of Biological Sciences

We are seeking a postdoctoral researcher to work on evolutionary genomics/ modeling of Tasmanian devils and Tasmanian devil facial tumor disease, a transmissible cancer. This NSF-funded international collaboration builds on over 20 years of mark-recapture data tracking the spread of the unique infectious tumor across

Tasmania and consequent endangerment of the iconic Tasmanian devil. As the top predator in Tasmania, devil declines altered the native mammal community via trophic cascades. This project bridges ecology and evolution by combining ecological and evolutionary modeling, field ecology and evolutionary genomics to predict future community dynamics. The successful applicant will have an unprecedented opportunity to analyze tens of thousands of mark-recapture records, thousands of devil genotypes and hundreds of tumor samples taken both before and after epizootics to: model coevolutionary dynamics, test for selection throughout both genomes, predict phenotypic evolution of Tasmanian devils aided by pedigree reconstruction, and functional genomics studies aided by a CRISPR-Cas9 system. The position is centered in the lab of Dr. Andrew Storfer (https://storfer-lab.org/) at Washington State University, with the possibility for scholarly exchanges with University of South Florida, University of Tasmania and Griffith University in Australia. WSU has state-of-the-art facilities, including the WSU Genomics Core (https://labs.wsu.edu/genomicscore/) and the WSU Kamiak High Performance Computing cluster (https://hpc.wsu.edu/).

Review of applications will begin on August 15, 2020 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics experience is required. A background in evolutionary modeling is strongly preferred. Desired qualities also include experience in population genomics, infectious disease evolution, and/or cancer genomics. Start date is negotiable, but is anticipated to be between October, 2020 and January, 2021. Salary and benefits are competitive. Position is for 1 year, with continuation for additional year(s) pending satisfactory progress. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu). Inquiries prior to application are also encouraged.

WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.

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Andrew Storfer, PhD Professor School of Biological Sciences Washington State University Pullman, WA 99164 USA Phone: (509) 335-7922 Fax: (509) 335-3184 astorfer@wsu.edu www.storfer-lab.org andrew.storfer@gmail.com

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WoodsHole MA TransgenerationalInheritance

Post Doc at MBL - Genetic and Epigenetic Mechanisms of Transgenerational Inheritance

Marine Biological Laboratory | Woods Hole, MA | Salary commensurate with experience and qualifications

A postdoctoral research position is available in the laboratory of Dr. Kristin Gribble at the Marine Biological Laboratory, Woods Hole, MA. The interests of the lab include the mechanisms and evolution of the biology of aging, and maternal and transgenerational effects on offspring health. We use rotifers as a model system for our work. For more information about our lab's work and a list of publications, see www.mbl.edu/jbpc/gribble . Qualified applicants will have the opportunity to study the genetic and epigenetic mechanisms of aging in a novel experimental model system, focusing on how maternal effects influence offspring health and lifespan. This NSF-CAREER funded research program will use experimental, genetic, biochemical, and bioinformatic approaches to elucidate the mechanisms of transgenerational epigenetic inheritance.

Applicants should posses a Ph.D. in molecular biology, cell biology, biochemistry, genetics, bioinformatics, or a related field. The ideal candidate will have a record of scientific rigor, productivity, and creativity; the ability to work independently and as part of a team; and a strong publication record. Excellent oral and written communication skills are required. Highly motivated individuals with experience in other model systems and a background in biochemistry, cell/molecular biology, epigenetics, and/or bioinformatics are encouraged to apply. Salary will be commensurate with experience and qualifications.

Applicants must apply for this position via the Marine Biological Laboratory careers website: https://www.mbl.edu/hr/employment/. Please submit: a cover letter with a brief description of your research experience and how your expertise will contribute to research on the mechanisms of parental effects and transgenerational inheritance; a CV including a list of publications, and contact information for three references.

Jennifer Larkum <jlarkum@mbl.edu>

WorkshopsCourses

Marseilles RADCamp Oct7-10

Dear all,

over the last 10 years, there was a huge development of studies using restriction site associated DNA sequencing (RAD-Seq) in molecular ecology, population genetics, molecular phylogenetics and species delineation. RAD-Seq datasets provide sub-genomic sampling at the scale of thousands or tens of thousands of genome wide loci. These larger datasets provide more robust phylogenetic estimates, finer scale population delineation, information about adaptive variation, and can provide additional sources of information such as evidence of historical introgression. The process of organizing and making sense of the vast quantities of reads that come back off a sequencing instrument is non-trivial, and of great consequence.

RADCamp workshops are designed to introduce ipyrad (https://ipyrad.readthedocs.io/en/latest/), a unified and self-contained RAD-Seq assembly and analysis framework, which emphasizes simplicity, performance, and reproducibility. In these workshops we proceed through all the steps necessary to quality control and assemble a typical RAD-Seq dataset, including pre- and post-assembly data filtering. Additionally, we introduce the ipyrad 'analysis' API which provides a powerful, simple, and reproducible interface to several widely used methods for inferring phylogenetic relationships, population structure, and admixture.

More information available here: https://-radcamp.github.io/ RADCamp workshops are normally geared toward practicing field biologists with little or no computational experience. Workshop attendees will need to bring a laptop computer, and their own RAD data if they have some.

The next session of the RADCamp will take place in Marseilles (Provence, France) from October 7th to October 10th. The first two days will be dedicated to training per se. The third day is optional and will be kept for any additional requested instruction, open discussions, and guided help with empirical data assembly.

More precisely the training will take place at the Luminy campus, inside the Calanques National Park—: http://www.calanques-parcnational.fr/fr. This session is funded by the Eccorev Research Federation, the Environmental Genomics Research Group, the IMBE laboratory and the Aix-Marseille University.

There are no registration fees, and participants should manage on their own for accomodations. Only lunches will be provided. The number of participants is limited to 20. If you are interested please send a mail to radcamp2020@osupytheas.fr with a short CV, and a description of your project(s) with RAD sequencing.

Thanks

The organising commitee,

Joana Boavida, Alex Baumel, Didier Aurelle, Isaac Overcast

–

Didier AURELLE

Courriel: didier.aurelle(at)univ-amu.fr / didier.aurelle(at)mio.osupytheas.fr

MaÃtre de Conférences *Aix-Marseille Université / Institut Pythéas* MIO / Institut Méditerranéen d'Océanologie < https://www.mio.univ-amu.fr/ > UMR AMU / CNRS / IRD

Campus de Luminy - OCEANOMED Bâtiment Pacifique 13288 MARSEILLE cedex 09 FRANCE

Didier AURELLE <didier.aurelle@mio.osupytheas.fr>

Online Bioinformatics Sep7-11

Dear all,

the Physalia Summer School in Bioinformatics will be held online from the 7th to the 11th of September: (https://www.physalia-courses.org/courses-workshops/-course68)

We will start by gaining experience with the Linux command line which is fundamental for running the analysis that the rest of the week will be based on. We will therefore dedicate one day to introduce basic and advanced Linux concepts for processing data on Amazon cloud (AWS), and then introduce concepts and background on each analysis step as we progress. Overall, we will cover a broad range of software and analyses from quality assessment of sequencing runs, through assembling and annotating small genomes, RNAseq and differential gene expression, and phylogenomics with NGS data. Primarily focussed on Illumina data, we will also look at the different requirements and opportunities when utilising long read data (Nanopore/PacBio).

Please check out the programme: (https:/-/www.physalia-courses.org/courses-workshops/-course68/curriculum68/)

Here is the full list of our 'ONLINE' courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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

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Online ConGen Sep7-18

ConGen 2020 Online: Population Genomics, Conservation Genetics & Data Analysis Workshop

Early Registration Discount: Submit Payment by July 15th and Reserve Your Place for $790

Theme:New this year is slightly more focus on genome sequencing, assembly, and re-sequencing of whole genomes to prepare participants and instructors for the future which will involve far more whole-genome data production and analyses.

Instructors:Craig Primmer, Maren Wellenreuther, Eric Anderson, Chris Funk, Brian Hand, Paul Hohenlohe,Marty Kardos, Brenna Forester, Joanna Kelley, Gordon Luikart, Mike Miller, Rena Schweizer,Amanda Stahlke, Robin Waples, and more TBA.

When: September 7-18, 2020

Where:Online due to Covid-19

For details on ConGen-2020: see http://www.umt.edu/-ces/conferences/congen/ Course Objective:The goal of ConGen is to provide training in conceptual and practical aspects of data analysis to understand the evolutionary and ecological genomics of natural and managed populations.

Emphasis will be on next-generation sequence (NGS) data analysis (RADs, DNA capture, and whole-genome sequence analyses, and gene expression) and interpretation of output from recent novel statistical approaches and software programs. The course promotes interactions among early-career researchers (students/participants) and leaders in population genomics to help develop the "next generation" of conservation and evolutionary geneticists. We will identify and discuss developments needed to improve data analysis approaches.

This course will cover analysis methods including the coalescent, Bayesian, and likelihood-based approaches. Special lecture sessions and hands-on exercises will be conducted on population structure, detecting selection, and genetic monitoring (of Ne, FST, etc.), landscape genomics, inbreeding detection (RoH), GWAS to identify adaptive loci, genomic vulnerability assessment and more. It will also include lectures and hands-on activities on gene expression mechanisms underlying rapid adaptation to environmental change.

Who should apply:Advanced Undergrads, M.S. & Ph.D. students, post-docs, faculty, agency researchers, and population biologists that have taken at least one university-level course in population genetics and a course in population ecology.Priority will be given to persons with their own NGS data to analyze and/or experience analyzing NGS data.

Registration & Cost:The cost to participate in ConGen 2020 is $790 US if you pay before July 15th or $850 US if you pay after July 1st. This includes lectures (live and recorded) by 12 expert instructors, question & answer sessions (live and recorded), question and answer sessions, copies of all lecture PowerPoint slides, hands-on exercise work sheets with dummy datasets, along with ConGen-2020 Swag (T-shirt, mug). Course materials will remain available for many months after the end of the course to all students in a box repository including all recorded lectures. Scholarships are available based on availability and financial need.

Participants will also receive advice installing programs through multiple online help session and also through tutorials and email. Students with PC can receive help installing a Linux virtual machine on their PC in the weeks BEFORE the course. Linux line commands will be used for several analyses during the course. A brief tutorial on Linux will be given the first day for those interested in learning Linux line commands important for population genomics data analysis.

The course will be Online this year using Zoom along with a static forum/blog for writing questions to and getting answers from instructors (during and after each lecture). Participants outside North American time zones (e.g., Europe, Australasia) can watch recorded lectures (if they cannot participate live) after lectures are given and still participate in Q & A sessions and blogs within a few days after each lecture. Because all lectures and hands-on sessions are recorded (in Zoom), participants can watch (or re-watch) them the next day and still ask questions and get instructor feedback (via the blog or live).

This course is sponsored by the American Genetic Association, the Journal of Heredity, NASA (the National Aeronautics and Space Administration), NSF (the Dimensions in Biodiversity program), along with PacBio, DoveTail Genomics, support from publications such as eDNA, Evolutionary Applications, Conservation Genetics and more TBA. It includes 12 expert instructors and hands-on data analysis using your data (with instructors) and dummy data sets provided by instructors. It has led to publications describing main topics and outcomes of the course in past years, with the goal of facilitating data analysis for population geneticists worldwide.

Sincerely,

Leif Howard Lab Technician Montana Conservation Genomics Lab (406) 552-5448

“Howard, Leif” <leif.howard@umconnect.umt.edu>

Online CulturalEvolution

Subject line: Online. Dynamics of cultural evolution

ANNOUNCEMENTS

New Online Tutorials: Dynamical Systems in Cultural Evolution http://www.dysoc.org/news#cesmodules The Center for the Dynamics of Society Complexity (DySoC) and the Cultural Evolution Society (CES) announce a new online learning series presenting basic and applied lessons in the dynamics of cultural evolution. To truly understand how culture evolves, scientists often turn to mathematical models to shed light on how culture and life history have interacted in shaping who we are and what we might become.

The CES online learning series, which includes seven modules, has been developed with self-guided study in mind. Through a variety of online learning methods, students will be able to independently work through the material to gain both a theoretical understanding of the method and practical experience using it.

The concepts and techniques covered in these modules are intended to facilitate interdisciplinary conversations and collaborations. The modules could serve as a basis for intensive short courses, seminars, or as components of a regular quarter or semester course.

The modules were created by scholars from around the world through a competitive process as a part of a grant from the John Templeton Foundation with principal investigators DySoC Director Sergey Gavrilets and past CES President Peter J. Richerson. Technical assistance was provided by the National Institute for Mathematical and Biological Synthesis.

Four of the seven modules were released June 16th, available at http://www.dysoc.org/cesmodules . They are as follows:

Models of Social Dynamics: An Introductory Module (created by Paul E. Smaldino, Cognitive and Information Sciences, University of California, Merced). This module takes an interdisciplinary approach to modeling social behavior, drawing on insights from across the social sciences and evolutionary ecology. It focuses on constructing and analyzing simulations using the NetLogo programming language.

Animal Cultures: Core Discoveries and New Horizons (created by Andy Whiten, University of St Andrews, UK; Lucy Aplin, Max Planck Institute for Animal Behaviour, Germany; Nicolas Claidière, CNRS, Aix-Marseille University, France; Rachel Kendal, University of Durham, UK). This module offers an overview of core discoveries and new developments in the study of animal cultures. The significance of animal culture for evolutionary biology and ecology, understanding human cultural evolution, and conservation are highlighted.

The Neverending Story: Cultural Evolution and Narratives (created by Joseph Stubbersfield, Psychology Department, Heriot-Watt University, Edinburgh, UK; Jamie Tehrani, Anthropology Department, Durham University, Durham, UK; Oleg Sobchuk, Max Planck Institute the Science of Human History, Jena, Germany). This module explores the universal and uniquely human behavior of narrative and how cultural evolution theory has provided vital insights into the transmission and evolution of narratives and why some become culturally successful.

Foundations of Cultural Evolution: A Question + Tools Approach (created by Adrian Bell, Department of Anthropology, University of Utah). An introductory guide to the body of formal theory in the study of the cultural evolution in humans and other animals, this module guides participants through the basic machinery of dynamic models and key results from a variety of cultural evolution topics.

The remaining modules will be released this summer. They include Modeling the Dynamics of Cultural Diversification; Dynamic Models of Human Systems; and Cultural Evolution of Dynamic Learning.

Sergey Gavrilets <gavrila@utk.edu>

Online ENMTools Aug10-12

Dear evoldir members,

Transmitting Science is offering the LIVE ONLINE course 'ENMTOOLS: A HANDS-ON WORKSHOP'

Instructor: Dr. Dan Warren (Senckenberg Biodiversity and Climate Research Center Germany) Dates: August 10th-12th, 2020

COURSE OVERVIEW:

In this workshop students will be introduced to the ENMTools R package, which is a package for constructing niche and distribution models and using them to test hypotheses about patterns of niche evolution. ENMTools contains a streamlined workflow for making, visualizing, and projecting models, as well as new methods for evaluating model predictions, statistical significance, and biases in the model construction and projection process.

It also implements Monte Carlo tests addressing many fundamental questions regarding niche evolution, such as: - Are two species' environmental associations identical? - Are two species' environmental associations more or less similar than expected based on the available habitat in their ranges? - Are biogeographic boundaries determined by environmental gradients? - What are the patterns of niche evolution across clades?

This course will comprise 9 hours of live online lessons plus 6 hours of pre-recorded classes.

For more information and registration: https://bit.ly/ENMTools Contact: haris.saslis@transmittingscience.com

All the best,

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com

haris.saslis@gmail.com

Online EvolQuantGenetics Sep14-18

Dear evoldir members,

Transmitting Science is offering the LIVE ONLINE course 'Introduction to Evolutionary Quantitative Genetics'

Instructor: Dr. Erik Postma (University of Exeter, UK)

Dates: September 14th-18th, 2020. 9:00-12:00 & 14:00-17:00 (GMT+1, London time)

A FULL SCHOLARSHIP is available for this course. Deadline for scholarship applications is July 31st.

COURSE OVERVIEW:

The response to both natural and artificial selection critically depends on the additive genetic variances and covariances underlying the traits subject to selection.

As a consequence, understanding the genetic basis of complex morphological, life-history, physiological, ornamental and behavioural traits is crucial if we are to understand their evolutionary potential, and the evolutionary process in general.

Quantitative genetics uses the phenotypic resemblance among related individuals to infer the role of genes and the environment in shaping phenotypic variation. Depending on the species, we can use data obtained from breeding experiments under controlled conditions (e.g. insects, plants), or from individual-based monitoring programs in the wild (e.g. birds and mammals). Especially the latter has benefited greatly from the application of animal model methodology, originally developed in animal breeding to identify individuals of high genetic merit. By simultaneously using the resemblance among all individuals in the pedigree, these methods provide more precise and accurate estimates of genetic and non-genetic variance components (heritabilities and genetic correlations). Furthermore, they allow for the estimation of individual-level genetic effects (breeding values), and thereby the inference of evolution.

In this course we will cover everything from basic quantitative genetic theory and statistics to advanced mixed model-based approaches. You will learn how to estimate genetic variances and covariances in wild and captive populations, and how to test for evolutionary change. Along the way, you will be exposed to a range of general statistical methods (including generalised and mixed models), the R packages MCMCglmm and ASReml-R in particular. Furthermore, we will discuss a number of landmark papers that have put the concepts and methods covered during the lectures and practicals into practice to address fundamental evolutionary questions. You are strongly encouraged to bring your own data (if you have them), which you will be able to work on during the course and which will allow you to put the theory into practice.

For more information and registration: http://bit.ly/intro-evol-quant-genetics Contact: haris.saslis@transmittingscience.com

All the best,

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com Haris Saslis <haris.saslis@gmail.com>

Online IntroNGS Sep7-11

Dear all,

we have the last 3 seats left on our "Summer School in Bioinformatics" which will be held online (via Zoom) from the 7th to the 11th of September (2-8 pm Berlin time).

General Topic: Understanding and Working with Next Generation Sequencing Data

Course website: https://www.physalia-courses.org/courses-workshops/course68/ Instructors: Dr. Daniel A. Pass (Cardiff University) and Dr. Christoph Hahn (University of Graz)

The course is aimed at researchers with a biological background but with no to basic hands-on experience with NGS data. This course will introduce participants into the field of NGS biology, understanding both the concepts and handling of the data. We will cover a broad range of software and analyses from quality assessment of sequencing runs, through assembling and annotating small genomes, RNAseq and differential gene expression, and phylogenomics with NGS data. Primarily focussed on Illumina data, we will also look at the different requirements and opportunities when utilising long read data (Nanopore/PacBio). This course will be accompanied with sessions on the use of the Linux command line, and docker which is the preferred platform for most bioinformatic analyses, as well as software containers, through Docker or Singularity, with particular focus on best practices for reproducibility.

Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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

Online PhylogeneticComparativeMethods Nov30-Dec4

Dear all,

the second edition of the Physalia course on "Phylogenetic Comparative Methods", will be held online from the 30th of November to the 4th of December.

Course Website: https://www.physalia-courses.org/-courses-workshops/course44/ Instructors:

1) Dr. Alex Dornburg (Research Curator of Ichthyology, North Carolina Museum of Natural Sciences, USA)

2) Dr. Bruno Frédérich (Université de Liège, Belgium)

This course will introduce participants to the theoretical and practical aspects of generating ultrametric trees, reconstructing trait evolution and investigating rates of lineage diversification. It will consist of both lectures to cover theory, as well as practical tutorials.

For more information about the programme, please visit our website: https://www.physalia-courses.org/courses-workshops/course45/curriculum45/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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

Online RADseq Nov2-6

Dear all,

registrations are now open for our course "RADseq data analysis" which will be held ONLINE in November (2nd-6th).

Course website: (https://www.physalia-courses.org/-courses-workshops/course16/)

In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis using Stacks. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

This course is aimed at researchers and technical workers who are or will be generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS,$B!D(B).

Instructors: Dr. Naiara Rodriguez-Ezpeleta, Dr. Natalia Diaz Arce (Azti Tecnalia, Spain) and Dr. Tereza Manousaki (Hellenic Centre for Marine Research, Greece).

For more information about the programme, please visit our website: https://www.physalia-courses.org/courses-workshops/course16/curriculum-16/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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

Online SpeciationGenomics Dec7-11

Dear all,

registrations are now open for our 4th edition of the Speciation Genomics course with Dr. Mark Ravinet (University of Nottingham, UK) and Dr. Joana I. Meier (University of Cambridge, UK).

The course will be held online in December (7th-11th): https://www.physalia-courses.org/courses-workshops/course37/ This course will provide a thorough introduction to the growing field of speciation genomics. The course aims to take students from the initial steps required for handling raw sequencing data to demographic modelling and inference of genome-wide signatures of selection and introgression. Through a combination of lectures covering key theoretical and conceptual topics, alongside hands-on exercises, participants will learn the most important computational approaches used in speciation genomics. This will include a heavy emphasis on data visualization and intepretation. After completing of the course, the participants should be able to begin using NGS data to shed light on the genomic aspects of speciation in their study system of choice.

Learning Outcomes:

1.Handling NGS data from raw reads to genetic variants

2.Applying basic population genetic statistics

3.Visualizing the genetic structure

4.Inferring demographic history

5.Identifying regions under divergent selection or barriers to gene flow

6.Understanding the potential and limitations of different methods to detect regions under selection

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 15771084054

info@physalia-courses.org

Online TeachingEvolution Aug24-28

Dear colleagues,

Transmitting Science is offering a new live ONLINE course on teaching evolution: LESSONS IN SCIENTIFIC THINKING: UNDERSTANDING EVOLUTION.

Dates: August 24th-28th, 2020. 9:00 to 11:00 online live lessons (GMT+1, London time)

Instructor: Dr. Brian Metscher (University of Vienna, Austria)

The course is intended to help participants develop advanced and subtle thinking skills to improve their understanding and teaching of central evolutionary and scientific concepts.

This course is intended for 'V University faculty or secondary teachers who will teach scientific thinking or evolution 'V Faculty in teacher education 'V Graduate students in any field 'V Anyone interested in being able to understand science better

In addition to online lectures (10 hours), the course will include reading/viewing assignments, writing assignments, and group discussions (7.5 hours). Each lesson will include other resources for teaching the information and concepts (readings, exercises, videos).

More information and registration: https://www.transmittingscience.com/courses/scientific-communication/lessons-in-scientific-thinking-understanding-evolution/ Best regards

Sole

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

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

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.