EvolDir

January 1, 2021

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

Online EvolSpeciesRanges Mar8-10

Save the date!

8-10 March 2021, virtual conference over 3 half days on the Evolution of Species Ranges

Hosted by the Centre for Marine Evolutionary Biology, University of Gothenburg, Sweden

Organised by Marina Rafajlovic, Roger Butlin and Kerstin Johannesson

Participation open to all those interested in the dynamics of species ranges

More information will be available at www.gu.se/en/cemeb Registration will open in the New Year

– Roger Butlin

Professor of Evolutionary Biology Animal and Plant Sciences The University of Sheffield

Guest Professor Marine Sciences University of Gothenburg

r.k.butlin@shef.ac.uk

Online EvolutionEcol Dec2

Dear EvolDir,

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

—

Wed 2 Dec

Professor Ruth Mace (Dept. of Anthropology, University College London, UK)

"The behavioural ecology of religious belief and practice"

—

When: 5PM GMT / 9-10AM PST, 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

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

Online EvolutionEcol Dec9

Dear EvolDir,

Join us for the next week of our popular online seminar series in Evolution and Ecology. This will be the last EvoEcoSeminar of 2020, but we will return in the new year.

—

Wed 9 Dec

Professor Dolph Schluter (Biodiversity Research Centre, Dept. of Zoology, University of British Columbia, Canada)

“Fitness maps to a large-effect locus in introduced stickleback”

— Abstract: Beneficial variants with large fitness effects can contribute to adaptation in new environments under certain conditions. Genes having large effects on phenotypic differences between populations are known from numerous taxa, but fitness effect sizes have rarely been estimated. We mapped fitness over a generation in an F2 intercross between a marine and a lake stickleback population introduced to a freshwater pond. A QTL map of the number of surviving offspring per F2 female detected a single, large-effect locus near Ectodysplasin (Eda), a gene having an ancient freshwater allele causing reduced bony armor and other changes. F2 females homozygous for the freshwater allele had twice the number of surviving offspring as homozygotes for the marine allele, producing a large selection coefficient, s=0.50Â±0.09 SE. Correspondingly, the frequency of the freshwater allele increased from 0.50 in F2 mothers to 0.58 in surviving offspring. We compare these results to allele frequency changes at the Eda gene in an Alaskan lake population colonized by marine stickleback in the 1980's. The frequency of the freshwater Eda allele rose steadily over multiple generations and reached 95% within 20 years, yielding a similar estimate of selection, s=0.49Â±0.05, but a different degree of dominance. These findings are consistent with other studies suggesting strong selection on this gene (and/or linked genes) in fresh water. Selection on ancient genetic variants carried by colonizing ancestors is likely to increase the prevalence of large-effect fitness variants in adaptive evolution.

When: 5PM GMT / 9-10AM PST, 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

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

Online PoeciliidFishEvolution Feb26

Dear EvolDir

Join us for a one-day Virtual Forum on the Ecology and Evolution of Poeciliid Fishes. The forum will be held on Friday, February 26, 2021, 9 AM to 6 PM CST, through Zoom. Abstract submissions are due on January 15, 2021 (see below). Attendance is free of charge for everybody, but registration by February 19, 2021 is required for logistical reasons.

We're excited to present four amazing keynote speakers:

Sarah Fitzpatrick (W.K. Kellogg Biological Station, Michigan State University): "Playing 'God' with Guppies: Informing Conservation with a Model Experimental System"

Kate Laskowski (Department of Evolution & Ecology, University of California Davis): "You're Unique Just Like Everyone Else: What a Clonal Fish Can Tell Us About Behavioral Individuality"

Molly Schumer (Department of Biology, Stanford University): "The Genetic Basis of a Lethal Incompatibility Between Hybridizing Swordtail Species"

Jaime ZÃºñiga-Vega (Departamento de Ecología y Recursos Naturales, Universidad Nacional Autónoma de México): "Superfetation and Matrotrophy in Viviparous Fishes: Ecological Correlates and Tests of Adaptive Hypotheses"

Besides the keynote talks, we invite anyone to submit an abstract for a talk. Two formats will be available: (1) 12-minute talks for people that would like to present their research. (2) 3-minute mini-talks for people that just want to introduce themselves and their interests, including undergraduate students and starting graduate students that may not have any data yet.

Networking opportunities for students will round out the program. Additional information on the virtual forum, including abstract submission and registration, is available on the designated website: https://sulfide-life.info/virtual-forum/ We hope to have a fun and laid-back day full of exciting research and opportunities for people to put faces to names during the networking activities. If you have any questions or suggestions, please don't hesitate to contact us.

With best wishes, Michi Tobler (tobler@ksu.edu) Zach Culumber (zwc0001@uah.edu)

Michi Tobler Division of Biology Kansas State University 116 Ackert Hall Manhattan, KS

http://sulfide-life.info Michi Tobler <tobler@ksu.edu>

UppsalaU Postdoc Mar2

Linnean Centre postdoc symposium at Uppsala 2 March 2021

On March 2nd next year, we will be part of the eighth postdoc symposium of the Linnean Centre for Plant Biology (LCPU) in Uppsala. The idea behind the event is to bring together selected postdoc candidates and Linnean Centre group leaders to plan for the submission of joint postdoc fellowship applications to international and national funding bodies such as EMBO, Marie Sklodowska-Curie Actions. The best qualified applicants will be invited to present their PhD work in a zoom seminar and have direct interviews with group leaders and their research teams to discuss potential projects. Each year 15-25 % of the applications are funded.

The Plant Ecology and Evolution program is part of the Department of Ecology and Genetics, at the Evolutionary Biology Centre (EBC), Uppsala University. Our research covers a broad range of topics in plant science at all levels of organisation, from the genomic level to species community and ecosystem functioning (see details below).

To know more about LCPU and for application conditions see https://lcpu.se/ More about our research groups:

Charlotte Jandér Evolutionary Ecology (https://sites.google.com/view/charlottejander) Species interactions, mutualisms, adaptation, behavioural ecology, tropical ecology, pollination, herbivory, microbiomes, conservation biology, chemical ecology

Sophie Karrenberg, Ecological Genetics (https://karrenberg.weebly.com/) Speciation, Sex chromosome evolution, Adaptation, biased sex ratios, reproductive barriers

Martin Lascoux, Population genetics (https://lascouxlab.wordpress.com/) Population genomics inferences (in particular demography), Evolution of polyploidy and mating systems, Genetic architecture of quantitative traits, Local adaptation, Evolution of mutation and Distribution of Fitness Effects

Pascal Milesi, Evolutionary genomics (https://milesilab.wordpress.com/) Population / Comparative genomics, Architecture of complex traits, role of genomic structural variation in adaptation, CNVs

Bob Muscarella, Forest ecology (https://bobmuscarella.weebly.com/) Tropical forest ecology, Biogeography and geographic distributions, demographic performance along abiotic gradients, response to natural and anthropogenic disturbances, biodiversity patterns

Nina Sletvold Evolutionary ecology (https://www.ieg.uu.se/plant/sletvold-group/) Plant-animal interactions, plant reproductive ecology, natural selection, conservation biology, population viability modelling, conservation genetics, plant demography

Jon Sgren Evolutionary ecology (https://www.ieg.uu.se/plant/agren-group/) Ecology and genetics of plant adaptation, plant-animal interactions, plant reproductive ecology, mating system evolution, quantitative genetics, pollination, herbivory

Do not hesitate to circulate the announcement to those who might be interested.

Best regards Martin Lascoux

Martin Lascoux Department of Ecology and Genetics EBC, Uppsala University Norbyvägen 18D 75236 Uppsala Sweden Tel +46 (0) 18 471 64 16 Fax +46 (0) 18 471 64 57 https://lascouxlab.wordpress.com När du har kontakt med oss pÃÂ¥ Uppsala universitet med e-post sÃÂ¥ innebär det att vi behandlar dina personuppgifter. For att läsa mer om hur vi gor det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy Martin Lascoux <martin.lascoux@ebc.uu.se>

GradStudentPositions

AMNH NewYork ComparativeBiology

We are pleased to announce that we are accepting applications for our Comparative Biology Ph.D. Program, Graduate Fellowships Program, and Postdoctoral Research Fellowships Program at the Richard Gilder Graduate School at the American Museum of Natural History.

Details about the Fall 2021 Comparative Biology Ph.D. Program and Graduate Fellowships Program can be found on https://www.amnh.org/research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/doctoral-student-fellowships . Details about the Postdoctoral Research Fellowships Program can be found on https://www.amnh.org/research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/postdoctoral-research-fellowship-program . The UPDATED DEADLINE for all three programs is Friday, January 8, 2021 for this cycle.

Please contact us (info-rggs@amnh.org) if you need any further information.

Richard Gilder Graduate School American Museum of Natural History https://www.amnh.org/research/richard-gilder-graduate-school Anna Manuel Richard Gilder Graduate School American Museum of Natural History Central Park West at 79th Street New York, NY 10024-5192 Tel: 212-769-5055 amanuel@amnh.org

Anna Manuel <amanuel@amnh.org>

Australia EvolutionFungalDisease

Degraded urbanised landscapes come at a cost to species' health and as such may present novel opportunities for new emerging infectious disease outbreaks.

This PhD project will use the eastern water dragon as a study system to explore the fitness cost of city life and link these findings to the emergence of a novel emerging infectious fungal disease (Nannizziopsis barbatae) which is threatening Australian reptiles. It will use a replicated design across an urban gradient and measure several phenotypes linked to immunocompetency, diet and microbiome. These will include telomere length, glucocorticoids, fatty acids and skin microbiomes composition. We expect this position to provide the candidate with training in fieldwork, molecular laboratory work and bioinformatics. We are a research lab that welcomes and cherish diversity and values team work.

Relevant literature linked to the study system:

https://doi.org/10.1038/s41598-020-77865-7 https://doi.org/10.1111/mec.15240 https://doi.org/10.1111/1365-2435.13337 https://doi.org/10.1093/jue/juz005 https://doi:10.1111/mec.14042 Prior to submitting a full application, in the first instance, please submit an expression of interest and a curriculum vitae to Associate Professor Celine Frerecfrere@usc.edu.au. Shortlisted applicants will then be asked to submit a full HDR program and scholarship application.

Associate Professor Celine Frere ARC Future Fellow University of the Sunshine Coast

mobile: 0423312893 celinefrerelab.com

Celine Frere <cfrere@usc.edu.au>

Brno 2 FishBroodParasitism

TWO PHD POSITIONS ARE AVAILABLE

TOPIC: Fish Evolutionary Ecology: Brood parasitism, Coevolution

REICHARD LAB (reichardlab.eu)

Institute of Vertebrate Biology, Czech Academy of Sciences, Brno

Two funded PhD student positions are available at the Institute of Vertebrate Biology, Czech Academy of Sciences, located in Brno, Czech Republic. Formal start of PhD. study is expected in September 2021, potential earlier start of the work can be financially supported.

The successful candidates will work on brood parasitism, primarily on the cuckoo catfish and their cichlids hosts and/or bitterling fishes and their mussel hosts using experimental, molecular and theoretical modelling methods/approaches.

For experimental work, access to well-equipped fish breeding facility and an outdoor mesocosm system is granted.

QUALIFICATIONS - MSc. in Biology or a related discipline. Experience with experimental work using fish, MHC laboratory work and/or mathematical modelling of evolutionary processes is welcome.

No TUITION, decent SALARY from the research project and STIPEND from the Masaryk University (expected enrolment at Masaryk University in Brno) ensure good standard of living.

APPLICATION PROCEDURE

For applications, please submit a CV and explain your motivation to apply for this position in a Cover Letter (single page is sufficient). Email your application to reichard@ivb.cz

All applications submitted until 31 January 2021 will be fully considered. Selected candidates will be interviewed by Skype.

For informal enquires and more details, feel free to email reichard@ivb.cz

Martin Reichard <reichard@ivb.cz>

CityUNewYork EvolutionaryBio

The Calamari lab at the City University of New York (CUNY) seeks applicants for a PhD position to study the intersection between gene expression and regulation and anatomical variation in fossil and living animals. United by our focus on changes in gene expression and regulation during development, geometric morphometrics, and phylogenetic comparative methods, the successful applicant will join our ongoing efforts to understand the evolution of new morphology, especially horns, antlers, and other bony cranial outgrowths in even-toed hoofed mammals (cattle, antelopes, deer, giraffes, etc.) and stem cell populations in rodent molars.

The Calamari lab is located at Baruch College in Manhattan, and works extensively with the facilities at the American Museum of Natural History (AMNH). The graduate student will have ample opportunities to join Calamari lab collaborations with scientists at AMNH, the University of California, San Francisco, and the New York Consortium of Evolutionary Primatology, among other institutions.

The ideal candidate will have some experience in programming related to bioinformatics (genome assembly, high-throughput gene expression, single cell sequencing, and other analyses) or geometric morphometrics. Qualified applicants with backgrounds in biology, paleontology, or other related fields are welcome.

Potential applicants should contact Zachary Calamari (zachary.calamari@baruch.cuny.edu) with a description of their experience, research interests, and CV. The successful applicant will be enrolled full time at the CUNY Graduate Center in the Ecology, Evolutionary Biology, and Behavior subprogram of the Department of Biology. Applications to the CUNY Graduate Center to start in the Fall 2021 semester are due January 1, 2021. More information about applying to the program can be found here: https://www.gc.cuny.edu/Prospective-Current-Students/Prospective-Students/Admissions . The Calamari lab and CUNY are inclusive research communities; students from backgrounds underrepresented in STEM are strongly encouraged to apply.?

Zachary Calamari, PhD Assistant Professor Department of Natural Sciences PhD Program in Biology Baruch College and the Graduate Center, CUNY

Zachary Calamari <Zachary.Calamari@baruch.cuny.edu>

FUBerlin HoneybeeVirus

** 3-year Doctoral position on honey bee - virus evolution. Deadline for applications: 21 December 2020 **

The project aims to gain a greater understanding of the evolution and consequences of virus virulence in the honey bee Apis mellifera. Deformed Wing Virus (DWV) is thought to be a major cause of honeybee loss in the northern hemisphere. The impact of DWV has been significantly exacerbated by the arrival of the ectoparasitic mite Varroa destructor, which can effectively transmit virus between bees. In this project, we will carry out in vivo evolution experiments with the aim of understanding the genomic basis of virus virulence. We will work closely with other members of the VIROINF network (www.viroinf.eu) to enable in depth bioinformatic analysis of virus genomes, and to develop methods to identify (co)evolving sites and potential epistatic interactions responsible for adaptive evolution. Overall, the project will seek to understand the evolutionary drivers of virus spread and damage in the honeybee, a species of significant economic and ecological importance.

We are a member of VIROINF. The project will be carried out in close coordination and collaboration with other members of the wider VIROINF consortium (www.viroinf.eu).

Activities: - Research in the area of genomics with a focus on experimental drivers of virus virulence evolution - Preparation and analysis of transcriptomic (RNA-seq) und genomic data - Programming / Statistics / data analysis - Project planning (experimental design) und hypothesis formulation - Preparation and carrying out lab experiments - Work with honey bees - Understanding of project-related literature - Work activities are expected to lead to the successful completion of a doctorate.

Eligibility criteria: - Masters in (Bio)informatics, (Micro)Biology - The applicant must not have resided in Germany for more than a total of 12 months during the last 3 years. - The joint VIROINFO training program entails travel between participating European partners, including extended secondments to institutes other than the FU Berlin.

Desired expertise: - Background / strong interest in genomics and evolution - Lab experience in molecular biology - Good programming knowledge is an advantage - High level of written and spoken English - Good team and interpersonal skills - Proven ability to work independently - Experience: previous participation in projects or practical work in topic-related research is an advantage.

Applications should be written in English and include the following documents: (1) A cover letter with a brief explanation of motivation (not more than one page). (2) A curriculum vitae with details of your research experience and any publications. (3) Names of 2-3 potential contacts as references. When sending your application by e-mail (preferred), please send as a pdf-document.

For informal enquiries about the position, please get in touch with Dino McMahon (dino.mcmahon@fu-berlin.de).

Deadline for applications: 21 December 2020

Application documents should preferably be sent by PDF to the above contact, or by post to:

Dino McMahon Unter den Eichen 87 12205 Berlin Germany

“McMahon, Dino Peter” <dino-peter.mcmahon@bam.de>

ImperialCollegeLondon InsectRanges

Hello,

I have a position open in my lab, which is described below. Please note that it’s open to anyone from any country.

The critical role insects play in pollinating crops and wildflowers means understanding their responses to climate change is vital for predicting food security and ecosystem resilience. Populations can respond to environment variation in a number of ways, including their behaviour such as phenology (the timing of life-history events like emergence) and morphology (e.g., wing shape). Such responses can have important, cascading consequences for ecosystems, inducing mismatches in timing such as plant flowering and pollinator emergence. Yet whilst ecologists understand the significance of these consequences, work has been constrained to mostly data from the last 30-40 years. Lacking historic data about populations before climate change limits our ability to mechanistically model responses, leaving us without a longer-term context of recovery especially after ’outlier’ years. Hence, we urgently require baseline data from the earlier part of the last century if we are to understand populations’ phenological and morphological variation before and after the recent major climate and land-use changes.

In this PhD studentship you will address this gap by studying natural history specimens collected over the past 150 years. The project will primarily assess butterfly and bee responses to climate change, but other insect pollinator taxa may be studied. To do this, you will be working with a unique and large dataset, including tens of thousands of digitised bees and hundreds of thousands of butterflies from across the UK, as well as data from over 750 natural history collections worldwide that use the Symbiota data platform. You will use specimen label information and morphometric approaches to understand functional trait responses, whilst helping to develop bioinformatic tools to gather this information.

Using this data we will build mechanistic models of when and how insects can adapt to climate change without necessarily having to shift their ranges, and compare this to known species distribution changes. Ultimately the project will develop accurate forecasts of species' distributions and, critically, ecosystem service delivery, in order to help climate change mitigation planning.

If you are interested in applying for this position, please follow the instructions online here (https://www.findaphd.com/phds/project/the-evolution-of-species-distributions-president-s-phd-scholarship/?p123758).

Thanks,

Will Pearse

—

Measuring phylogenetic structure? Try install.packages('pez')

Will Pearse (pearselab.com) < http://pearselab.com/ > Senior Lecturer, Imperial College London

Will Pearse <will.pearse@imperial.ac.uk>

JLUlGiessen EvolutionaryBiology

The Systematics & Biodiversity Lab of the Department of Animal Ecology & Systematics announces the opening a 3-year PhD position in the frame of the DFG project "Unraveling the Pontocaspian biodiversity crisis" starting 1 January 2020.

The main objective of this proposal is to use mollusks as model taxon to disentangle the effects of the taxonomic crisis, the sampling crisis and the biodiversity crisis using state-of-the art museomics, targeted field work as well as modelling and species delimitation approaches to explain the sharp decline of endemic species in the Pontocaspian region.

Specifically, we aim 1) to assess species-level relationships of Caspian Sea mollusks based on artificial intelligence, using among others ancient DNA, proteomics, 3D-morphometrical and ecological information, 2) to identify potential refugia in the Pontocaspian region (deeper and subterranean waters, limans, satellite lakes) based on predictive modelling and targeted field work, 3) to assess sampling effects on the number of endemic species reported over time using sampling-success and stable isotope analyses, and 4) to quantify the differential contributions of the taxonomic crisis and the sampling crisis on the loss of endemic Caspian Sea mollusk species to understand the extent of the current biodiversity crisis using multivariate analyses.

The applicant should

' have at least basic knowledge of molecular genetics, phylogenetics and statistical analyses. Background in morphometric studies and experience with the statistical environment R are desirable;

' hold a M.Sc. degree (or equivalent) in Biology, preferably with background in Biodiversity, Biogeography or Evolutionary Biology research;

' be fluent in English, both in writing and speaking; background in German is preferable;

' be willing to interact with the scientific community and present research results at scientific meetings. We offer

' a constructive and modern working environment;

' an international and interdisciplinary team;

' flexible office hours;

' a salary corresponding to 65% of a full position (65% of TV-L/TV-H E13).

' Please send your CV and publication record along with a motivation letter (1'2 pages), contact information of two referees and copies of your exam certificates until 10 December 2020 to Prof. Dr. Thomas Wilke, Department of Animal Ecology & Systematics, Heinrich-Buff-Ring 26-32, 35392 GieÃÂen, Germany.

—

Darwin Scholarship: "Unravelling the phylomorphospace development in freshwater gastropods to understand larger scale evolutionary dynamics"

The Systematics & Biodiversity Lab of the Department of Animal Ecology & Systematics announces the opening of a 3-year PhD position in the frame of a "Darwin Scholarship" funded by the Justus Liebig University Giessen. The lab led by Prof. Dr. Thomas Wilke conducts research in freshwater and marine Evolutionary Biology, Biodiversity and Biogeography, and Marine Holobiomics.

The focus of the current project will be on unravelling the phylo-morphospace development in selected groups of freshwater gastropods to understand evolutionary dynamics on a larger scale. Research will involve the setup of phylogenetic frameworks, dating of molecular trees using the fossil record, biogeographic reconstructions as well as 2D/3D morphometric applications to quantify shell morphology. Most data are already available at the

Systematics & Biodiversity Lab or partner institutes, and the project can start immediately.

The applicant should ' have at least basic knowledge of molecular genetics, phylogenetics and statistical analyses. Background in morphometric studies and experience with the statistical environment R are desirable;

' hold a M.Sc. degree (or equivalent) in Biology, preferably with background in Biodiversity, Biogeography or Evolutionary Biology research;

' be fluent in English, both in writing and speaking; background in German is preferable;

' be willing to interact with the scientific community and present research results at scientific meetings.

We offer ' a constructive and modern working environment; ' an international and interdisciplinary team; ' flexible office hours; ' a tax-free scholarship of 1200 EUR per month + 150 EUR monthly allowance for travels and material.

' Please send your CV and publication record along with a motivation letter (1'2 pages), contact information of two referees and exam certificates as a single PDF to Dr. Christian Albrecht (Christian.Albrecht@allzool.bio.uni-giessen.de) until 8 January 2021. Target appointment is as early as possible.

"Albrecht, Christian" <Christian.Albrecht@allzool.bio.uni-giessen.de>

MartinLutherU RapidEvolution

The Martin Luther University Halle-Wittenberg, in cooperation with the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, offers the following position at the earliest possible starting date and initially limited until 30th September 2021:

Doctoral Researcher (m-f-d) on the flexpool project 2: "Harnessing the power of RADseq data to achieve a more mechanistic understanding of rapid evolution"

as part-time employment (65 %), an extension for further 2.5-3 years is possible and dependent upon successful renewal of DFG funding for iDiv (evaluation in spring 2021).

The salary will be up to Entgeltgruppe 13 TV-L, if the personal requirements and tasks are fulfilled. The workplace will be mainly the Hensen lab at MLU Halle. However, parts of this interdisciplinary project will also take place at the Durka lab (UFZ Halle) and at the Onstein lab (iDiv Leipzig).

The project: This integrative project will apply RAD-seq analyses to identify molecular mechanisms of rapid evolution in native and non-native Conyza canadensis populations. Landscape genomics will unravel adaptive and non-adaptive drivers of the global genomic structure of this cosmopolitan weed. Available common garden data will allow studying genomic associations for intraspecific trait variation for phenotypic (competitive ability) and metabolomic data (root exudate profiles). The project will be supervised by the iDiv members Isabell Hensen (MLU Halle), Walter Durka (UFZ Halle) and Renske E. Onstein (iDiv Leipzig).

Tasks: - Performing population genomic lab work and data analyses - Publishing scientific papers in peer-reviewed journals - Presenting results at national and international conferences - Interactions with molecular and evolutionary ecologist at MLU, UFZ and iDiv - Travelling for interactions with collaborators from the University of Montana - Active participation in the yDiv graduate school - Qualification goal: PhD in population genomics

Requirements: - M.Sc. or equivalent scientific university degree in a project-related field (e. g., population genetics, plant genomics, population ecology, plant ecology and evolution, invasion biology) - Statistical skills, experience with R - Expertise and experience in population genetics are advantageous - Experience in working with data pipelines is also advantageous - Profound English communication skills (spoken and written) - Strong organizational skills - Interest and ability in working in international and interdisciplinary teams - High intrinsic motivation and team spirit

The Martin Luther University Halle-Wittenberg gives priority to applications from severely disabled candidates with equivalent qualifications. Women are particularly encouraged to apply. Queries concerning the application process should be directed to Mrs. Christa Genz (christa.genz@idiv.de), for project-related questions, please contact Professor Isabell Hensen (isabell.hensen@botanik.uni-halle.de). Submission deadline is 27th January 2021. Selected candidates will be invited to the online Flexpool recruitment symposium on 23rd and 24th February 2021.

Application should include: - Cover letter describing motivation for the project, research interests and relevant experience - Complete curriculum vitae including names and contact details of at least two scientific references - Digital copy of master certificate or equivalent

Kindly send your application, quoting the reference number 4-15437/20-D via our application portal at https://apply.idiv.de. While we prefer applications via this portal, hard-copy applications may also be sent to: German Centre for Integrative Biodiversity Research - iDiv (Halle-Jena-Leipzig), Mrs. Dr. Christa Genz, PuschstraÃÂe 4, 04103 Leipzig.

The position is offered with reservation of possible budgetary restrictions. Application portfolios will not be returned, application costs will not be reimbursed. iDiv is committed to establishing and maintaining a diverse and inclusive community that collectively supports and implements our mission to do great science. We will welcome, recruit, develop, and advance talented staff from diverse genders and backgrounds.

Christoph Rosche <christoph.rosche@botanik.uni-halle.de>

MaxPlanck AnimalMicrobeSymbiosis

The Max Planck Research Group on Mutualisms offers a graduate position in microbial symbiosis, evolutionary biology and developmental biology.

Introduction:

Housed in the Max Planck Institute for Developmental Biology, the research group studies the molecular basis behind the establishment of host-microbe symbioses. Contextualized through our work on leaf beetles and their pectinolytic mutualists, and by leveraging a broad range of methodologies, our aim is to study these partnerships across multiple biological scales.

Available projects:

Symbiont role in shaping leaf beetle physiology and ecological range

Outlook and responsibilities:—

Candidates will be trained to combine computational and experimental approaches in order to characterize the molecular underpinnings behind the establishment of specialized symbioses in herbivorous beetles. Specifically, we are interested in how symbionts are integrated into their hosts' developmental cycle, and the regulatory and physiological implications of long-term coevolution between host and microbe. The ideal candidates are expected to apply their expertise and interests in molecular biology, ecology, genomics, proteomics and/or microscopy to formulate hypothesis-driven research and participate in collaborations with other members of the group.

The laboratory is part of a collaborative environment equipped with state-of-the art infrastructure and a highly collegial community. With access to excellent core facilities within the Institute for Developmental Biology (including platforms for microscopy, proteomics, and metabolomics, and sequencing and high-performance computing facilities), the applicant will be in a position to develop and pursue independent multidisciplinary questions, consistent with the dynamic research environment in Tübingen and its International Max Planck Research School (IMPRS).

Applicants should have a bachelor's or master's degree in biology, entomology, evolutionary biology, bioinformatics, developmental biology, microbiology, chemistry or a related field. Prior research experience in sequence data analysis, physiology, bioinformatics, fieldwork, and/or molecular techniques are desirable. We offer a stimulating environment, a tractable study system, and the opportunity to combine a number of approaches to better understand the intricacies of host-microbe symbioses.

Application information:—

Expected start date in position: Summer/Fall 2021. Funding is available throughout the length of your training. A completed application includes emailing the following to Dr. Hassan Salem (hassan.salem@tuebingen.mpg.de):

1) —A statement of research interests (1-2 pages), describing how your past experiences will inform your future research in the group. Articulating concrete questions, hypotheses and/or approaches is highly encouraged. 2) —Curriculum vitae (1-2 pages). 3) —Contact information for two references familiar with your background and training.

Please include all the materials in a single .pdf file. Applications are due on January 30th, 2021.

Additional information: www.mutualisms.net Hassan Salem, Ph.D. Max Planck Research Group Leader Mutualisms Research Group Max Planck Institute for Developmental Biology Tübingen, Germany 72076 Email: hassan.salem@tuebingen.mpg.de Website: www.mutualisms.net Hassan Salem <hassan.salem@tuebingen.mpg.de>

MaxPlanck Tubingen EvolutionaryGenomics

PhD studentship on evolutionary genomics in Tubingen The Department for Algal Development and Evolution at the Max Plant Institute for Developmental Biology in TÃÂ¼bingen has an opening for a PhD thesis in the context of the ERC grant TETHYS.

Over the last few years, the brown algae have emerged as a highly valuable group to study the evolution of sex chromosomes and reproductive systems because they exhibit a remarkable diversity of sexual traits and because there have been multiple transitions between sexual systems over a relatively short evolutionary time period (less than 200 my). The maintenance of a high level of diversity of sexual features in a single, evolutionarily young group is outstanding among the eukaryotes, and points to a complex evolutionary history of the underlying regulatory systems. Recent discoveries in our group regarding the evolution of UV sex chromosomes in the brown algae have created an unprecedented opportunity to access the basis of the turnover between sexual systems and their broad impact on the evolution of this key lineage.

We are looking for a creative, enthusiastic and ambitious PhD student interested in unravelling the molecular basis and evolutionary processes underlying the evolution of sex chromosomes in the brown algae, in particular to tackle the genetic and genomic basis of transitions between sex determination systems. The student will use already available genomes and transcriptomes of several brown algal species where transitions from sex chromosomes to hermaphroditism occurred independently, in order to understand the molecular and evolutionary causes and consequences of these turnovers.

We are an international research group, and during your stay you will interact with experienced researchers with a range of backgrounds, from bioinformatics to genetics, genomics, cell biology, ecology and physiology, who will provide supervision and ensure a productive training period. You will gain experience in cutting edge techniques and after an initial training period you will be able to work independently.

If you are interested, please send your CV and a brief outline of your goals and interests to Susana Coelho (susana.coelho@tuebingen.mpg.de).

You can check our website (https://www.eb.tuebingen.mpg.de/department-of-algal-development-and-evolution/), and phone/email for informal discussions. More PhD projects are available ibn our group if you are interested in development and evolution, seaweeds, genetics, evolutionary genomics and marine biology.

Susana Coelho, PhD Department of Algal Development and Evolution Max Planck Institute for DevelopmentalBiology Max-Planck-Ring 5 72076 TÃÂ¼bingen Tel.: +49 7071-601-1307 E-mail: susana.coelho@tuebingen.mpg.de

Susana Coelho <susana.coelho@tuebingen.mpg.de>

MonashU ClimateChangeAdaptation

Monash U Australia/Graduate Position/Immediate start

Predicting species responses to climate change represents one of the greatest challenges for biologists. Current predictions focus on sensitivity to thermal stress, but they ignore species interactions. Species interactions especially competition shape all aspects of a species' ecology, including the capacity of species to respond to climate change. Failure to consider the role of competitive interactions in shaping species responses limits our ability to predict species vulnerability to climate change.

Species can respond to climate change by adapting to future climates via evolutionary change, shifting distributions to track optimal climates or going extinct. These responses will alter community dynamics and composition, leading to changes in the direction, frequency, and intensity of competition. Thus, the combined effects of rising temperatures, altered community composition, and altered competitive interactions will directly impact biodiversity and extinction risk across all levels of biological organisation. Indeed, climate change-induced shifts in species interactions are already driving species extinctions.

Current assessments of risk primarily focus on whether species harbour sufficient genetic variation in key traits to enable adaptive responses to occur. Yet, species do not evolve in isolation, but rather in communities whose composition and competitive interactions will define their risk and adaptive capacity in changing climates.

The need to incorporate competition into predictions of climate change risk is widely acknowledged. But we lack the empirical foundations to do so. Using Drosophila this project will examine the role of inter-specific competition in shaping species thermal performance and capacity to adapt to climate change and in doing so further our understanding of the role of biotic interactions in species vulnerability to climate change.

We are seeking a student who is highly motivated and passionate about evolutionary biology. Preferred candidates will have experience in evolution, ecology and thermal physiology, although experience in these areas is not necessary. The project will involve a combination of field work and lab-based experiments. There will be opportunities for the successful applicant to pursue their own scientific ideas within the aims of the project. The successful candidates will be supervised by Dr Vanessa Kellermann and Prof Carla SgrÃ² and will be based at Monash University's School of Biological Sciences.

The successful applicant will be awarded a scholarship that covers salary (current rate is $27,862 AUD tax-free per year), and a waiver of student fees, international students are welcome to apply, however preference will go to domestic students due to COVID19 and border restrictions.

Interested applicants should submit a CV, a copy of their academic transcript and a cover letter outlining their research interests to Vanessa.kellermann@monash.edu. For links to the PhD application process at Monash University go to vanessakellermann.com.

Vanessa Kellermann <vanessa.kellermann@monash.edu>

NortheasternU GenomicsMachineLearning

A position is available for a graduate student (PhD) in the Lotterhos Lab at Northeastern University. Applicants should be interested in applying machine learning algorithms to the study of landscape/seascape genomics, for applied problems in restoration. The successful applicant will participate in an NSF-funded project to develop and evaluate algorithms for studying adaptation to multivariate environments from genomic data, and for testing those algorithms in a field setting in the Eastern Oyster.

The Lotterhos Lab at Northeastern University located at NU's Marine Science Center, near the vibrant city of Boston.To better describe complex marine systems and improve predicability, our research uses theory and experiment to inform each other and develops novel statistical methodology to integrate data across biological, spatial, and temporal scales. Conceptually, we are interested in how feedbacks between ecological (from abiotic to biotic interactions) and molecular processes (from DNA sequence evolution to expression and epigenetic modifications) can lead to rapid evolutionary change that in turn affects how species interact with their environment. We are interested in central problems in marine systems such as the influence of climate on dispersal, recruitment, and local adaptation - but we also study broader problems in molecular ecology such as the inference of loci under selection from genome scans.To address these pressing issues in biological science, we use a combination of field surveys, experiments, mathematical modeling, genomics, and bioinformatics.

Northeastern's PhD program in Marine and Environmental Sciences trains high-caliber and independent scientists whose research addresses fundamental and applied marine and environmental science questions at local, regional, national, and global scales.

How to apply: Application deadline: 14 January 2021; Website:https://phd.northeastern.edu/program/marine-and-environmental-sciences/ For more information about the position, please contact Dr. K. E. Lotterhos (k.lotterhos@northeastern.edu).

K. E. Lotterhos, PhD (she/hers) Assistant Professor Department of Marine and Environmental Sciences Northeastern University Marine Science Center 430 Nahant Rd Nahant, MA 01908 I respond to email mid-day on weekdays

Katie Lotterhos <k.lotterhos@gmail.com>

NTNU Norway MolecularEvolParasites

We have a vacancy for a PhD student at the Norwegian University of Science and Technology and the Norwegian Institute for Nature Research in Norway.

PhD Candidate in molecular ecology/parasitology (194823) | NTNU - Norwegian University of Science and Technology (jobbnorge.no)

Dr. Frode Fossøy Senior Research Scientist

Norwegian Institute for Nature Research - NINA Postal address: P.O. Box 5685 Torgarden, NO-7485 Trondheim, NORWAY Delivery/Visiting address: Høgskoleringen 9, NO-7034 Trondheim, NORWAY Phone: +47 99 69 23 03-Fax: +47 73 80 14 01 -www.nina.no Frode Fossøy <Frode.Fossoy@nina.no>

PortlandStateU ConsequencesOfSomaticMutation

Graduate position: Genomics of Somatic Mutation Accumulation and Clonal Evolution in /Mimulus/

A graduate position (PhD or MS) is available in the Cruzan lab at Portland State University as part of a collaborative NSF-funded project focused on understanding the consequences of clonal evolution and natural selection on somatic mutation accumulation in plants. Mutation accumulation is intrinsically different in plants compared to animals, because the same germ cells that subtend vegetative growth are responsible for gamete production. Somatic mutations can occur with each mitotic division during stem growth; consequently, plants have enormous potential to accumulate mutations, but the effects of these mutations on adaptation is unknown. This project will use genomic and greenhouse experiments to identify the fitness consequences of somatic mutations for plants in the next generation, using /Mimulus/ as a model system. This work will be conducted in collaboration with PIs, graduate, and undergraduate students at Portland State University (Cruzan lab) and the University of Oregon (Streisfeld lab).

Interested individuals should contact Mitch Cruzan (Cruzan@pdx.edu) that includes a brief statement of your background and research interests.

Mitch Cruzan, Department of Biology, Portland State University, Portland, OR

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

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

cruzan@pdx.edu

QueenMaryU London 3DGenomeEvolution

PhD position available in the lab of Dr Chema Martin (Queen Mary University of London) in collaboration with Oxford Nanopore Technologies to dissect the evolution of 3D genome structure with Pore-C Nanopore sequencing.

Background: The 3D structure of the genome - the set of DNA molecules with the guidelines to build an organism - is fundamental for proper expression of the genetic information contained in it [1]. However, how this 3D structure evolves and is influenced by other features of the genome is still unclear. This is because our understanding of this biological phenomenon is mostly limited to a handful of model organisms and by the fact that current methods to reconstruct the 3D structure of genomes depend on short-read sequencing. In late 2019, Oxford Nanopore Technologies (ONT) released Pore-C, a method to apply long-read sequencing to reconstruct 3D genome structure that overcomes current limitations in chromatin conformation approaches [2]. In parallel, the Martín-Durán lab is establishing a set of marine segmented worms (annelids) as research model systems for comparative evolutionary genomics [3]. What are the genomic features controlling 3D genome structure in annelids? How do these mechanisms generate variability in 3D genome structure among species? Can we develop Pore-C as a widespread approach to reconstruct 3D genome structure?

In this project, you will rigorously answer these questions combining state-of-the-art experimental and computation approaches in a unique academic-industry collaborative environment.

- You will have access to large genomic databases, and in-house live organisms to fuel your investigation. - You will gain experience of molecular techniques (epigenomics, nanopore long-read sequencing), bioinformatics (pipelines to analyse Pore-C data), and statistics. - You will be encouraged to develop your own ideas and hypotheses.

Benefits: This is a BBSRC LIDo iCASE PhD fully funded position, including home (UK) tuition fees and a tax-free stipend in the region of 17,285. The student will become part of Queen Mary's Doctoral College, which provides training and development opportunities and financial support for research. The student will also have access to a Researcher Development Programme designed to help recognise and develop key skills and attributes needed to effectively manage research, and to prepare and plan for the next stages of their career. In addition, the student will enjoy a 6-months placement at Oxford Nanopore Technologies headquarters in Oxford (UK), where the students will integrate within the research and development team.

Skills/Qualifications: In a multidisciplinary project like this, candidates are unlikely to have a background in all disciplines involved. The most important qualification is motivation, enthusiasm and that the project appeals to you. However, previous computational experience would be important. We can envisage strong candidates coming through a variety of routes including: - practical molecular biology - developmental and cell biology - biotechnology - computational biology

Application: To apply, students should have a 1st class BSc degree or have received a MSc in a relevant field (i.e. molecular biology, genetics and evolutionary genomics, developmental and cell biology, biotechnology, bioinformatics) or are about to finish their MSc. For more information check https://www.lido-dtp.ac.uk/apply References: 1. Rowley, M.J., Corces, V.G. (2018) Organizational principles of 3D genome architecture. Nat Rev Genet 19, 789-800. https://doi.org/10.1038/s41576-018-0060-8 2. Netha Ulahannan, et al. (2019) Nanopore sequencing of DNA concatemers reveals higher-order features of chromatin structure. bioRxiv 833590; doi: https://doi.org/10.1101/833590 3. José M. Martín-Durán, et al. (2020) Conservative route to genome compaction in a miniature annelid. Nature Ecology and Evolution. https://doi.org/10.1038/s41559-020-01327-6 Chema Martin <chema.martin@qmul.ac.uk>

TexasAMU CorpusChristi AquacultureGenomics

A PhD position, beginning in Fall 2021, is available in the Marine Genomics Lab at Texas A&M University - Corpus Christi (https://marinegenomicslab.tamucc.edu). Research topics for the position are flexible, but will center around genomics and breeding of aquaculture species such as Eastern oyster in Texas and the wider United States. The position is offered through the Marine Biology program at Texas A&M University - Corpus Christi.

Desired qualifications:

- A Master's degree in a related field - Experience with processing and analysis of genomic datasets - Experience working in Unix/Linux and R

Interested candidates should send the following to Chris Hollenbeck (christopher.hollenbeck@tamucc.edu): - CV - A short cover letter detailing experience and research interests - Copies of unofficial transcripts

Christopher.Hollenbeck@tamucc.edu

TU Madrid EngineeringEvolutionPlantBacteria

EVOLUTION-PROOF ENGINEERING APPROACHES FOR PLANT-ASSOCIATED MICROBES

A 4-year, fully-funded PhD position opportunity is open to Chinese nationals to conduct doctoral research in the Evolutionary Systems Genetics of Microbes Lab (cutt.ly/EvolSysGen) on the topic "Evolution-proof engineering approaches for plant-associated microbes". The successful candidate will join a multicultural research team focused on understanding evolutionary principles of microbial evolution (see link above). She/he will employ a combination of cutting-edge experimental and computational approaches to find ways to anticipate and prevent the evolution of microbes of interest in agriculture (both harmful and beneficial). Strong candidates will show previous experience in plant-microbe interaction assays and/or genetic engineering of bacteria. Bioinformatics expertise will considered a plus. The position will be funded by the China Scholarship Council and the Technical University of Madrid (Spain) Cooperative PhD Programme. Up to 20 scholarships are available in this call, each offering 100% of tuition fees for the full duration of the PhD studies (4 years) a grant for living costs and one return flight from China. Candidates should hold a MSc in a relevant field (i.e. molecular biology, microbiology, evolutionary genetics and genomics, biotechnology). In addition, they should show proof of English proficiency (IELTS 6.5 or TOEFL 90, this requirement is waived if English is the only language of instruction for your current or previous level of studies).

Interested candidates please send a single PDF file with a cover letter and a CV including publication list to a.couce@upm.es. Application deadline is January 31th although early applications are strongly encouraged. Candidates short-listed for interview will be additionally requested up to two recommendation letters. Please include the word "EvolProofPhD" in the subject line.

– Dr Alejandro Couce Evolutionary Systems Genetics of Microbes Lab Centre for Plant Biotechnology and Genomics (CBGP, UPM-INIA) Technical University of Madrid, Spain

phone: +34 910679195 website: cutt.ly/EvolSysGen address: Campus de Montegancedo, M-40 (Km 38), 28223 Madrid

A Couce <a.couce@upm.es>

TU Munich MolEvol PlantPathogenDefence

The Chair of Phytopathology at the Technical University of Munich, TUM School of Life Sciences, hires a

PhD. Student in the field of

Molecular evolution of pathogen defence in wild tomato species.

We are interested in understanding the diversity of pathogen resistance within wild plant species. Therefore we study different populations from a diverse and geographically differentiated tomato species, Solanum chilense. We have shown that populations show different levels of defence against a range of pathogens and have identified patterns of differential selection for defence-associated genes. However, the implications of these findings on a molecular level remain unknown.

We are looking for an enthusiastic PhD student to investigate the underlying molecular mechanisms and the effects on plant defence mechanisms in an evolutionary context, using a combination of genomics, transcriptomics and metabolomics. The applicant must have a very good MSc in biology, biochemistry or bioinformatics, with a strong theoretic background. Knowledge and practical experience in molecular plant sciences and/or bioinformatics are required. English skills, both written and spoken, are essential.

The project will be carried out in the group of Dr. Remco Stam at the Chair of Phytopathology (Prof. Dr. Ralph Hückelhoven). The chair hosts several research groups studying molecular biology of plant pathogens and is well equipment to study defence responses on different levels. The project is integrated into the SFB924 "Molecular mechanisms regulating yield and yield stability in plants" and benefits from many collaborations and direct access to state of the art technology for cell biological and biochemical analysis and next generation sequencing on the The TUM Life Science campus in Freising-Weihenstephan.

The Technical University of Munich wishes to increase the percentage of employed women. Women are therefore explicitly encouraged to apply. Handicapped persons with equivalent qualification will be given preference. The salary is according to German income level TV-L E13.

Please send your comprehensive application including a letter of motivation (1 page), your CV, certificates, list of publications, and names of 2 potential referees as a single pdf file by email to: remco.stam@tum.de Informal inquiries can be made on the same address.

The position is to be filled in April 2021.

Reviewing applications will start 15 January 2021, until a suitable candidate has been found.

Website of the lab: www.remcostam.com Related publications Population studies of the wild tomato species Solanum chilense reveal geographically structured major gene-mediated pathogen resistance. P.S Kahlon, S.M. Seta, G. Zander, D. Scheikl, M.H.A.J. Joosten, R. Hückelhoven and R. Stam* (2020) BioRxiv https://doi.org/10.1101/2020.05.29.122960 The de novo reference genome and transcriptome assemblies of the wild tomato species Solanum chilense. R. Stam*%, T. Nosenko%, A.C. Hörger, W. Stephan, M. Seidel, J.M.M. Kuhn, G. Haberer and A. Tellier (2019) G3 1 (9) 3933-3941

Subsets of NLR genes show differential signatures of adaptation during colonization of new habitats. R. Stam*, G.A. Silva-Arias and A. Tellier (2019) New Phytologist 224: 367-379

The wild tomato species Solanum chilense shows variation in pathogen resistance between geographically distinct populations. R Stam*, D Scheikl, A Tellier (2017) PeerJ 5, e2910

Remco Stam <stam@wzw.tum.de>

UAberdeen MusselGenomics

Applications are invited for a fully funded PhD position (Ecological Genomics) in the School of Biological Sciences at the University of Aberdeen to start autumn 2021.

The freshwater pearl mussel (Margaritifera margaritifera) was once widely distributed across the Northern Hemisphere but is now considered rare across most of its range. Some of the largest remaining populations exist in northwest Scotland, making it a pressing conservation priority for the region. Here, you will integrate genomics and modelling to predict how the pearl mussel will respond to climate change. Previous studies have demonstrated the utility of this combined approach for identifying highly vulnerable populations of vertebrate, but this project will be the first to apply this to an endangered invertebrate model in an applied context. By identifying highly vulnerable populations across Scotland, isolating the drivers of mussel decline and predicting future suitable habitat, the student will contribute to the conservation of an iconic component of Scottish biodiversity.

You will benefit from a supervisory team with strengths in evolutionary biology, conservation genetics and aquatic biology and from a department with diverse research interests and a strong cohort of PhD students. You will gain valuable skills in fieldwork and data collection, molecular work, population genomics, ecological modelling, bioinformatics, science communication and writing, among other skills. You will be based at the University of Aberdeen but will have the opportunity to visit the UHI Rivers & Lochs Institute in Inverness and work alongside NatureScot. The University of Aberdeen offers a variety of social clubs for students and is committed to equality and diversity, while the region itself boasts extensive cultural and outdoor opportunities.

We are looking for an enthusiastic student with a desire to learn new skills and an interest in integrating ecology and evolutionary theory for species conservation. You will hold a minimum 2:1 Honours degree (or equivalent) in biology, zoology, genetics or another relevant field. A master's degree in a relevant subject with some experience in population genetics or modelling is desirable. This opportunity is open to UK and international candidates (including EU nationals) and provides funding to cover stipend, UK level tuition fees and a research and training support grant (RTSG).

DEADLINE: January 20th, 2021

More information about the position and application details can be found here: https://www.abdn.ac.uk/sbs/-postgraduate/super-dtp-opportunities–736.php Kara Layton <karakslayton@gmail.com>

UAlabama Tuscaloosa EvolutionTardigrades

UAlabamaTuscaloosa.Integrative_Tardigrade_Biology

I am seeking highly motivated PhD applicants to join my lab at the University of Alabama, Tuscaloosa to study tardigrade biology ranging from molecular ???omics??? perspectives through to their macroevolutionary dynamics, beginning in the Fall of 2021. The successful applicants will join a diverse team of postdoctoral researchers and graduate students employing integrative approaches (genomics, transcriptomics, metabolomics, cytology, morphometrics, population genetics, phylogenomics, ecology and evolutionary modeling) to unpack the fascinating biology of these so-called ???toughest animals on earth??? and their interactions with their cryptogamic habitats. Potential projects include but are not limited to phylogenetic comparative method development, comparative morphometrics, genome sequencing and differential gene expression analysis of tardigrades and / or their host cryptogams, signaling molecule characterization, or tardigrade systematics. Graduate students will also be expected to participate in tardigrade discovery outreach, working with local middle and high school students to find and describe tardigrade species using combinations of morphological keys and DNA barcoding approaches. Successful applicants will be supported by research and teaching assistantships that cover tuition and living expenses. Applicants must have previous research experience in related areas (preference will be given to candidates with a MS in hand), strong analytical, laboratory or field skills, and the ability to work independently as well as collaboratively. Under-represented minority candidates are particularly encouraged to apply. Interested candidates should email a CV, contact details for at least 2 references, and a short description of their research interests and experience to:

Dr. Jason Pienaar Department of Biological Sciences The University of Alabama Tuscaloosa

jpienaar@ua.edu 205-348-5999

See https://jpienaar.people.ua.edu/ for more information on the lab and https://bsc.ua.edu/ for information on the department, faculty, and application procedures.

Review of applications will begin on January 10th, 2021 and continue until the position is filled.

Jason Pienaar jpienaar@ua.edu

"Pienaar, Jason" <jason.pienaar@ua.edu>

UArctic Norway AncientDNA

A PhD position is available at The Arctic University Museum, The Arctic University Museum of Norway and Academy for Fine Arts, with the research group IceAGenT < https://www.iceagent.no/ > and ECOGEN < https://www.ecogen.no/ >.

The Arctic University Museum seeks candidates who wish to obtain the degree of Philosophiae Doctor (PhD). The position is on reconstructing past terrestrial ecosystems using ancient DNA methods. The position is for a period of four years. The nominal length of the PhD program is three years. The fourth year is distributed as 25 % each year, and will consist of teaching and other duties for the Arctic University Museum of Norway.

Deadline 4th of January 2021 https://www.jobbnorge.no/en/available-jobs/job/194273/phd-candidate-in-sedimentary-ancient-dna Prof. Inger Greve Alsos Tromsø University Museum NO-9037 Tromsø Norway Telephone: +47 77 62 07 96 Telefax: +47 77 64 51 05 Email: inger.g.alsos@uit.no http://en.uit.no/ansatte/inger.g.alsos http://ecogen.no/ https://www.iceagent.no/ http://svalbardflora.no/
Inger Greve Alsos <inger.g.alsos@uit.no>

UDebrecen SocialBehavourShorebirds

PhD position available at Department of Evolutionary Zoology and Human Biology, University of Debrecen, Hungary.

Supervisors: Primary - Dr Andras Kosztolányi (Univ Vet Med Budapest, Hungary), Dr Grant.C. McDonald (Univ Vet Med Budapest, Hungary), Prof Tamás Székely (Univ Debrecen Hungary, & Univ Bath, UK)

Application Deadline date: 16 January 2021

Project title: Evolutionary consequences of the social environment

Background In nature, individual animals live and reproduce in complex ecological environments, facing challenges from extreme weather, food shortages and predation. These challenges are predicted to drive the evolution of diverse behavioural and life-history strategies, allowing individuals to maximise their reproductive success. Crucially, individual animals rarely live in isolation, and are instead embedded within complex social networks characterised by diverse social interactions including cooperation, aggression, mating and parenting. Thus, while ecological variation may shape the evolution of individual behavioural strategies, social interactions between these behaviourally distinct individuals will in turn feedback to shape the evolutionary responses of animals to their environment. Uncovering the role of the social environment in mediating the responses of animal populations to their ecological environment remains a key challenge, particularly in the context of ongoing climate change and human disturbance.

This PhD project will focus on shorebirds (plovers) that nest on the ground. Our previous research has demonstrated that plovers vary in their position in social networks and that patterns of sociality predict the formation of mating pairs. However, it is not known to what extent individuals express consistent behavioural differences (i.e. animal personalities), how personalities relate to their position in social networks and the different environmental and climactic conditions where the plovers breed. The PhD student will develop approaches to investigate the role of the social environment in mediating the breeding biology of plovers and the evolutionary and ecological outcomes of animal personality.

Primary supervisor Dr Kosztoanyi's main interest is to understand how life histories and ecology influence social behaviour and parental care (https://elvonalshorebirds.com/group/core-team/andas-kosztolanyi/). Co-supervisor Dr McDonald researches how the social structure of animal societies impacts on reproduction (https://sites.google.com/view/grant-c-mcdonald/home) and co-supervisor Prof Szekely's key interests include the evolution of mating systems and the conservation of shorebird populations (https://researchportal.bath.ac.uk/en/persons/tamas-szekely).

Objectives (1) Test the link between consistent differences in individual behaviour, life-history and the ecological environment. (2) Test the role of personality in organising plover social structure. (3) Test the impact of social structure on breeding strategies and reproductive success of individual birds.

Approach The research project will use field studies of natural populations of Kentish plover in remote areas e.g. on the island of Maio, Cabo Verde. The breeding biology of Kentish plover is well characterised and much of the methods are routinely used in plover fieldwork meaning parental behaviour, life history traits and breeding success are easily monitored. In addition to detailed population monitoring, the research will develop methods to quantify behavioural responses of individual Kentish plovers, as well design and implement experimental manipulations in the field. Novelty

This project will reveal how animal personality and sociality shape the demographic and evolutionary outcomes of natural populations. Moreover, the results will be of keen interest to conservation biologists. Shorebird populations are declining globally as a result of human disturbance and predation associated with climate change. This research will provide key information for how animal personality and sociality mediate species responses to local ecology, providing important steps forward in linking the study of social behaviour with practical conservation management.

Training The student will be primarily affiliated with Debrecen University, Hungary (https://www.edu.unideb.hu/) and the University of Veterinary Medicine Budapest, Hungary (https://univet.hu/en/). Debrecen is the 2nd largest city in Hungary, and Debrecen University is one of the prestigious universities in Central Europe with a large international student community. The student would be based within the Department of Evolutionary Zoology and Human

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

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UEastAnglia SongbirdGenomics

Dear colleagues,

A PhD opportunity is available in my group to work on germline-restricted chromosomes of songbirds. More information here: https://www.findaphd.com/phds/project/expression-and-elimination-of-the-avian-germline-restricted-chromosome-suha-u21sciec/?p127113 Please forward this ad to interested colleagues. Application deadline is January 15.

Please stay safe and best wishes, Alex

Alexander Suh <alexander.suh@ebc.uu.se>

UEdinburgh PlantEvolutionaryGenomics

I am advertising two PhD positions in plant ecology and evolutionary genomics:

1. Ecological genomics of the British Flora

This project uses the British flora as a model system to explore the evolutionary and ecological processes shaping regional plant diversity.

This research will use an integrated approach to link genetic variation to ecological variables to better understand the assemblage of species in the British flora. The British flora is an ideal study system as it is manageable in size with ~1400 native species, has an excellent ecological and genetic resource base (e.g. over 40 million plant occurrence records), and can act as a tractable model for the wider impacts of global change. The project will draw on genome data from the Darwin Tree of Life Project, a major new initiative to generate complete genome sequences for all ~60,000 British native organisms. For selected genera of ecological interest, genomic resequencing data will be generated to investigate population dynamics and postglacial history, as well as the impact of recent changes in distribution. Depending on their interests, the student will have a choice of study species, and may choose to take the project in the direction of more ecological work (e.g. comparing traits between taxa accounting for genetic relatedness) or genomic research (e.g. comparing genome structure of divergent taxa).

For more details please see here: https://www.ed.ac.uk/e4-dtp/how-to-apply/our-projects/project?item'7 2. Growing on the edge: The genomic basis of coastal adaptation in eyebrights

Local adaptation enables plant populations to survive in extremely harsh environments. Coastal habitats present a suite of challenging conditions with plants exposed to drying oceanic salt spray and osmotically stressful high salinity soils. Despite adaptation to saline environments being a ubiquitous feature of coastal plant populations, little is known about adaptation to these conditions. In particular, the genetic basis of salt tolerance has rarely been characterised in natural populations, and whether adaptation to coastal environments comes at a cost for colonising new (non-coastal) habitats is not known.

This project will use British native species of eyebrights to study adaptation to coastal environments. There are 21 native eyebright species, with taxa found in a wide range of environmental conditions. These species are a useful system for investigating coastal adaptation as populations are widespread along the coast and inland, these species are experimentally tractable and can be grown in common garden conditions and at field sites, and there are a range of genomic tools for linking phenotype to genotype. We test the hypothesis that as adaptation to coastal habitats is extremely common we expect it to involve the fixation of pre-existing (standing) genetic variation found in inland populations.

The core of the project will involve growing coastal and inland Euphrasia species under experimental conditions where coastal stressors are simulated, and under benign conditions. This experiment will look at the phenotypic and transcriptomic (gene expression) changes associated with these environments. The research will also involve population genomic sequencing of pairs of coastal and inland plants to look at the extent of immigration between contrasting environments.

For more details please see here: https://www.findaphd.com/phds/project/eastbio-growing-on-the-edge-the-genomic-basis-of-coastal-adaptation-in-eyebrights/?p125789 Please get in contact directly with any informal enquiries: Alex [dot] Twyford@ed.ac.uk. http://twyford.bio.ed.ac.uk/opportunities The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

TWYFORD Alex <Alex.Twyford@ed.ac.uk>

UExeter Cornwall Evolution

Biological Sciences PhD Studentship (NERC GW4+ DTP funded):

Disentangling the drivers of life-history evolution in the wild: Artificial selection meets natural selection in a unique avian island population.

For all information, including on how to apply, visit http://www.exeter.ac.uk/studying/funding/award/?id=4007 Lead Supervisor: Dr Erik Postma, University of Exeter, Centre for Ecology and Conservation, e.postma@exeter.ac.uk

Additional Supervisors: Dr Sinead English, University of Bristol, School of Biological Sciences Dr Jinliang Wang, Zoological Society of London Prof Marcel Visser, Netherlands Institute of Ecology Prof Alastair Wilson, University of Exeter, Centre for Ecology and Conservation

Location: Penryn Campus, University of Exeter, Penryn, Cornwall

Project background: Despite a large body of theory describing how genetic variation and selection shape adaptive evolution, theoretical predictions often appear to be at odds with what we observe in real-world populations. Although the apparent ubiquity of so-called evolutionary stasis (i.e. selection and heritability but no evolution) has triggered many attempts to refine our predictions by incorporating the complexities that are typical of wild populations, this crucially assumes that evolution is in essence predictable. However, is natural selection strong enough to overcome the effects of random drift and gene flow, especially in small populations?

Aims and methods: You will quantify the roles of natural selection, gene flow and drift in shaping the evolutionary dynamics of clutch size, a key life-history trait. You will do this by capitalising on i) over 60 years of individual-based data for an island population of great tits (Parus major) on the Dutch island of Vlieland, and ii) a unique eight-year experiment that combined strong artificial selection on clutch size with cross-fostering and clutch size manipulations. Thereby you will provide an insight into the evolutionary dynamics of wild populations in general, and their capacity to respond to natural and human-induced selective pressures. To this end, you will use statistical/quantitative genetic approaches to infer the role of genes and the environment in shaping variation in clutch size and fitness, and the relationship between them. This project capitalises on a uniquely rich and powerful dataset that allows for answering a wide range of questions, and you are encouraged to develop the project according to your interests.

Training: You will be part of a large and vibrant group of researchers working on a diverse range of questions in evolution, ecology and behaviour. You will receive training in, among others, quantitative and population genetics, the statistical analysis of large datasets and computer simulations, as well as nest monitoring and bird handling. This will be provided by the (co-) supervisors and their group members in both the UK (Penryn, Bristol and London) and The Netherlands (Wageningen). Finally, you will attend postgraduate courses and present your results at national and international conferences.

Eligibility: This project is one of a number that are in competition for funding from the NERC Great Western Four+ Doctoral Training Partnership (GW4+ DTP). NERC GW4+ DTP studentships are open to UK and Irish nationals who, if successful in their applications, will receive a full studentship including payment of university tuition fees at the home fees rate. A limited number of full studentships are also available to international students which are defined as EU (excluding Irish nationals), EEA, Swiss and all other non-UK nationals.

The closing date for applications is Friday 8 January 2021 2359 GMT.

For all information, including on how to apply, visit http://www.exeter.ac.uk/studying/funding/award/-?id=4007 "Postma, Erik" <E.Postma@exeter.ac.uk>

UHeidelberg PlantEvolutionaryGenomics

PhD position (Heidelberg University, Germany)

Deadline for application: 15.01.2021

PhD position (65%) in plant evolutionary genomics (d/f/m)

Who we are: We are working at the interphase of organismal biology, systematics and taxonomy, and evolutionary biology. Our team has a wide range of expertise from taxonomy and field work towards comparative genomics and database management. Our group "Department of Biodiversity and Systematics" (https://www.cos.uni-heidelberg.de/index.php/m.koch?l=_e) is embedded into the excellence center COS (Centre for Organismal Studies at Heidelberg University).

What we offer: - A motivating and innovative working environment at our university - Full access to modern facilities and infrastructure at a strong research institution - Scientific exchange, flexibility, independence and self-responsibility - Extensive options of vocational training (meetings, workshops, conferences) - Excellent opportunities for cooperation and networking preparing its own scientific career - A great chance to receive your doctoral degree and joining an excellent doctoral training programme (HBIGS) - TV-L E13 (65%), limited to 3 years

HU is an equal opportunity employer. Qualified people of all gender are encouraged to apply. HU strives to increase the proportion of women. Applicants with disabilities will be given preference, if they essentially have the same qualifications.

Job description The position is embedded into a DFG funded research project (Evolutionary principles and the genomic basis of convergent evolution in tribe Arabideae, Brassicaceae family“) and continues our evolutionary work on Brassicaceae (Nature Comm. 2020, ps://doi.org/10.1038/s41467-020-17605). The successful candidate will be focusing on analyzing whole-genome sequence data and elaborating on the genomic footprints of parallel and convergent evolution in selected independent biological replicates. Additional data will come from other sources such as GBIF and physiological experiments to define key traits to be studied in detail.

The candidate ideally has - A strong background in the field of genomics or transcriptomics - Enthusiasm for and competence in large-scale data management and handling - First experience and some conceptual competence with multivariate statistics, modelling and relevant languages (e.g. R, Python, etc.) - An intrinsic and high motivation in developing strong skills in scientific writing - A high interest to work within a team and motivate other students to contribute

Job requirement An excellent diploma or master's degree in biosciences or close disciplines is mandatory, same as excellent knowledge of English and pronounced writing skills. We also expect some interest in plant species biology, ecology and evolutionary history.

The starting day is scheduled latest with March, 1st, 2021 (part-time 65%, fixed-term for 3 years) If you are interested, we are looking forward to receive your comprehensive standard application documents as one single PDF file. Please send the documents to: Prof. Dr. Marcus Koch and Dr. Christiane Kiefer using marcus.koch@cos.uni-heidelberg.de. We will arrange ZOOM meetings to discuss applications continuously until the position is filled (latest January 20th, 2021).

As part of your application for a position at Heidelberg University (HU), you are transmitting personal data. Please note our data protection information in accordance with Art. 13 General Data Protection Regulation (GDPR; Datenschutzgrundverordnung DSGVO) on collection and processing of personal data in the context of your application (https://www.uni-heidelberg.de/-md/studium/interesse/bewerbung/verfahren/-infoblatt_zum_datenschutz_fur_bewerber_innen.pdf). By submitting your application, you confirm that you have read HU's data protection information.

"Kiefer, Dr. Christiane“ <christiane.kiefer@cos.uni-heidelberg.de>

Ujyvaskyla EarlyLife

Apply for a PhD position at the University of Jyväskylä!

We are seeking an outstanding PhD (graduate) student to lead an exciting project 'Non-genetic mediators of anthropogenic stress during early life' at the Department of Biological and Environmental Sciences, University of Jyväskylä, Finland.

One of the outstanding questions in biological sciences is to understand how organism may respond and potentially adapt to human-induced changes. Understanding the mechanisms underlying responses to environmental stressors can help us to predict changes to future challenges (e.g. Taborsky, Ruuskanen et al. 2020). Developing organisms are particularly sensitive to environmental and anthropogenic stressors (e.g. Ruuskanen et al. 2019), and early-life stress can have long-lasting effects on phenotype and performance.

Two recently discovered mechanisms that could mediate long-lasting effects early life-stress are changes in epigenetic markers regulating gene expression (Laine, Ruuskanen et al. 2020) and gut microbiome (Ruuskanen et al. 2020 Lavrinienko et al. 2018, 2020), yet their role in outside captive model species has been poorly studied. In this project, we study whether early-life stress by radiation - a key anthropogenic stressor - is mediated via these mechanisms, using a wild population of passerine birds at the Chernobyl nuclear accident site as a model. This project thus combines ecophysiology and -toxicology and molecular biology. The student will gain versatile skills in field work and experimental designs, physiological measurements, molecular methods and bioinformatics.

We are looking for a candidate with a MSc degree in ecology, ecotoxicology, physiology, molecular biology or other relevant field, and experience in field work in wild populations and some laboratory skills. High motivation to learn molecular and bioinformatic skills is essential, and excellent English writing and verbal communication skills are expected.

The candidate will supervised and working in the group of Suvi Ruuskanen (Assistant Professor, JYU), see group pages here: https://sites.utu.fi/ruuskanengroup/ Apply for the position here: https://www.jyu.fi/science/en/bioenv/research/doctoral-programme/phd-posts/2021/call Deadline 15.1.2021, with expected start date in August 2021. NOTE: There are 3 positions open in the call, out of the 5 projects that are being advertised (see the link above).

For further details, please contact Suvi Ruuskanen (suvi.ruuskanen@gmail.com)

Happy holidays!

Suvi Ruuskanen, TCSM Research Fellow, University of Turku Assistant Professor in Environmental Physiology, University of Jyväskylä

Mobile +358503256547

Twitter: @RuuskanenSuvi Ruuskanen Group pages https://sites.utu.fi/ruuskanengroup/ Suvi Ruuskanen <skruus@utu.fi>

UKentucky EvolutionaryBiology

The University of Kentucky Department of Biology is recruiting Ph.D. and Masters degree students now!

Application Deadline: *January 1st, 2021*

Program Highlights

- Access diverse research areas including: - developmental, regeneration, and stem cell biology, physiology, genomics, evolutionary genetics, evolutionary ecology, macroecology, mathematical biology, neuroscience, behavior, and circadian rhythms - Join a specific lab or rotate in >1 lab - Competitive stipend (Nine month salary $22,000 pre-quals, $24,000 post-quals) - Tuition scholarship & health insurance included

To find out more, please attend our *Virtual Open House 12/18/2020 12-2pm*. Go to https://biograd.as.uky.edu/ to find out more and register for the open house and get a Zoom link. – 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>

UKoblenz AnimalPopulationGenetics

Job announcement

University of Koblenz-Landau, Institute for Integrated Natural Sciences PhD Position in Animal Population Ecology

Application deadline: 15th January 2021

The Department of Zoology, Institute for Integrated Natural Sciences, at the University of Koblenz-Landau, Campus Koblenz, invites applications for a

PhD Position.

Starting date: April 1st 2021 Duration: 3 years Salary: German salary scale (TV-L 13, 50%) Teaching obligation (in German or English): 2 hours per week

We invite applications from highly motivated candidates with passion for and experience in research related to animal population ecology. Specifically, we will investigate population structure and connectivity in selected animal species. The successful applicant will (1) hold a M.Sc. degree (or equivalent) in biology or another relevant discipline, have (2) a solid background in population ecology, (3) experience with experimental designs in ecology and according statistical analyses, (4) be capable of pursuing field work, and (5) have an excellent command of the English language. Experience with molecular methods and population / landscape genetics (SNPs) will be advantageous.

Our department works mainly in the fields of evolutionary ecology and conservation biology. For further information please visit:

https://www.researchgate.net/profile/Klaus_Fischer . The University of Koblenz-Landau is an equal opportunity employer.

Applications should include (1) a cover letter with short statements of motivation and research interests, (2) scientific CV with degree certificates, and (3) contact details of two academic referees. Applications should be submitted electronically as a single PDF file to bewerbung@uni-koblenz-landau.de before January 15th 2021. Please mention your name and the call number (94-2020) in your application and in the header of your email.

For any enquiries please contact Prof. Dr. Klaus Fischer via e-mail:

klausfischer@uni-koblenz.de

Prof. Dr. Klaus Fischer Institut für Integrierte Naturwissenschaften Abteilung Biologie Universität Koblenz-Landau Universitätsstraße 1 D-56070 Koblenz

klausfischer@uni-koblenz.de Phone: +49-261-287-2238

Klaus Fischer <klausfischer@uni-koblenz.de>

UKonstanz SGN PaleoEnvironmentalDNA

PhD and Postdoc opportunities in the PHYTOARK project

Dear all,

We currently have three openings in the multidisciplinary team of researchers in the “PHYTOARK” project funded by the Collaborative Excellence Program of the Leibniz Competition, one postdoc and two PhD positions (see separate posting for the postdoc position).

Background. PHYTOARK - “Predicting the future from signatures of the past: using living sediment archives and ancient DNA to understand responses of marine primary producers to environmental changes” - is an interdisciplinary collaborative project that looks into the Holocene history of the Baltic Sea to investigate past patterns of phytoplankton biodiversity change on the levels of communities and populations and integrates this change with Holocene and Anthropocene climate warming. The results are used in ecosystem models to develop novel tools for the assessment and prediction of ecosystem functioning under global change. The project will be carried out by a network of German and international partners. Network partners within Germany are located at the Institute of Baltic Sea Research Warnemuende (IOW), Senckenberg Research Institute (SGN), University of Hamburg and University of Konstanz.

PhD Topic 1 - Ancient Community Dynamics of Phytoplankton This PhD project will investigate phytoplankton community dynamics and biodiversity patterns through the Holocene history of the Baltic Sea. The PhD candidate will be based at the Senckenberg Research Institute (SGN) and the LOEWE Centre for Translational Biodiversity Genomics (LOEWE- TBG), with Prof. Dr. MikloÃBaÃ. Application deadline January 10th, 2021 - complete advert here https://bit.ly/-

3h2YwlK For scientific enquiries please contact miklos.balint@senckenberg.de

PhD Topic 2 - Population Genomic Analyses of Phytoplankton Species using Sedimentary Ancient DNA In this PhD project, we will generate population genomic data of a diatom and a dinoflagellate species from sediment cores spanning the Holocene. We will establish assays based on existing genomic references and use these on DNA extracted from sediments. The PhD candidate will be based at the University of Konstanz, with Prof. Dr. Laura Epp. Application deadline January 19th, 2021 - complete advert here: https://bit.ly/37x7moA For scientific enquiries please contact laura.epp@uni-konstanz.de

Best regards, the PHYTOARK team

Prof. Dr. Laura Epp University of Konstanz Limnological Institute Junior Professor for Environmental Genomics in Aquatic Systems Mainaustraße 252 78464 Konstanz / Egg Germany

Office Phone: 0049 7531 88 3391 Mobil Phone (frequent home office): 0049 176 6477 6818 laura.epp@uni-konstanz.de https://www.researchgate.net/profile/Laura_Epp https://www.limnologie.uni-konstanz.de/en/ag-epp-environmental-genomics/ Laura Epp <laura.epp@uni-konstanz.de>

ULeeds PinnipedEvolutionaryGenomics

Evolutionary genomics of life-history adaptations and disease susceptibility in pinnipeds

PhD studentship, University of Leeds UK, open to UK, EU, and International students

Closing date 5th January 2021

Pinnipeds (seals, sea lions, fur seals and walrus) are keystone marine predators, and sentinels for marine ecosystem health. Advances in genomics technologies are opening up the possibility to identify and dissect the genetics and molecular evolution underlying the adaptions of pinnipeds to the marine environment and the startling variation in ecology and life history present within the family. Understanding these mechanisms not only provides fundamental insights into the process of evolution, but is also important for assessing species vulnerability and responses to potential future environmental change.

This project will build on rapidly growing genomic resources for pinnipeds, including de novo seal genome assemblies generated by the Goodman/O'Connell labs and other colleagues in the Pinniped Genome Consortium at the University of Helsinki and University of Copenhagen. These provide an opportunity to use comparative genomics to examine key aspects of pinniped ecology and evolution including physiological adaptations underpinning different life-history strategies and among species variation in disease susceptibility. We will use a variety of genomic approaches including de novo sequencing of seal genomes, and population genetic studies at the genomic level using methods such as ddRAD. The student can expect to gain experience in cutting edge DNA sequencing and genomics methods, together with developing skills in bioinformatics, comparative genomics, molecular evolution and population genetics analysis. There will opportunities to visit collaborators from the Pinniped Genomes consortium including Denmark and Finland.

More information and how to apply: https://panorama-dtp.ac.uk/research/the-evolutionary-genomics-of-life-history-adaptations-and-disease-susceptibility-in-pinnipeds/ Enquiries: s.j.goodman@leeds.ac.uk

Dr Simon Goodman School of Biology Manton Building University of Leeds Woodhouse Lane Leeds, LS2 9JT, UK

Tel: +44-(0)113-3432561, Fax: +44-(0)113-3432835 Email: s.j.goodman@leeds.ac.uk Web: http://www.goodmanlab.org/ Skype: simon.j.goodman Twitter: @DrSimon_Goodman

Simon Goodman <S.J.Goodman@leeds.ac.uk>

UMBC Maryland 3 MateChoiceSpeciation

Three PhD positions are available in the Mendelson lab at the University of Maryland Baltimore County (UMBC) to study mate choice and speciation. One NSF-funded PhD research assistantship and two PhD teaching assistantships are available. The RA will test hypotheses derived from information theory about mate choice and signal evolution in wild populations of darter fish. The TA positions are more flexible, and research will be designed to fit the joint interests of student and mentor.

UMBC is a minority-serving institution with a mission of inclusive excellence located a short distance from Baltimore, MD, USA. Catonsville offers the quiet and affordable life of the suburbs, with a vibrant harbor city to the east and rolling green mountains to the west. The Mendelson lab recently moved into a newly constructed interdisciplinary science building with tons of natural light and a new aquatic facility. We are one of several active labs in ecology and evolutionary biology at UMBC.

Please contact tamram@umbc.edu with a statement of interest and CV, and we can set up a video chat. Application deadline for the department of Biological Sciences is January 1.

– Tamra C. Mendelson, Ph.D. Professor & Associate Chair Department of Biological Sciences University of Maryland Baltimore County 1000 Hilltop Circle, Baltimore MD 21250 tamram@umbc.edu - www.mendelsonlab.net Tamra Mendelson <tamram@umbc.edu>

UNewOrleans EvolutionaryPhysiologyFish

Graduate Position:UNewOrleans.EvolutionaryPhysiologyFish

I am seeking motivated applicants to our Integrative Biology Ph.D. program to begin in the Fall of 2021. The successful applicant will undertake research on the evolutionary and ecological physiology of hypoxia tolerance in estuarine fish. The successful applicant will be supported by a graduate assistantship (teaching and/or research) including a waiver of tuition and non-resident fees. Applicants must have previous research experience in related areas, strong analytical skills, and the ability to work independently as well as collaboratively. Interested students should send a CV and a short description of their research interests to:

Dr. Barney Rees Department of Biological Sciences University of New Orleans brees@uno.edu 504-280-6743

For examples of recent research see:

*Reemeyer & Rees. 2020. JEB jeb.228098. doi:10.1242/jeb.228098 *Townley et al. 2017. AJP 312: R412-R425, doi: 10.1152/ajpregu.00402.2016 *Rees & Matute. 2018. PBZ 91: 1046-1056, doi: 10.1086/699596.

See http://www.uno.edu/cos/biology/index.aspx for information on the department, faculty, and application procedures.

Review of applications will begin on February 1, 2021 and continue until the position is filled.

Bernard B Rees <brees@uno.edu>

UPorto 2 EvolutionaryGenomics

Graduate position: UPorto.2.EvolutionaryGenomics

We are looking for 2 graduate students interested in applying to 4-year PhD fellowships from the Portuguese Science and Technology Foundation (FCT), to pursue PhD degrees in Evolutionary Genomics in research group EVOCHANGE - Genomics of Evolutionary Change (https://cibio.up.pt/research-groups-1/-details/evochange), led by José Melo-Ferreira (https:/-/sites.google.com/site/meloferreiraj) at CIBIO-InBIO, University of Porto (https://cibio.up.pt/).

Research Subjects: 1) Evolutionary genomics of colouration (details in https://bit.ly/39zwgFK). 2) Genomics of ancient hybridization (details in https://bit.ly/-2JlsOUy).

Application Deadline: 14 January 2021.

The selected candidates will be invited to apply to 4-year PhD Fellowships of Fundação para a Ciência e a Tecnologia (FCT, Portugal), in the call expected for the first trimester of 2021 (see information about the previous call at https://www.fct.pt/apoios/-bolsas/concursos/individuais2020.phtml.en). Monthly salaries are compatible with living costs in Portugal (BD in https://www.fct.pt/apoios/bolsas/docs/-Tabela_Valores_SMM_LOE_2020.pdf), and the fellowships cover social security and tuition fees. If funded, the student is expected to enroll in a PhD program at the University of Porto (http://www.biodiv.pt/). The PhD projects are expected to start in October 2021.

Required qualifications: - A Master (MSc) degree in Biology, Evolution, Genetics, Bioinformatics or related fields is required. If any of the stated degrees was obtained abroad, the formal recognition of the degree in Portugal and the conversion of the obtained grades to the Portuguese scale are required at the time of the application to FCT (more information at https://www.dges.gov.pt/-en/pagina/degree-and-diploma-recognition). - Candidates should be highly motivated and demonstrate strong interest in Evolutionary Biology. - Preference will be given to candidates with background in evolutionary and population genetics and experience in analyses of high-throughput sequencing data, and knowledge of programming languages, such as Unix, Python/Perl and/or R, and with a track record demonstrating these skills. - Good writing and communication skills in English, excellent teamwork skills, and ability to work independently. - The successful applicant must be resident in Portugal at the start of the PhD.

How to apply: - Application deadline: 14 January 2021; - Inquiries and Applications should be directed to José Melo-Ferreira (jmeloferreira@cibio.up.pt; meloferreiraj@gmail.com) indicating the research subject you are applying to. - Applications should be written in English and must include the following information: 1) a motivation letter describing the candidate's profile, research interests and suitability for the role; 2) a Curriculum Vitae, summarizing the academic path, research experience, publications and other qualifications deemed relevant; 3) copy of the BSc and MSc certificates, and course grades; 4) names and contact information of two referees.

Jose Melo-Ferreira <jmeloferreira@cibio.up.pt>

UPorto ParallelEvolution MarineSnails

Graduate Position: UPorto.ParallelEvolution_MarineSnails

We are looking for candidates interested in applying for a 4-years PhD fellowship from the Portuguese Science Foundation (FCT) on the topic of Parallel Ecotype Evolution and Speciation in Marine Snails (flat periwinkles: *Littorina fabalis* and *L. obtusata*). The project will use an interdisciplinary approach involving a strong genomics component (bioinformatics skills), morphological and ecological analyses, as well as demographic modelling, to test for parallel divergence between *L. fabalis *ecotypes at different geographic scales and evaluate the role of natural selection and gene flow in the diversification of this system. Although most samples for this project have been already collected, the student will have the opportunity to do field work in different geographic regions (e.g. Iceland and Iberian Peninsula). We are seeking for a highly motivated and independent person with a scientific background, interest in evolutionary biology, that enjoy problem-solving and team work, has flexibility in learning new tasks and concepts, and has excellent data handling and communication (orally and written) skills (in English).

The selected candidate will apply for a FCT PhD fellowship scheme at the beginning of 2021 (information for the 2021 call is not yet available in the FCT website but see the previous call here https://www.fct.pt/-apoios/bolsas/concursos/individuais2020.phtml.en), under the supervision of researchers working evolutionary genomics of adaptation and speciation, including myself (https://scholar.google.com/citations?user=-ubDybpQAAAAJ&hl=en; https://orcid.org/0000-0001-6635-685X; https://rmigueldefaria.wixsite.com/farialab-1) and two co-supervisors (to be defined based on the selected applicant main interests). The student will work in close collaboration with an enthusiastic international network of researchers in evolutionary genomics of adaptation and speciation in Littorina (including Roger Butlin (https://www.sheffield.ac.uk/biosciences/people/-bms-staff/academic/roger-butlin) from the University of Sheffield, UK; Kerstin Johannesson from the University of Gothenburg, Sweden; Anja Westram from IST, Austria; and Juan Galindo, University of Vigo; among others) and will be integrate in a very dynamic, interactive and international research group (Evolutionary Genetics and Genomics, https://cibio.up.pt/-research-groups-1/details/evolgen/team) led by Miguel Carneiro (https://scholar.google.pt/citations?user=-onCfzJ4AAAAJ&hl=pt-PT), at CIBIO/InBIO (https:/-/cibio.up.pt/), a laboratory of excellence in the study of Biodiversity and Evolutionary Biology.

If funded, the student is expected to enroll in a PhD program at the University of Porto (e.g. BIODIV: http://www.biodiv.pt/), one of the best Portuguese universities that is located in a very attractive European city (Porto), which hosts a diverse community of international students. The fellowship amount is fixed by FCT and is in line with the living costs in Portugal (https://www.fct.pt/apoios/bolsas/docs/-Tabela_Valores_SMM_LOE_2020.pdf). Importantly, the fellowship is tax-free and the social security/national health system is covered by FCT. Only citizens from other member-states of the European Union, third-party states citizens, stateless individuals or citizens holding a political refugee status can apply to FCT fellowships. Candidates should have a completed BSc or MSc degree by the beginning of 2021, when they will apply for the PhD fellowship. If successful, the student is expected to start the PhD before the end of 2021. Highly motivated students should send me a letter explaining the motivation to pursue a PhD on the above-mentioned topic and describe your scientific expertise, a CV, and other documents that you wish to be considered, as well as the name and contact of two references. All applications must be submitted by the 31st of December 2020. Selection results will be communicated by the beginning of January 2021.

Rui Faria, PhD

1. Researcher at:

CIBIO/InBIO, Research Center on Biodiversity and Genetic Resources

University of Porto, Portugal

2. Visiting Researcher at:

Department of Animal and Plant Sciences

University of Sheffield, United Kingdom

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UReading PlantDiseaseEpidemiologyEvolution

Smart control of crop diseases: how can we best combine fungicides and plant resistance genes?

PhD studentship, University of Reading, UK, open to UK, EU, and international students. Submission opens 13 January 2021; deadline 8 February 2021.

About the project:

This multidisciplinary PhD project will investigate the epidemiology and evolutionary adaptation of the major fungal pathogen of wheat Zymoseptoria tritici (Zt) to control measures – fungicides and disease resistance genes, thereby using evolutionary biology to tackle one of the most urgent problems in agriculture. The methodology combines mathematical modelling, machine learning and field experimentation.

Zt causes septoria tritici blotch (STB), the most damaging disease of wheat in Europe and one of the largest constraints on wheat production globally. The disease is especially serious in the UK because of conducive climatic conditions. It is becoming increasingly difficult to control STB, because Zt is capable of rapidly evolving resistance to fungicides and adapting to disease-resistant wheat varieties and environmental conditions. It is recognized that no single control measure is durable in the face of the pathogen's notorious adaptive capacity, hence the two key control methods - fungicides and disease resistance genes in wheat - need to be combined in a manner that optimizes not only control efficacy in the short term, but also their sustainability in the longer term. This interdisciplinary project will make a major contribution to this goal using a powerful combination of large-scale field experimentation with novel high-throughput phenotyping techniques, bioinformatic analyses, state-of-the-art machine learning and mathematical modelling approaches.

In the first phase, a field experiment will be conducted during two consecutive years to investigate the STB epidemic development in a large number of different wheat genotypes. The amount of disease will be measured using both the conventional visual assessments and novel digital phenotyping approaches, and the daily weather data will be recorded. The data on epidemic development will be linked to genomic data already available for the wheat population under study, and in this way you are likely to identify new genetic bases of STB resistance in wheat. In the second phase, powerful machine learning techniques will be used to combine the three types of data (disease measurements, weather data and wheat genomic data) and construct a model predicting the seasonal STB epidemic development. Finally, in the third phase of the project, the outcomes of the two previous phases will be incorporated into a mathematical modelling framework (epidemiological/evolutionary model) that describes how the pathogen population changes over time in its interaction with the host population of wheat plants. The model will incorporate the effect of two control measures: fungicides and STB resistance genes in wheat. This will allow you to optimize choices of fungicide treatment programmes and disease-resistant wheat cultivars that maximize net benefit of growers over a short term of a single growing season. You will then be able to compare the outcomes with the predicted net benefit over a longer term of a number of consecutive growing seasons, taking into account disease levels, weather variables and wheat genomes.

Training opportunities:

The student will acquire inter-disciplinary skills in designing and conducting large-scale field experiments with crop pathogens, acquiring large datasets with the help of novel digital phenotyping approaches, use machine learning and mathematical modelling to extract knowledge from data. The student will receive extensive training by the supervisory team in computer programming to handle large and complex data sets and conduct mathematical and computational modelling using Linux, Python and R. The student will have access to advanced computational infrastructures, such as the high- performance computing clusters available at Aberystwyth University, and via Supercomputing Wales, and receive appropriate training in their usage. The student will be embedded within the extensive international collaborative network of the supervisory team that includes plant pathologists, genomics experts, modellers and practice-oriented researchers, enabling the student to make use of these diverse sets of expertise. A three-month placement with Syngenta will provide the student with the industry's perspective on the project's outcomes, expanding the range of possible employment options after the completion of the project. The unique combination of empirical, mathematical and computational skills as well as a valuable professional network developed in the course of the project will increase the student's chances to find a high-profile job in academia, governmental agencies or industry.

Student profile:

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URhodeIsland Phylogenomics

PhD or Masters Student position in Phylogenomics / Bioinformatics

A graduate student position is available in the Schwartz Lab in the College of the Life Sciences and the Environment at the University of Rhode Island to work on projects in phylogenomics starting in Fall 2021. The lab is focused on understanding evolutionary history using genomic datasets. We also develop methods and software for researchers interested in empirical questions. The student will be expected to use computational tools to examine phylogenetic datasets, but will have some flexibility to develop a project related to their interest. Opportunities for collaboration at URI and elsewhere are also possible.

Required skills and expectations: * B.S. or M.S. in Evolution or Bioinformatics or a related field (e.g. Biology) * Background and interest in phylogenetics and evolution * Commitment to participating in a collaborative and inclusive lab environment * Prior research experience (e.g. summer internship, work in a research lab) * Interest in computational research

Preferred skills: * Experience with genetic sequence data including building phylogenies * Experience coding in R, Python, or another language * Experience working in an HPC environment * Demonstrated writing skills

This position will be partly funded by URI RA support and partly by an NSF grant. The student will also be expected to TA (for example Introductory Biology lab). Students from backgrounds that have been excluded from science due to ethnicity or race are particularly encouraged to apply. Questions are always welcome, especially if you are interested but not sure about the research or your experience. It is always best to ask.

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 student will be a part of the Biological and Environmental Sciences graduate program in the College of the Environment and Life Sciences, with a specialization in Evolutionary Biology (https://web.uri.edu/cels-gradprograms/bes/emb/) or Cell and Molecular Biology (https://web.uri.edu/cels-gradprograms/bes/cmb/).

For more information please read about research in the lab (https://schwartzlaburi.github.io/research.html) and the expectations and responsibilities (https://schwartzlaburi.github.io/positions.html). Prior to applying to the graduate program please send your CV and a cover letter (rsschwartz@uri.edu) outlining your research interest and how they might intersect with mine.

Rachel Schwartz, PhD Assistant Professor Department of Biological Sciences College of the Environment and Life Sciences The University of Rhode Island Kingston, RI 02881

Office: CBLS 377 Phone: 401-874-5404

"rsschwartz@uri.edu" <rsschwartz@uri.edu>

USBohemia Czechia PhenotypicConvergenceButterflies

Graduate position: USBohemia_Czechia.PhenotypicConvergenceButterflies

New PhD Position: Phenotypic convergence in Neotropical skipper butterflies (Please, feel free to distribute to all potential candidates) Closing date: December 31, 2020

You will be part of an exciting project studying the role of species interactions in the diversification of skipper butterflies (family Hesperiidae) in the Neotropics. The goal of the PhD position is to test competing hypotheses for understanding the evolution of convergent phenotypes. It is expected to obtain measurements of shape and color variation in butterfly wings across species, and to test potential drivers of phenotypic similarity using geometric morphometrics and an available species-level phylogeny.

You will also carry out experiments in the field (rainforest in Peru) in collaboration with our partners at the Natural History Museum in Lima (Depts. of Entomology and Ornithology). We will measure defense strategies in butterflies against avian predators (e.g., unpalatability, escape ability) using bird enclosures. These data will allow quantifying the strength of predator selection on the evolution of butterfly wings.

The project will provide novel knowledge on phenotypic convergence among unrelated butterfly species at both the phylogenetic and the community levels. The overall aim of the PhD work is to bring in deep understanding of butterfly wing phenotype evolution driven by predator-prey interactions.

Priority will be given to candidates who have coauthored at least one scientific publication (including submitted and accepted manuscripts). Experience with conducting fieldwork in the tropics, handling birds in manipulative experiments and/or using geometric morphometrics and phylogenetic comparative methods are desirable. Due to fieldwork in Peru, basic language skills in Spanish are advantageous.

The results will be part of a larger multidisciplinary framework aiming at determining the role of biotic and abiotic factors in the diversification of Neotropical butterflies at different evolutionary and ecological scales. As part of the research activities of our international team, multiple avenues for networking will be possible, including our collaborators Dr. Marianne Elias (Natural History Museum, France; http://tiny.cc/Elias), Dr. Andre V. L. Freitas (University of Campinas, Brazil; http://tiny.cc/Freitas) and Dr. Katerina Sam (Biology Centre, CAS; https://multitrophicinteractions.blog/).

The applicant must have the following qualifications: - Master???s degree in biology or related fields (must be awarded prior to the starting date). - Good communication skills in English, written and spoken. - Independence in learning and working, with documented productivity.

It is expected that you will enroll into the associated PhD program (4 years) at the Faculty of Sciences, University of South Bohemia (https://www.prf.jcu.cz/en). The scholarship will be a combination of research grant salary (50%, from the Biology Centre, Czech Academy of Sciences, https://www.entu.cas.cz/en/) plus student stipends (50% from the University of South Bohemia), fully covering living expenses with a comfortable margin in the Czech Republic. The research facility is in Ceske Budejovice, a charming historical city in the south of the country, within an easy reach of Prague and Vienna. Our working environment (Department of Ecology, led by Prof. Vojtech Novotny, http://tiny.cc/Novotny) is highly diverse and international (16 nationalities from 4 different continents).

The application is by e-mail (to pavel.matos@entu.cas.cz) and must be written in English. The following documents must be attached in one single PDF file: - Cover letter, stating your motivation, how your background and skills fit the project, and your potential plans for this position (max. 2 pages). - CV, including contact details of at least two referees that are familiar with your work.

The deadline for applications is December 31, 2020. The top ranked candidates will be selected for an interview in English (by phone/skype). The start date is upon agreement, but the successful applicant is expected to start during spring 2021.

For further information, please do not hesitate to contact me.

Dr. Pavel Matos-Maravi Biology Centre, Czech Academy of Sciences Branisovska 31, 37005, Ceske Budejovice, Czech Republic Email: pavel.matos@entu.cas.cz Web: http://pavelmatos.wordpress.com Matos Maravi Pavel Fortunato <pavel.matos@entu.cas.cz>

USouthBohemia 3 ArthropodEvolution

Two PhD Studentships are available to work on the project

Do entomopathogenic fungi drive arthropod diversity gradients via host negative density dependence?

Two highly motivated postgraduate students are sought to join a project exploring interactions between entomopathogenic fungi and arthropods in tropical forests. We hypothesise that host-specific entomopathogenic fungi reduce the chance that any single arthropod species can become highly abundant, hence maintaining arthropod diversity. We will explore whether this mechanism can contribute to explaining arthropod diversity patterns across the arthropod phylogeny, and in relation to elevation, anthropogenic habitat disturbance, and future climate change. We envisage that one student will focus on elevation and climate change, and the other on anthropogenic habitat change. Students will conduct field sampling for fungus-infected arthropods and assess arthropod population sizes, experimental eradications of fungi in the wild, experimental exploration of climate impacts in the laboratory, molecular identification of arthropods and fungi in the lab, and statistical analysis of results, including incorporation of fungus-arthropod network data into the LifeWebs database (www.lifewebs.net). There will also be opportunities to develop the project in a direction of the students' own choosing. Duties will include spending extensive periods of time in the field in Malaysian Borneo.

The successful applicants will join the Ant Research Group (http://antscience.com/) at the Institute of Entomology, Biology Centre Academy of Sciences, Ceske Budejovice, Czech Republic, under the supervision of Tom Fayle (http://www.tomfayle.com/index.htm), Shuang Xing (https://xingshuang.weebly.com/about.html), and Vojtech Novotny (department web). The laboratory is a dynamic, multinational group studying ant ecology, evolution and biogeography, and is embedded within the Department of Ecology and Conservation Biology, a world-class centre for interaction network research with regular publications in Science, Nature and other leading journals. The research facility is in Ceske Budejovice, a charming historical city in the south of the country, within easy reach of Prague and Vienna.

The deadline for applications is January 15th 2021, with an expected start date of April 1st 2021 (negotiable). The students will receive a scholarship from the University of South Bohemia and employment on an ongoing grant from the Czech Science Foundation for the 4-year PhD course, sufficient to cover living expenses in Czech Republic. Applicants from all countries are eligible.

Required - A master's degree (non-negotiable requirement for PhD study in Czech Republic). - Interest in the ecology of fungi and/or insects (particularly ants, which are likely to make up the majority of sampled and infected arthropods). - 1st or upper second (2.1) undergraduate degree in ecology or related subject (or equivalent: https://tinyurl.com/y2kcw2c8) - Enthusiasm for working in the field for extended periods of time in challenging conditions in tropical rain forest. - Ability to work independently, manage small teams of assistants, and collaborate with other team members. - Fluency in spoken and written English. - Experience in the use of ecological statistical analyses.

Desirable - Previous experience of tropical field work. - Research experience with fungus or insect ecology. - Experience with basic ecological molecular lab work relating to use for species identification. - Experience with scientific publishing in the above fields.

To apply please send a CV, contact details for three references, and cover letter stating qualifications, previous work and motivation for this position to Shuang Xing (xingshuangbjfu@gmail.com). If you would like to discuss the project further, please feel free to contact Tom Fayle (tmfayle@gmail.com).

A PhD Studentship is available to work on the project

Does competition really structure ant communities in tropical forest canopies?

A highly motivated postgraduate student is sought to join a project that aims to explore the relative contribution of biotic (interspecies competition, forest structure) and abiotic effects (climate) on the structuring of canopy ant communities in tropical rain forests. The student will conduct field surveys, and perform experimental transplants of ant colonies across different forest systems and between dominant species territories in New Guinea, a region with globally high insect and plant diversity. In addition to innovative manipulations of species composition, the project will include functional and phylogenetic measures of ant community diversity, and behavioural and thermal-tolerance

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UStAndrews EvolutionInComplexAdaptiveSystems

*Evolution in complex adaptive systems *

Last chance to apply for a fully funded PhD studentship exploring the evolution of complex forms of developmental plasticity including learning, culture and adaptive immunity, working with Kevin Laland (Biology, St Andrews), Thomas Pradeu (Immunology, CNRS & Bordeaux) and Richard Watson (Computer Science, Southampton). Deadline December 15. https://www.findaphd.com/phds/project/dstl-uk-french-studentship-evolution-in-exploratory-and-selective-developmental-mechanisms/?p114553 Professor Kevin N Laland, PhD, FRSB, FRSE

Centre for Biological Diversity School of Biology University of St Andrews Sir Harold Mitchell Building St Andrews Fife, UK, KY16 9TF tel: 01334 463568 e-mail: knl1@st-andrews.ac.uk http://lalandlab.st-andrews.ac.uk/ https://nicheconstruction.com/ http://extendedevolutionarysynthesis.com twitter: @EES_Update < https://twitter.com/ees_update?lang=en >

– Thomas Pradeu CNRS Senior Researcher in Philosophy of Science Immunology Unit ImmunoConcEpT, UMR5164, CNRS & University of Bordeaux Stanford University CASBS Fellow < https://casbs.stanford.edu/people/current-fellows > (2020-2021) Team Leader Conceptual Biology and Medicine Group < https://www.immuconcept.org/conceptual-biology-medicine/ > PI ERC Starting Grant Immunity, Development, and the Microbiota (IDEM) < http://erc-idem.cnrs.fr/ > Coordinator of the Institute for Philosophy in Biology and Medicine < https://www.philinbiomed.org/ > (PhilInBioMed) Associate Editor, Biology & Philosophy < https://link.springer.com/journal/10539 > 146 rue Léo Saignat 33076 Bordeaux, France & IHPST < https://www.ihpst.cnrs.fr/en > Pantheon-Sorbonne University 13 rue du Four, 75006 Paris, France

Thomas Pradeu <thomas.pradeu.list@gmail.com>

UStAndrews Scotland ExplainingHumanHandedness

Applications are invited for a 3.5 year PhD studentship in the research groups of Prof Andy Gardner and Dr Silvia Paracchini at the University of St Andrews, Scotland.

The studentship is fully-funded and covers tuition fees (including at the Home and Overseas rate), a living allowance and research costs. Candidates of all nationalities are eligible to apply. Default start date is Sep 2021, although this is flexible.

The deadline for applications is 5 Jan 2021.

== About the Project Around 10% of people are left-handed, across all cultures and ethnicities. Although sidedness is observed in most species, the strong rightward population bias of handedness is characteristic of humans. Human handedness correlates with language hemispheric dominance, which typically resides in the left hemisphere, and is thereby linked with traits related to lateralized brain function, including language acquisition, cognition, personality, dyslexia, autism and schizophrenia. Accordingly, explaining handedness holds the key to understanding multiple facets of the human experience.

Handedness has a strong biological basis and is established during foetal development. It is also clearly heritable, with the prevalence of left-handedness increasing to 19.5% and 26.1% among children born to one or two left-handed parents, respectively, and with twin-studies pointing to a heritability of ~25%. However, genomic studies have identified only a small number of genes that are associated with handedness, and these appear to account for a very small proportion of its overall heritability. Accordingly, a major challenge for handedness research is to explain the "missing heritability".

For right-handedness to predominate while left-handers remain present at a lower - but substantial and fixed - frequency implies that there is both a basic evolutionary advantage to right-handedness and also a frequency-dependent advantage to individuals of the rarer type. Such a frequency-dependent advantage has been suggested to arise in relation to combat, whereby left-handers are able to surprise opponents that are more used to fighting against right-handers. In support of this social-evolutionary hypothesis, a left-handedness advantage has been observed in combat sports, and the somewhat higher incidence of left-handedness among men than women is consistent with combat having traditionally been a male-dominated activity.

In this social-evolutionary view of the balance between right- versus left-handedness lies a potential explanation for the missing heritability. Genes underpinning social adaptations are expected to express at different levels according to the parent from which they are inherited, yet these parent-of-origin effects - so-called "genomic imprinting" - are not considered in standard genomic approaches that seek to link genes with phenotypes. Therefore new theoretical models and analytical approaches are need to understand the biology of handedness. The project aims to identify new genes contributing to handedness, and to develop a completely novel framework for the integration of theoretical and empirical approaches in the study of social traits more generally.

This is a unique opportunity for a fully-funded interdisciplinary PhD project that will combine social evolutionary theory and genome analysis to establish the role for parental genotype in deciding an individual's handedness. Training will be provided in both areas of the project. The PhD researcher will work under the supervision of Prof Andy Gardner (School of Biology) to develop novel mathematical models to formalise this social-evolutionary hypothesis and thereby derive explicit predictions as to patterns of gene expression for genes that promote versus inhibit the development of left-handedness. Genetic analysis on already-available datasets will be supervised by Dr Silvia Paracchini's (School of Medicine)

The successful applicant will have an undergraduate degree in Biology or other relevant subject, an ability for logical and creative thinking, and a passion for evolutionary genetics and multidisciplinarity. We particularly encourage applications from women and from BAME individuals.

== References Gardner A & Ãbeda F (2017) The meaning of intragenomic conflict. Nature Ecology & Evolution 1, 1807-1815.

Hitchcock TJ, Paracchini S & Gardner A (2019) Genomic imprinting as a window into human language evolution. BioEssays 41, 1800212.

Papadatou-Pastou M, Ntolka E, Schmitz J, Martin M, MunafÃ² MR, Ocklenburg S & Paracchini S (2020). Human handedness: A meta-analysis. Psychological Bulletin 146, 481-524.

Pettigrew KA, Frinton E, Nudel R, Chan MTM, Thompson P, Hayiou-Thomas ME, Talcott JB, Stein J, Monaco AP, Hulme C, Snowling MJ, Newbury DF & Paracchini S (2016) Further evidence for a parent-of-origin effect at the NOP9 locus on language-related phenotypes. J Neurodevelop Disord 8, 24.

== How to Apply Full details are given here:

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UStirling OysterGenomics

This 4 year PhD project is part of a competition funded by EASTBIO BBSRC Doctoral Training Partnership. This opportunity is open to UK and International students and provides funding to cover stipend and UK level tuition (Please state if your institution will provide funding to cover the difference in fees). Please refer to UKRI website and Annex B of the UKRI Training Grant Terms and Conditions for full eligibility criteria.

The prospective student will be part of a multidisciplinary group at the Institute of Aquaculture in the University of Stirling and at The Roslin Institute and will acquire expertise in bivalve biology and genetics. The student will initially analyse the currently available datasets, by using statistical and bioinformatic tools, to build hypothesis of domestication signatures in the oyster populations to then further analyse publicly available sequencing data, pick out informative SNPs and potentially develop a low-density panel to facilitate the screening of oyster samples. The student will also oversee the functional analysis of genes in the identified genomic regions using gene expression profiling, which will give us a better idea of potential biological mechanisms underlying the selection signatures

This is a full-time PhD Project

About the Project:

Aquaculture has become a fast-growing industry called to play a crucial role in future food production. Among a vast number of aquaculture species being cultured, Pacific oyster is the most widely farmed oyster species, providing socio-economic benefits to many coastal communities and generating yearly revenues at approximately US$1.2 billion worldwide (FAO, 2018).

The domestication process by which wild animals or plants adapt to human-altered environmental conditions is recent in aquaculture species compared to terrestrial animals. However, the practice has expanded quickly over the past few decades and breeding programs have been stablished for many important aquaculture species such as Atlantic salmon, tilapia, rainbow trout, among others. These breeding programs have been focused on the improvement of productive traits, i.e. growth rate.

A positive (natural or artificial) selection causes phenotypic changes in the organisms but also underlying genetic changes involving an increase in the frequencies of favourable allelic variants and, consequently, a decrease of genetic variation in the loci under selection which with time will leave signatures of selection noticeable at the genome level. In particular, more information is needed to understand how selection practices have affected Pacific oyster populations, globally, in terms of levels of inbreeding, genetic diversity and the genomic regions/genes under selection.

The reduction of genetic diversity in a population may affect disease resistance and the adaptability to environmental changes (Allendorf, 1980). Therefore, it is crucial to survey the genetic diversity within or between selected lines and wild populations for successful hatchery management of species. Breeding companies face a challenging problem on how to keep genetic diversity over generations. Analyses of these selection signatures in domestic animals can provide further insights into the genetic basis of adaptation to diverse environments and genotype/phenotype relationships. The development of genetic markers for monitoring the genetic variation in wild populations and selected lines is highly desired. The identification of such regions under selection is important since they would highlight loci that are linked to economically relevant characteristics such as growth, disease resistance or adaptation to environments.

Next-generation sequencing and high-throughput genotyping technologies play a fundamental role in genetic studies by for example allowing the development of genomic resources such as the identification of single nucleotide polymorphism (SNP) or the quantification of mRNA expression levels, making possible the comparison of multiple samples or populations.

More information can be found at: https://www.findaphd.com/phds/project/eastbio-genome-wide-identification-and-analysis-of-signatures-of-selection-in-pacific-oyster/?p126238 If any questions, please contact Dr. Alejandro Gutierrez at alejandro.gutierrez@stir.ac.uk

The University achieved an overall 5 stars in the QS World University Rankings 2020 UK Sports University of the Year 2020 (Times Higher Good University Guide) The University of Stirling is a charity registered in Scotland, number SC 011159.

Alejandro Gutierrez <alejandro.gutierrez@stir.ac.uk>

UTromso AncientMetagenomicsMethods

PhD research fellowship to develop sedimentary ancient DNA bioinformatic methods at the Arctic University Museum of Norway in Tromso, supervised by Assoc. Prof. Peter Heintzman.

Ancient DNA extracted from sediments and other environmental sources is an emerging and fast-moving field that has the potential to revolutionize our ability to reconstruct past communities at unprecedented temporal resolution. However, computational methods for processing, identifying, and analyzing total ancient DNA from sediments are still rudimentary. The goal of the position is to therefore develop novel bioinformatic methods for the optimal processing of metagenomic sequence data generated from complex and degraded biological remains. The project will use a combination of published and recently generated data sets from lake, cave, permafrost, and archaeological sites across the Pleistocene and Holocene of Europe, Asia, and North America, as well as simulated data sets to test and verify the developed methods. You will gain expertise in bioinformatics, metagenomics, ancient DNA/palaeogenomics, molecular biology, palaeoecology, and analysis of large genomic data sets.

The position is for a period of four years, of which three years are dedicated to research. The fourth year is distributed as 25% each year, and consists of teaching, outreach, sys-admin work, and/or other duties for the Arctic University Museum.

Apply here: https://www.jobbnorge.no/en/available-jobs/job/194286/phd-fellowship-to-develop-sedimentary-ancient-dna-methods Deadline for applications is 20th December 2020. Start date is flexible, but should be within 6 months of the application deadline.

For more info, please contact: peter.d.heintzman@uit.no / Twitter: @PalaeoPete

Cheers, Pete Heintzman

Pete Heintzman <peteheintzman@gmail.com>

Vienna PopulationGenetics

Reminder: apply by Jan 17, 2021 Start date: Sept 2021 (or earlier)

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

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

Available topics include:

- Evolution from de novo mutations - influence of elevated mutation rates. - Evolution of sex-specific neuronal signaling. - Genome evolution in columbines. - Genomic architecture of reverse selection. - Inference of selection signatures from time-series data. - Long-term dynamics of local Drosophila populations. - Molecular genetics of epigenetics. - Seed ecology. - Structural variation and genome evolution. - Temperature adaptation in Drosophila: phenotypic adaptation. - Understanding polygenic adaptation.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by January 17, 2021 will be considered. Two letters of recommendation need to be sent directly by the referees.

Depending on the project, PhD degrees will be awarded either in genetics, mathematics or statistics. PhD students will receive a monthly salary based on currently EUR 2.205,60 before tax according to the regulations of the Austrian Science Fund (FWF).

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

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

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

Jobs

BinghamtonU SUNY ComputationalBiology

Assistant Professor (Tenure track) position in Computational Biology at Binghamton University SUNY

Job posting link: http://-binghamton.interviewexchange.com/-jobofferdetails.jsp?JOBID=126757 About Binghamton University: Binghamton University is a world-class institution that unites more than 130 broadly interdisciplinary educational programs with some of the most vibrant research in the nation. Our unique character - shaped by outstanding academics, facilities and community life - promotes extraordinary student success. Binghamton merges rigorous academics, distinguished faculty and state-of-the-art facilities to engage and challenge its 18,000 students. The high-achieving Binghamton student body also represents a great diversity of life experiences, from first-generation college-goers to international students. Beyond their talent, these classmates share a desire to shape the future through technology, insight, intellectual exploration and community service.

Job Description: The Department of Biological Sciences at Binghamton University (SUNY) (https://-www.binghamton.edu/biology/) invites applications for a tenure-track Assistant Professor position in any area of computational biology. The ideal candidate will develop an original research program that addresses fundamental questions about complex biological systems using and/or developing quantitative and computational tools for the analysis of large datasets. We especially encourage applicants who are working at the level of genomes, transcriptomes, proteomes, metabolites, and/or cell populations to investigate genetic interactions, gene expression regulation, biological networks, and/or their evolution. Priority will be given to applicants whose research program complements departmental strengths in Genetic and Molecular Interactions, Global Change Biology, and/or Infectious Diseases.

The successful candidate must have a PhD in Biology or a related field (e.g. Statistics, Math) and will join a diverse biology department with over 30 tenured/tenure-track and teaching faculty members. The university is committed to encouraging interactions among data scientists on campus through a newly developed Transdisciplinary Area of Excellence in Data Science which provides seed grants, hosts seminars and data salons, and assists in developing educational resources. Computational infrastructure on campus is available through the Spiedie high performance computing cluster (with increases in capacity currently being implemented). The successful candidate will contribute to the department's teaching mission through undergraduate and graduate courses in their areas of expertise and will mentor graduate and undergraduate students.

The Department of Biological Sciences is committed to equity and inclusion and is actively working to increase diversity amongst its faculty. Members of groups historically underrepresented in computational biology and those from non-traditional backgrounds are strongly encouraged to apply. Additionally, evidence of a commitment to advancing equity and inclusion through research, teaching, and/or service will be valued.

Requirements: The successful candidate must have a PhD in Biology, Computational Biology, or a related field (e.g. Statistics, Math). Applicants must have received a PhD (or equivalent) degree by the anticipated start date (fall 2021).

Additional Information: The State University of New York is an Equal Opportunity/Affirmative Action Employer. It is the policy of Binghamton University to provide for and promote equal opportunity employment, compensation, and other terms and conditions of employment without discrimination on the basis of age, race, color, religion, disability, national origin, gender identity or expression, sexual orientation, veteran or military service member status, marital status, domestic violence victim status, genetic predisposition or carrier status, or arrest and/or criminal conviction record unless based upon a bona fide occupational qualification or other exception.

As required by title IX and its implementing regulations, Binghamton University does not discriminate on the basis of sex in the educational programs and activities which it operates. This requirement extends to employment and admission. Inquiries aboutsex discrimination may be directed to the University Title IX Coordinator or directly to the Office of Civil Rights (OCR). Contact information for the Title IX Coordinator and OCR, as well as the University's complete Non-Discrimination Notice may be found here. Pursuant to Executive Order 161, no State entity, as defined by the Executive Order, is permitted to ask, or mandate, in any form, that an applicant for employment provide his or her current compensation, or any prior compensation history, until such time as the applicant is extended a

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CentreC Kentucky GeneticsEvolutionaryBiology

Assistant or Associate Professor of Biology Centre College invites applications for a tenure-track position in Biology at the rank of Assistant or Associate Professor to begin in August 2021. We seek a teacher-scholar who will enhance the learning and teaching environment at Centre College with their lived experience, ideas, perspectives, and scholarship. The candidate must have a Ph.D. in the biological sciences or related field by the time of appointment, demonstrate a commitment to excellence in teaching at a nationally-ranked liberal arts college, and display enthusiasm for teaching the following classes: an introductory genetics course and its associated lab, an introductory biology course (evolution, biodiversity, and ecology) and its associated lab, and additional upper-level classes in the candidate's area of interest which might include, but are not limited to: anatomy, physiology, evolution, or botany. Collaborative research with undergraduates is expected and supported. The program strongly encourages applications from candidates who have experience teaching and mentoring a diverse student body.

Centre College is committed to an environment that welcomes and supports diversity. As noted in the Statement of Community < http://centre.smartcatalogiq.com/en/2018-2019/Faculty-Handbook/Introduction/Statement-of-Community >, Centre strives to create an environment where individuals of diverse backgrounds have the opportunity to exchange ideas and share in the richness of mutual experiences. Therefore, the Biology program strongly encourages applications from candidates who further diversify our faculty, who celebrate the rich diversity of our student body, and who utilize inclusive and engaging pedagogical practices. A number of resources support faculty success, including a robust Center for Teaching and Learning, peer mentoring, and endowed funding for professional development.

Centre College is a highly selective liberal arts college of about 1,450 students, has one of the nation's premier study abroad programs and is among the top National Liberal Arts Colleges by U.S. News & World Report. Classes are small and academic standards are high. Centre graduates enjoy extraordinary success, with entrance to top graduate and professional schools, prestigious fellowships for further study abroad, and rewarding jobs. The College is located in Danville, Kentucky, a town of 18,000 recognized for its high quality of life. It is within easy driving distance of Lexington, Louisville, and Cincinnati. For information about the College, visit our web site at www.centre.edu . Centre College is a proud member of the Greater Kentucky Higher Education Recruitment Consortium: www.greaterkyherc.org. The Greater Kentucky HERC is a non-profit organization composed of a diverse group of colleges, universities, hospitals, government agencies, non-profit organizations, and members of private industry committed to recruiting and retaining a diverse, talented workforce. Member representatives include faculty, staff, human resources professionals, institutional leaders, and faculty relations experts. Centre College is an equal opportunity employer.

To apply, please go to http://apply.interfolio.com/ < http://apply.interfolio.com/44117 >44117 to submit a letter of application that includes your cover letter, CV, transcripts, three letters of recommendation, teaching philosophy, research interests, and a statement that explains the importance of diversity and inclusion and how you would contribute to and/or address issues of diversity and inclusion at Centre. Review of applications will begin January 4, 2021.

"Mark L. Galatowitsch" <mark.galatowitsch@centre.edu>

HudsonAlphaInst Biotechnology

The HudsonAlpha Institute for biotechnology hires in the fields of plants, geneticists, to bioinformatics. We have 3 positions open currently. They are: 1) Clinical Data Scientist/Bioinformatician I CSL https://hudsonalpha.applicantpro.com/jobs/1596529.html 2) Clinical Lab Technologist https://hudsonalpha.applicantpro.com/jobs/1590675.html 3) Plant Biotechnologist https://hudsonalpha.applicantpro.com/jobs/1556897.html Ava Rose-Schaefer, CPP HR Generalist aroseschaefer@hudsonalpha.org (p)256.327.9610 601 Genome Way Northwest Huntsville, AL 35806 https://hudsonalpha.org/ aroseschaefer@hudsonalpha.org aroseschaefer@hudsonalpha.org

Ithaca NY BioinformaticsProgrammer

The Mueller lab at the Boyce Thompson Institute (https://btiscience.org/) has an open position for a bioinformatics and web programmer to work on omics analysis and web-based data visualization for genomics and plant breeding database systems. The genomics databases (e.g. https://citrusgreening.org/) contain genomics, marker, phenotype and transcriptomics information with genome browsers, expression atlases and pathway databases. The breeding databases (e.g. https://cassavabase.org) contain extensive genotypic and phenotypic information for genomic selection breeding approaches, which requires extensive modeling and prediction algorithms, with appropriate visualization. This position has lots of flexibility and opportunities for collaboration, travel, and independent research. All researchers with relevant background in bioinformatics will be considered, regardless of the organism(s) previously studied.

Major Responsibilities

Major responsibilities include genomics and transcriptomics analysis, code development and maintenance for genomics and breeding websites. Knowledge of JavaScript, jQuery, HTML5, Perl, RESTful web services (BrAPI, https://brapi.org/), and a good working knowledge of Linux (Debian), git, and web servers (Catalyst, apache2, nginx), as well as Javascript graphical frameworks such as D3 are desired. Interacting with scientists, molecular biologists, students and breeders working in different international institutions, as well as travel will be involved.

Job Requirements

A background in programming, computational biology, or related field with strong interests in plant and/or vector biology and/or breeding is desired.

Application: http://bti.hrmdirect.com/employment/job-opening.php?req=1403469&&#job –

Surya Saha Sol Genomics Network Boyce Thompson Institute, Ithaca, NY, USA https://citrusgreening.org/ https://orcid.org/0000-0002-1160-1413 http://www.linkedin.com/in/suryasaha https://twitter.com/SahaSurya Surya Saha <ss2489@cornell.edu>

JohnInnesCentre PlantOrMicrobialEvolution

Group Leader search (John Innes Centre, Norwich, UK)

We have several positions available and are looking for creative early-career or established researchers who wish to develop exciting long-term independent programs in plant and microbial science and be part of the highly collaborative culture of the John Innes Centre (Norwich, UK).

We have two adverts out: one for Group Leaders in areas that are complementary with our science: < https://www.jic.ac.uk/vacancies/group-leaders-2/ > and one that is specifically targeted at Group Leaders who have a strong interest in studying wheat: < https://www.jic.ac.uk/vacancies/group-leader-wheat-research/ >. Our Group Leaders are similar to a tenure-track or tenured research professorship, with some teaching opportunities available at the University of East Anglia.

As an international centre of excellence in plant and microbial science, you will work alongside researchers covering a vast breadth of areas < https://www.jic.ac.uk/research-impact/ >. Although most of our researchers work on more cellular/molecular/developmental topics, please note that basic science and evolutionary ecology are within our remit, and we are interested in growing this area. Researchers studying the genetic/molecular and/or mechanistic underpinnings of ecology and evolution would be especially welcome.

We have state-of-the art technology and research platforms < https://www.jic.ac.uk/research-impact/technology-research-platforms/ > that support Group Leaders and their labs across all scientific disciplines, including bioimaging, biomolecular analyses, genomics and bioinformatics, and field, horticultural and (quarantine) entomology services. We also have a new purpose-built 110-hectare field experimentation station, bringing together labs and field research in one location.

We have a vibrant mentoring programme for all career levels, including a program that is specifically tailored to support those starting their independent careers. The collegial environment that we foster encourages strategic input at all levels.

Appointments can be made at any level (Tenure Track or Tenure) depending on experience and come with significant support (professional development, research and administrative). Start-up research funding is negotiable.

Interested applicants are invited to submit a description of (i) current research activities and (ii) short and longer-term research aims and potential strategic goals (each ~2-3 pages).

Apply online < https://jobs.jic.ac.uk/Details.asp?vacancyID=15854 > including a CV and names of three academic referees.

The deadline for applications is Friday 22nd January 2021 with interviews taking place mid-March 2021.

Click here < https://www.jic.ac.uk/training-careers/why-work-at-jic/ > for further information about working at the John Innes Centre, or contact Human Resources, John Innes Centre Norwich, NR4 7UH, UK, (+44) (0)1603 450149, quoting reference 1003975.

We are committed to equality of opportunity for all employees and will consider applications on the criteria above regardless of gender, ethnicity or other personal characteristics, beliefs and backgrounds.

The Institute holds a prestigious Athena SWAN Gold award in recognition of our inclusive culture, commitment and good practices towards advancing of gender equality. We are also a Disability Confident Employer and a Stonewall Diversity Champion. We offer an exciting, stimulating, diverse research environment and actively promote a family friendly workplace.

We welcome applications from candidates seeking full-time, part-time or other flexible working arrangements.

We strongly encourage applications from women and ethnic minorities.

"Kelsey Byers (JIC)" <Kelsey.Byers@jic.ac.uk>

LehighU EvolutionaryBiology

Tenure-Track Faculty Position in Evolutionary Biology Department of Biological Sciences Lehigh University

The Department of Biological Sciences at Lehigh University invites applications for a tenure-track position at the level of Assistant Professor. We are particularly interested in applicants studying natural populations, although all applicants investigating fundamental questions in evolutionary biology (broadly defined) whose research complements or enhances existing departmental strengths are welcomed. Hires are expected to develop an internationally recognized extramurally funded research program and contribute to the department's excellence in teaching.

Eligible applicants will hold a Ph.D. at the time of employment and have at least one year of postdoctoral research experience. To apply, please submit: (1) a cover letter, (2) curriculum vitae, (3) research statement, (4) teaching statement, (5) a statement of contributions to promote diversity and inclusion, and (6) have at least three letters of recommendation submitted to https://academicjobsonline.org/ajo/jobs/17733 . Founded in 1865, Lehigh University has combined outstanding academic and learning opportunities with leadership in fostering innovative research. Recognized among the nation's highly ranked research universities, Lehigh offers a rigorous academic community for nearly 7,000 students. Lehigh University has some 5,000 undergraduates, 2,000 graduate students, and about 550 full-time faculty members. Lehigh University is located in Bethlehem, PA., a vibrant and historic area. Over 820,000 people live in the Lehigh Valley, which is in close proximity to New York City and Philadelphia.

For additional information contact BIOS Faculty-Search Committee Chair at inbios@lehigh.edu or by mail at 111 Research Drive, Bethlehem, PA 18015. http://www.lehigh.edu/~inbios/ The initial deadline for applications is February 1st, 2021.

Lehigh University is especially interested in candidates who can contribute, through their research, teaching and/or service, to the diversity and excellence of the academic community. Lehigh University is the recipient of an NSF ADVANCE Institutional Transformation award for promoting the careers of women in academic sciences and engineering.

—- Amber M. Rice, Ph.D. (Pronouns: she, her, hers) Associate Professor and Co-Director of Graduate Program

Department of Biological Sciences, Lehigh University 111 Research Drive, B217 Bethlehem, PA 18015 USA Lab website: https://wordpress.lehigh.edu/amr511/ Follow us on Twitter: @amberricelab

Amber Rice <amr511@lehigh.edu>

MichiganStateU StaffRes EvolEcolDiseases

The newly-established Wale Lab < http://www.ninawale.com/ >in the Department of Microbiology and Molecular Genetics seeks a Research Assistant II to assist with the development of exciting new research at the interface of ecology and evolutionary biology, infectious disease biology and molecular biology. This full-time position involves research on two host-pathogen systems: a mouse model of malaria and a little-studied, highly-virulent bacterium of zooplankton, which the Wale lab is establishing as a new model of infectious disease dynamics.

Duties

The successful applicant will be a highly-motivated, organized and creative researcher, who enjoys working independently. They will i) design and develop new assays and experimental protocols for the collection of data in both study systems, ii) collect, analyze and (if the applicant is interested in doing so) write up experimental data for publication, iii) oversee and coordinate laboratory operations and maintenance. While duties will largely be experimental, the position may require up to 20% administrative activities, including ordering of equipment, maintenance of health and safety standards, assistance with IACUC applications and maintenance of laboratory records/protocols. The Research Assistant will also train, supervise and collaborate with undergraduate and graduate students, and postdoctoral fellows. Dr. Wale is committed to the inclusion of Research Assistants in all aspects of laboratory life, from inclusion on (and leading of) publications to lab meetings and other laboratory activities.

This position is initially for one year, with extension contingent on performance and available funding. Please note that Dr. Wale is committed to funding this position for the long term, if the right candidate is found.

Desired Qualifications

Experience in culturing previously-unculturable microbes is desirable, as is experience with flow cytometry, microscopy and molecular methods (quantitative PCR, cloning etc.). Experience working with BSL-2 pathogens and with mice is desirable but not a prerequisite. Experience preparing data for publication and for submission for grant proposals. Strong interpersonal skills, including the capacity to communicate with researchers in a variety of different scientific fields and at different stages of academic training. A graduate degree (MS or PhD) in microbial ecology, microbiology,or molecular biology, or equivalent experience, is desired. A driver's license is preferable.

Apply & contact

For more information & to apply, please go to www.careers.msu.edu/en-us/job/504343/research-assistant-ii and/or contact Dr. Wale at walenina@msu.edu. Review of applications will begin immediately; the closing date is *December 22nd 2020. *Apologies for cross posting.

– Nina Wale PhD Assistant Professor Dept. Microbiology and Molecular Genetics Biomedical & Physical Sciences Building Rooms 6118 (lab) & 6178 (office) 567 Wilson Road, East Lansing, MI www.ninawale.com @ninawaleEEB

Nina Wale <walenina@msu.edu>

Muenster Germany BeetleEvolutionaryGenomics

The Institute for Evolution and Biodiversity at the University of Münster, Germany, invites applications for a Junior Group Leader Wissenschaftliche/r Mitarbeiter/in (Salary level TV-L E13, 100%)

in the Plant Adaptation-in-Action group, headed by Prof Shuqing Xu (https://www.uni-muenster.de/Evolution/plantadapt/people/shuqingxu.shtml). The successful candidate may start as soon as possible, preferably before May 2021. The salary will initially be provided for three years, with possibility of extension. The emergence of agricultural pests and their resistance to pesticides is a remarkable example of rapid adaptation in a human-mediated evolutionary experiment. The Colorado potato beetle (CPB, Leptinotarsa decemlineata), an insect with little practical significance to crops 150 years ago, is now a devastating global pest of potato and other solanaceous crops and has evolved resistance to nearly all known insecticides. The remarkable resistance to insecticides and relatively short and well-known natural history thus make CPB an ideal system to study the mechanisms of insecticide resistance and evolutionary processes of agricultural pests. In this DFG-funded project, the candidate will lead a team to investigate the evolution of CPB and the mechanisms of insecticide resistance using interdisciplinary approaches.

During the course of the project, the candidate will mature his/her scientific skills and develop independence in project planning and management skills. In addition, the candidate will gain the opportunity to improve their leadership skills by leading a research team consisting of one PhD student and several MSc and BSc students. The position serves as a stepping-stone for the candidate to pursue a faculty position.

Requirements: We are looking for a highly motivated researcher with a doctoral degree, or equivalent thereof, in biology, evolutionary genomics, bioinformatics or computer science. The candidate is expected to design, conduct and organize a large whole-genome resequencing project and conduct experimental work with high degree of independence. Thus, a background in bioinformatics and evolutionary genomics is required. Applicants must demonstrate experience in statistics and population genomics. Experience with pesticide resistance, animal evolutionary ecology, plant-herbivore interactions and molecular genetics are a plus. Our group consists of people of various nationalities and teamwork is essential for all projects in the group. Therefore, excellent communication skills, as well as proficiency in spoken and written English are expected. Good knowledge in German is a plus.

The University of Münster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. The University of Münster is committed to employing more staff with disabilities. Candidates with recognized severe disabilities who have equivalent qualifications are given preference in hiring decisions, although some restrictions related to specific project-related tasks may apply.

Applications must be in English and include:

(1) a motivation letter stating the research interests with reference to the stated requirements in no more than 2 pages, (2) a detailed CV including academic and extracurricular achievements, as well as details of all research experience, (3) an abstract of the PhD thesis, and (4) contact details of at least two referees.

Applicants should send their documents in one single PDF file to Prof Shuqing Xu (shuqing.xu@uni-muenster.de) with a subject line “Junior Group Leader Position - Your Name”. The application review will commence on 1st February 2020. The position will remain open until filled.

Prof. Dr. Shuqing Xu Institute for Evolution and Biodiversity University of Münster Hüfferstraße 1 D-48149 Münster E-mail: shuqing.xu@uni-muenster.de Phone: +49 251 83-21090

Shuqing Xu <shuqing.xu@uni-muenster.de>

Munich Germany AncientDNALabManager

Dear all,

The Palaeogenomics group of the Department of Veterinary Medicine, at the Ludwig-Maximilians-Universität Munich, is looking to appoint a Laboratory Manager at the earliest possible date.

The Palaeogenomics group (https://www.animal-palaeogenomics.com/), led by Prof. Laurent Frantz, is a newly formed group, part of the Institute of Palaeoanatomy, Domestication and the History of Veterinary Medicine, within the Department of Veterinary Medicine. Our group is broadly interested in evolutionary genomics, archaeology, conservation biology and sustainable agriculture. We exploit the power of ancient and modern genomics to contrast current patterns of genetic diversity to those in the past: this allows us to track evolutionary processes including artificial selection, extinction, speciation and domestication through time.

We are looking for a Laboratory Manager to facilitate the efficient operation of the ancient and modern DNA laboratories within the group. The contract is for an initial 1 year but is renewable for an additional 4 years, with the potential for longer-term extensions. The post-holder will lead the management and operation of the modern and ancient DNA facilities, sample processing, ancient DNA extraction, library preparation and sequencing. Additional roles include purchasing, shipments, safety and general organization, training members and visitors of the lab in established workflows, and interaction with other scientists, students and technicians. The post-holder will also have the opportunity to be involved in research projects and publications, as well as to purse their own research ideas.

Role:

- DNA extraction from biological substrates, and genomic library preparation. - Improvement of laboratory techniques through in-house optimization and innovation, and implementation of new advances and best practices. - Training other scientists in laboratory workflows. - Provide support for sample organisation including handling, shipping, managing internal databases, legal documentation and curation. - Assist with general administrative duties within research group, alongside other staff. - Assist with the maintenance and day-today operation of the specialized ancient and modern DNA facilities, instruments, and supplies, alongside other technical staff. - Assist with the managing consumables and reagent orders, maintaining stocks, and handling the shipment of libraries for sequencing, alongside other technical staff.

Profile:

- BSc, MSc, or PhD in Biological Sciences or in a field incorporating genomics, Next Generation Sequencing techniques, or equivalent qualification / experience (experienced technicians are also encouraged to apply). - Experience with (ancient) DNA extraction, library preparation and high-throughput sequencing. - Strong organisational skills. - Experience with training others in lab techniques (desirable). - Proficiency in English (prerequisite) and German (desirable). - An interest in Evolutionary biology and/or Archaeology (desirable).

We offer:

The Ludwig-Maximilians-Universität Munich is one of the largest and most prestigious research institutions in Germany and offers a wide range of training and development opportunities. The workplace is in a central location in Munich that can be easily reached by public transport. The contract is for an initial 1 year but is renewable for an additional 4 years, with the potential for longer-term extensions. The salary will be based on on TV-L. Part-time employment is generally possible. The university is an equal opportunity employer. Handicapped applicants will be given preference in the case of approximately equal qualifications. The University of Munich is interested in increasing the number of female faculty members and encourages women to apply.

To apply, please send a C.V, including contact of two referees, and a cover letter to Laurent.Frantz@palaeo.vetmed.uni-muenchen.de

The deadline for application is January 15th 2021

For enquiries or further questions please contact Prof. Laurent Frantz: Laurent.Frantz@palaeo.vetmed.uni-muenchen.de

https://www.uni-muenchen.de/aktuelles/-stellenangebote/technik/index.html Laurent Frantz <laurent.frantz@palaeo.vetmed.uni-muenchen.de>

NorthernIllinoisU ChairBiologicalSciences

Position Description

Northern Illinois University (NIU) invites applications for the position of Chair of the Department of Biological Sciences (BIOS) (https://www.niu.edu/clas/biology/-index.shtml). This is a 12-month tenured position with rank of associate or full professor to begin July 1, 2021.

We seek a Chair that is a strong communicator and will provide strategic, academic, and administrative leadership to distinguish the department in its research, teaching and service missions. The successful candidate will (1) promote excellence in undergraduate and graduate education and research and recruitment and retention of excellent students, (2) build bridges between departmental research emphases and other disciplines, departments, and institutions and (3) foster a transformation in faculty and staff development and composition to better serve an increasingly diverse community.

NIU is a public research university located in DeKalb, Illinois, an exurb of Chicago. Our 16,000+ student body is diverse, with many first-generation and minority students. NIU prides itself on student-centered approaches to teaching and research, and has social mobility, equity, and inclusion at the heart of its mission. Biological Sciences is one of the largest majors on campus and our department has faculty and students pursuing dynamic research agendas including biomedical, microbial, pedagogical, developmental, evolutionary and ecological questions utilizing nearby, world-class resources like Nachusa Grasslands, The Nature Conservancy, Fermi National Accelerator Lab, Argonne National Lab and the Chicago Proton Center. DeKalb is now home to the new Facebook strategic interconnected data center that uses local access to cloud on-ramps and surrounding energy grids. The proximity of DeKalb to Chicago provides easy access to Chicago's research and technology corridor, the arts and extensive nature preserves and parks. The Department of Biological Sciences is housed primarily in Montgomery Hall, a 112,000-square-foot facility. In addition to teaching and research laboratories, the department maintains live animal facilities, greenhouses, confocal and electron microscopy, and molecular core services (nucleic acid sequencing and qPCR).

Required Qualifications Ph.D. in the Biological Sciences, a history of excellence in teaching and research, relevant leadership, management and administrative experience, and a demonstrated commitment to diversity, equity, and inclusion.

Preferred Qualifications The field of specialization is open but should complement departmental strengths in molecular, cellular, and organismal biology.

Special Instructions Applications must include a (1) letter of interest, outlining the candidate's leadership and management experience, motivation, and qualifications for the position (2-3 pages); (2) a vision statement including research, teaching and fostering diversity, equity, and inclusion (3 page maximum); and (3) a current curriculum vitae with the names and contact information for three professional references. Review will commence for completed applications received by January 31, 2021, but applications will be accepted until the position is filled. NIUvalues diversity in its faculty, staff and student body. In keeping with this commitment, our academic community strongly encourages applications from diverse candidates and candidates who support diversity. Questions may be sent via email to the chair of the research committee, Dr. Linda Yasui at lyasui@niu.edu.

Posting date: December 4, 2020

Priority Review Date: January 31, 2021

Link to job posting: http://employment.niu.edu/postings/54555 Jennifer Koop, Ph.D. Assistant Professor Department of Biological Sciences Northern Illinois University 1425 W. Lincoln Hwy De Kalb, IL 60115 jkoop@niu.edu Office: 815-753-4215

Jennifer Koop <jkoop@niu.edu>

Surrey England Bioinformatics

Bioinformatics Research Scientist

Location: Egham, Surrey Salary: 40,000+ per annum, depending on experience Start: Immediately Duration: Permanent

Applications are invited for a Bioinformatics Research Scientist to join an expanding science-based start-up. The successful candidate will work closely with the members of the data and wider science teams to develop and validate state-of-the-art bioinformatics tools and processes for sequence-based biodiversity data. Applicants should have significant experience with metabarcoding data and the development of bioinformatics pipelines. Topics of current interest include data quality assurance, taxonomic assignment, and phylogeny-informed approaches for Illumina MiSeq metabarcoding data. Future work may focus on alternative technologies and approaches such as metatranscriptomics, shotgun metagenomics, and nanopore sequencing. Evidence of significant contribution to relevant research projects is required. The successful applicant will be comfortable working independently and as part of a wider team. They will be required to lead the development of the company's bioinformatics pipelines in close collaboration with the Lead Bioinformatician. Applicants must submit examples of their work as part of their application. The full specification can be found below. To apply please email careers@naturemetrics.co.uk including a CV and covering letter, and state that you are applying for the Bioinformatics Research Scientist role. There is no fixed deadline for applications and the position will be held open until we find the right candidate.

ABOUT NatureMetrics NatureMetrics is a high-growth start-up company leading the revolution in molecular biodiversity monitoring, enabling environmental managers to measure and monitor biodiversity with DNA-based tools. We have grown steadily for four years and are now expanding following a recent investment raise. We are a team of bright, enthusiastic individuals who are excited to be breaking new ground and disrupting the world of biodiversity monitoring. We take great pride in our work and are seeking new team members who will do the same. For more details, please visit www.naturemetrics.co.uk . Roles & responsibilities

General - Lead on the development and implementation of new bioinformatics pipelines in close collaboration with the Lead Bioinformatician - Work with the Bioinformatician to operationalise new solutions and integrate into SOPs - Refine existing pipelines where required - Lead on the bioinformatics component of projects that require a bespoke solution - Ensure that the outputs of bioinformatics pipelines are robust and of high quality - Contribute to scientific publications and reports - Contribute to the preparation of grant applications and tenders where relevant

Documentation - Maintain version-controlled, fully annotated scripts following NatureMetrics style guides - Write guides/explainers for developed tools suitable for different audiences - Prepare and contribute to reports and applications where relevant

Reporting - This role reports to the Lead Bioinformatician

Communication - Attend regular update meetings with the wider team - Update wider company, management or board on progress as required - Work collaboratively with the data and science teams

Person specification

Education & qualifications - You will have a PhD and postdoctoral experience in a relevant field - Specialist knowledge, skills & experience - Strong R and/or Python coding is essential, with good working knowledge of relevant packages - Experience with common command-line tools used in metabarcoding is required - Evidence of extensive metabarcoding data handling is required - Evidence of a leading role in relevant tool development is required - Particular expertise in quality control, taxonomic assignment, or appropriate phylogenetic methods would be an advantage - Strong Bash scripting and experience with Ubuntu would be an advantage

Interpersonal & communication skills - Organised & meticulous with effective communication skills - Able to work independently and as part of a team

Additional requirements - All applicants are legally required to demonstrate the right to work/permission to work in the UK

Terms & conditions

Location - The post is based at NatureMetrics Ltd, CABI Site, Bakeham Lane, Egham, Surrey, TW20 9TY - There is significant flexibility for regular home working

Working pattern and hours - The post is advertised at 40 hours a week Monday to Friday - Core hours are between 10am and 4pm - Applications for flexible working will be considered

Length of appointment - Full time, permanent

Jasmin Stewart <Jasmin@naturemetrics.co.uk>

UAE RENECO ConservationGenomics

We are looking for a highly motivated researcher to integrate our Conservation Genetics team, with a focus on Conservation Genomics. Our genetic research interests are genetic management of conservation programs (both in- and ex-situ), population genetic structure, sexual selection, aging and behaviour. The successful candidate must have proven academic background in Conservation Genomics. She / he will participate to ongoing research projects in Conservation Genomics in order to support RENECO's diverse conservation efforts; and will report to the head of the Conservation Genetics Division.

Duties will include: - Molecular laboratory techniques (e.g. DNA extraction, PCR, genotyping, ...) - Bioinformatic analyses of non-model species whole-genomes sequencing data (i.e. de-novo assembly, annotation, SNP identification, etc.) - Contribute to the management of the genetic laboratory - Mentoring undergraduate and graduate students - Genetic data management and analyses - Contribute to publication in peer-reviewed scientific journal - Participate in sampling collection in the field

Essential qualifications/skills include: - PhD and a Post-Doc in Conservation genomics or related subjects - Experience in conducting population genomics studies in non- model species - Experience in molecular biology - Solid data analysis skills and bioinformatics background are required. - Demonstrated ability to work independently, and as part of a team - Demonstrated ability to work on multiple assignments with overlapping deadlines - Demonstrated record of research productivity and publications

This is a full-time permanent position located in Abu Dhabi (United Arab Emirates) but willingness to travel in different countries is essential. Interested candidate can apply/inquire at hr-sourcing@reneco-hq.org. Please mention the reference RSCG/202012/RHQ as the subject of your email. Application materials include a cover letter describing your interest in the position and qualifications, a CV, and the names and contact information for at least two references.

Further information on RENECO research activities can be found at: https://www.researchgate.net/institution/-Reneco_International_Wildlife_Consultants LESOBRE Loïc <llesobre@reneco.org>

UBritishColumbia TeachingMolEcolEvol

The Department of Biology of the Irving K. Barber Faculty of Sciences at the University of British Columbia (UBC), Okanagan campus, requires an instructor to teach the following course during the Winter Session, 2020W, Term 2:

BIOL 468/568 (3) Molecular Approaches in Ecology and Evolution

Techniques for collecting molecular and population genetic data. Applications in ecology, evolution, and conservation. Characteristics of molecular markers, associated analytical approaches, emerging genomic technologies, and case studies.

Applicants with a PhD in the discipline or a related discipline, and relevant research and post-secondary teaching experience are preferred. This course will be taught on-line/remotely, so applicants living anywhere in Canada may apply. Relocation to Kelowna, BC is not a requirement for hire.

Interested applicants should submit a Curriculum Vitae (including but not limited to previous teaching experience), recent teaching evaluations (if available), and the name of three referees who have agreed to submit letters of reference directly to Barb Lucente at barb.lucente@ubc.ca.

Deadline for receipt of application is December 23, 2020. Please send application documents in electronic format using WORD or PDF files to: Barb Lucente at barb.lucente@ubc.ca.

For more information regarding the position, please contact Dr. Michael Deyholos at michael.deyholos@ubc.ca. All positions are subject to funding and enrolment.

UBC is one of the world's leading universities, and is consistently ranked in the top 40. The university has two distinct campuses, one in Vancouver and one in Kelowna. UBC's Okanagan campus, located in the city of Kelowna, has over 10,000 students in seven faculties, with strong undergraduate and graduate programs. Situated in the heart of the Okanagan Valley, one of the most scenic regions in Canada, it offers an intimate learning environment and excellent opportunities for regional, national, and international scholarly activities.

michael.russello@ubc.ca

UCalifornia Berkeley LabTech VertebrateZoology

Now Hiring! Lab Assistant Job ID 12775 We are currently seeking a Lab Assistant to join the Museum of Vertebrate Zoology to generate short-read sequencing libraries for a large-scale conservation genomics project: the California Conservation genomics Project (https://sites.lifesci.ucla.edu/eeb-CCGP/).

Apply here: https://jobs.berkeley.edu/ and reference position 12775

About us: The Museum of Vertebrate Zoology (MVZ) is a center for research and education in the biology of vertebrates fish, amphibians, reptiles, birds, and mammals. Founded in 1908, the Museum's mission is to document and increase understanding of the diversity of vertebrates, with particular emphasis on western North America. The superb collections are at the heart of the MVZ program, where methods of field biology are combined with modern laboratory techniques and analytical methods in a comprehensive, synthetic approach. Our goals are to remain at the forefront of international research on evolutionary biology from the perspectives of systematics, ecology, behavior, functional and developmental morphology, population biology, and evolutionary genomics, and to lead the way in using natural history collections for research, education, and solving problems in biodiversity conservation.

Responsibilities: - Plate-based DNA Extraction. - DNA handling and quantification. - Illumina short-read library preparation. - Post-library preparation assessment. - Optimization, troubleshooting, and repeats. - Project communication.

Required Qualifications: - Prior experience in working in a molecular biology lab, particularly with DNA extraction, PCR, agarose gel electrophoresis, DNA quantitation, and Illumina library preparation. - Meticulous record-keeping using a laboratory notebook and computerized records. - Basic computer skills for data entry in spreadsheets and use of databases. - Good communication skills (verbal and written) and ability to maintain working relationships in the laboratory as part of a team. - Ability to manage several tasks simultaneously. - Confidence to work independently after initial training but also to be comfortable in asking questions and for clarification. - Commitment to follow and enforce laboratory safety guidelines (both in terms of regular procedures and those specific to the prevention of the spread of SARS-CoV-2).

Education/Training: - BS in Biology and/or equivalent experience/training.

Preferred Qualifications: - Experience working with large-scale samples in 96-well plates. - Familiarity with SPRI (solid phase reversible immobilization) beads for DNA extraction, purification, and/or size-selection. - Previous use of high-throughput laboratory tools (plate reader, multichannel and repeater pipettes, and/or basic robotics)

Application Review Date - The First Review Date for this job is: December 24, 2020

Salary & Benefits - This position is a non-exempt, bi-weekly paid position. Hourly pay for this role is commensurate with experience. - For information on the comprehensive benefits package offered by the University visit: https://ucnet.universityofcalifornia.edu/-compensation-and- benefits/index.html

How to Apply - Please submit your cover letter and resume as a single attachment when applying. Use https://jobs.berkeley.edu/ and reference position 12775

Other Information - This is a one-year, full-time, 40-hours per week, Limited (temporary) Appointment. - This position is governed by the terms and conditions in the agreement for the Technical Unit (TX) between the University of California and the University Professional and Technical Employees (UPTE). The current bargaining agreement manual can be found at: http://ucnet.universityofcalifornia.edu/-labor/bargaining- units/tx/index.html - Per the UPTE Contract, Article 31, Section B - Â¿The automatic conversion to career status, as provided in Section B.2. above, will not occur when: c. The funding for the position is “one-time” funding, of eighteen months or less, or the employee was hired specifically to work on a short-term project lasting no more than one year.

Equal Employment Opportunity - The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, or protected veteran status. For more information about your rights as an applicant see: https://www.eeoc.gov/sites/default/files/migrated_file-

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UEdinburgh ResAssist ForestEvolution

Advanced Research Assistant, Borders Forest Trust Project 18 months, from 27,445 p/a Closing date 14/1/21

The Tree of Life (ToL) programme at the Sanger Institute is working with the Borders Forest Trust (BFT), the University of Edinburgh, NatureScot and the Royal Botanic Garden Edinburgh to sample genomic biodiversity across the extensive BFT estate. We intend to sample specimens of approximately 500 species of non-vertebrates, plants, bryophytes and fungi for genome sequencing. You will be part of the Tree of Life Core Laboratory team at the Sanger Institute, but will be largely based at the Conservation Genetics Laboratory in the University of Edinburgh. You will be supported by colleagues in Sanger and Edinburgh, and by Borders Forest Trust on-site staff. You will plan and carry out carefully organised field visits throughout the year to the extensive BFT estate, accompanied by experts from the Darwin Tree of Life project and others. You will coordinate sample collection to high standards of recording, and process samples, both on site and in our partner laboratory in the Conservation Genetics Group at the University of Edinburgh, before shipping them to Sanger Institute for genomic sequencing. You will keep meticulous digital records of specimens, and prepare reports for Darwin Tree of Life and BFT partners. As part of the field sampling, you will carry out monthly malaise trapping of flying insects, returning specimens to Sanger for BIOSCAN processing. The post will be split between the Sanger Institute and the University of Edinburgh, and will have the opportunity to develop other collaborative sampling projects (both terrestrial and marine).

You will be a biological sciences graduate with experience of both ecological fieldwork and molecular ecological or environmental genomics. You will have strong interpersonal skills and will be able to work effectively with a wide range of stakeholders, both internal and external. You will have the ability to organise and plan a programme of work, and will be able to problem-solve in order to ensure timely delivery of objectives.

More details and to apply: https://tinyurl.com/-araforest – The Wellcome Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

Sophie Potter <sp27@sanger.ac.uk>

UKLeuven Belgium EvolutionaryGenomics

At the KU Leuven and the Royal Museum for Central Africa (Belgium) we have an opening for a 50% tenure track Assistant Professor and 50% work leader in cichlid evolutionary biology (evolutionary genomics) Application deadline is 01 February 2021 Starting date is September 2021

The Department of Biology, Division of Ecology, Evolution & Biodiversity Conservation at KU Leuven and the Section Vertebrates of the Royal Museum for Central Africa (RMCA) jointly offer a full-time position (each with an appointment of 50 %). We are looking for candidates with an excellent research record and educational competence in the field of biology at the intersection of taxonomy and evolution of aquatic vertebrate radiations.

Duties Research You develop a research program at an international level in the evolutionary history of African cichlid fish radiations using an integrative approach combining morphology, ecology and genomics, within the framework of a FED-tWIN collaboration between KU Leuven and the Royal Museum for Central Africa (Project CichlidEcoEvo: Eco-evolutionary relationships in African cichlid radiations). The focus of this research profile is on the study of the cichlids of the Great African lakes as a model group for evolutionary research in Vertebrates.

The research must tie in with the ongoing research programme that focuses on Lake Edward and its nearby systems of lakes Kivu and Albert. On the mid and long term, you are expected to develop research avenues on the fish radiations of other African lakes and river systems.

You develop a research group in line with the strategy outlined in the FED-tWIN research profile and in synergy with research groups at KU Leuven and the RMCA. This FED-tWIN research profile specifically aims at developing a strong scientific collaboration between KU Leuven and RMCA.

You publish at the highest scientific level in the domain, you are able to obtain competitive financing, you develop international cooperation and you supervise master and PhD students at an international level.

Teaching You provide high-quality education in the domain of vertebrate biology, phylogeny, evolution and genomics, within the bachelor and master of Biology at the KU Leuven, with a clear commitment to the quality of the programme as a whole. You also contribute to the pedagogical project of the faculty and university by supervising bachelor projects and master theses and as a promoter of PhD students. You develop your educational project in accordance with the vision of KU Leuven on activating and researched-based education and make use of the opportunities for the educational professionalization offered by the faculty and the university.

Services Service provision is an important aspect of this FED-tWIN profile. This includes science management, science outreach, accommodating interns and visiting scientists, organising and/or contributing to training programmes, and answering questions from the general public. Specifically for the RMCA it also comprises the supervision of students of partner institutes in Africa, scientific advice for the set-up of permanent and temporary exhibitions, the further development of the rich fish and tissue collections, and contributing to the management of the associated databases, including genomic data.

Profile You have a PhD in biological or environmental sciences, obtained at the earliest 12 years before the submission date of the job application. The 12-year period is extended by one year for each maternity, parental and adoption leave, and for each long-term sick leave of yourself or your immediate family.

You have a strong research curriculum within the domain of biology, at the intersection of taxonomy and evolution of aquatic vertebrate radiations, that addresses fundamental research topics using a genomic, morphometric and phylogenetic toolbox. Expertise in the study of the African cichlid fish diversity is a bonus. The quality of your research is apparent from publications in leading international journals in the field. International research experience is a plus. You should have experience with field work and collection-based research, preferably on African fishes, and prepared to organize and conduct field work in Africa.

You have demonstrable qualities for academic education; educational experience is a plus. You have organizational skills and are collegial. You also have managerial capacities in an academic context.

Proficiency in English is required. The official administrative language at KU Leuven is Dutch. If you do not speak Dutch (or do not speak it fluently) at the start of your employment, KU Leuven will provide language training to enable you to take part in administrative meetings. Before taking on teaching in Dutch or English, you will be given the opportunity to learn Dutch or English, up to the required standard.

Offer Within the FED-tWIN framework, KU Leuven offers a 50% appointment as

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UKonstanz EvolutionaryGenomics

At the University of Konstanz in Germany we have an opening for an

Assistant Professor/Jr. Group leader in evolutionary biology (evolutionary genomics)

(starting date is on or around February 1st 2021)

The person we are looking for should be an evolutionary biologist who works on questions in either molecular evolution, and/or the genomics of speciation and adaptation. The position is intended for a Ph.D. biologist, ideally with prior postdoc experience, a strong publication record in evolutionary biology, and with expertise in evolutionary genomics. A total of three research groups two of which are headed by Junior Group Leaders make up the evolutionary biology group (~20 members total in the lab), in the Department of Biology at the University of Konstanz: http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=172 Our taxonomic emphasis is on fish, particularly on cichlids fish, but also other fish model systems are used in our research on comparative and speciation genomics and comparative developmental biology. We are especially interested in the origins of (convergently evolved) adaptations, speciation, and phylogenomics of the cichlid fish adaptive radiations from Nicaragua and Africa. But, we are open to anyone investigating other interesting taxa and questions. For publications of the lab see:

http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=92 . Space in a modern fish facility is available and the exclusive support of a 50% technician will be provided to this new group. Wet lab space, equipment, departmental facilities, including core-facilities in proteomics and genomics, and annual financial support for research expenses and student support, are provided by the University of Konstanz. The lab has sufficient space and state-of-the-art equipment for research in genomics, molecular, and developmental biology.

The University of Konstanz and the Department of Biology are among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the southern border between Germany and Switzerland. The position comes with a competitive salary, and excellent health and retirement benefits.

Appointments are initially for three years and are renewable for several years after that. Habilitation is possible, and a modest amount of teaching (in English at the BSc and MSc level) is required. The Assistant Professor is expected to acquire external funding and to supervise undergraduate, and graduate students as well as postdocs.

The University of Konstanz is an equal opportunity employer and tries to increase the number of women in research and teaching. The University of Konstanz is committed to further the compatibility of work and family life and has onsite child care facilities https://www.uni-konstanz.de/en/-equalopportunities/family/childcare/kinderhaus-knirps-co-child-care-centre/ . Additional information contact: a.meyer@uni-konstanz.de , phone: +49 7531 884163.

For our current research output see: https://scholar.google.com/citations?user=-qf6eWtgAAAAJ&hl=en&oi=ao Applications - including a statement of research interests/plans, a full CV and names and email addresses of 3 referees - should be emailed to: a.meyer@uni-konstanz.de.

Applications should be received by January 7th, 2021.

Prof. Dr. Axel Meyer Lehrstuhl f??r Zoologie undEvolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Christiane.Weber@uni-konstanz.de tel. + 49 (0)7531 88 3069

http://www.evolutionsbiologie-uni-konstanz.com/ Axel Meyer <prof.dr.axel.meyer@gmail.com>

UPortsmouth EvolutionaryBiology

The School of Biological Sciences is delighted to be able to appoint a number of new academic staff to further enhance our teaching and research in the Biological Sciences. We are expanding our team of lecturers and teaching fellows in areas including Plant Biology (including plant genetics), Biotechnology, Evolutionary Biology, Ecology and Zoology. Preference will be given to those able to contribute across multiple areas. We are seeking to appoint both lecturers/senior lecturers and teaching fellows to our team. Closing date is 10 January. (Posts are open to all nationalities.)

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

or Prof Scott Armbruster (scott.armbruster@port.ac.uk)

Detailed HR information about the positions is available at:

https://port.engageats.co.uk/ViewAttachment.aspx?enc=jmxpV+AcVus8i/wvT3FZXrrCOvCUGNWd9uca/tGZrAJjCe4gPnCqz54Ei2b0U3VbRYZB8Szfyl58OYGUH5wtTtiNOR9t3KPQIca/mWtWXNtdb9l/WWD+ql1nRiuXZa0m And about working at the University of Portsmouth at: https://www.port.ac.uk/about-us/working-at-portsmouth Application information is at: https://port.engageats.co.uk/LoginV2.aspx?enc=vDVLPY6BrOnmx9szwB5icMU/Bp97ap1BlI/jb0LhRYVeoh/cn5bYgvW+9EbbSw7a WS Armbruster University of Portsmouth, UK & University of Alaska Fairbanks, USA

W Scott Armbruster <wsarmbruster@alaska.edu>

UppsalaU MolecularEvolution

The Department of Ecology and Genetics (https://www.ieg.uu.se/?languageId=1) at Uppsala University seeks to further strengthen our research activities in the interface between evolution and genomics, and therefore announce a position as senior lecturer (associate professor) in molecular evolution, placed at the section of evolutionary biology (https://www.ieg.uu.se/evolutionary-biology/).

The full announcement and information on how to apply can be found at https://www.uu.se/en/about-uu/join-us/details/?positionId=364135 Deadline for applications is January 28, 2021.

Further information can be obtained from Prof. Hans Ellegren (Hans.Ellegren@ebc.uu.se).

The person appointed will be expected to perform research on molecular evolution in eukaryotic systems and be able to interact and give synergies with existing research within the section. The ranking of eligible applicants will be based primarily on research and teaching expertise, of which weight will be primarily given to research expertise. In assessing research expertise special weight will be attached to merits in both theoretical and empirical research on molecular evolution.

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

UppsalaU Sweden MarinePopGenomicsEvolution

The new research group of Andreas Wallberg is seeking a motivated candidate researcher with strong interests in evolutionary genomics. The successful candidate will join the group to carry out population genomics in marine zooplankton, including krill and copepods sampled across different oceans.

The Wallberg group studies multiple keystone species of krill and copepods of crucial importance to marine food webs and our research is motived by the poor state of knowledge of zooplankton and crustacean genomics in times of a rapidly changing world ocean.

The project that the successful candidate will join seeks to map and compare genome function and variation across the genomes and natural ranges of different species, using a combination of short-read and long-read techniques and analytical methods. The main aim of the project is to advance our insights into how these plankton is genetically adapted to their environment, including the identification of genes and mechanisms that contribute to adaptation, in order to better understand how they may respond to continued climate change.

Type of employment: Full-time, temporary position for a period of one year with eventual possibility to extension.

Information is provided by: Andreas Wallberg, andreas.wallberg@imbim.uu.se

Welcome with your application by January 7, 2021, UFV-PA 2020/4403.

More information at: https://uu.varbi.com/en/what:job/jobID:366024/ – Andreas Wallberg

Tel. +46-(0)-184714231 Mob. +46-(0)-709428262

Visiting address: Uppsala biomedicinska centrum BMC Husargatan 3 SE-751 23 Uppsala Sweden

Postal address: Uppsala biomedicinska centrum BMC Box 582 SE-751 23 UPPSALA Sweden

Andreas Wallberg <andreas.wallberg@imbim.uu.se>

VrijeU Amsterdam PlantMicrobeInteractions

ASSISTANT PROFESSOR ECOLOGY AND EVOLUTION OF PLANT-MICROBE INTERACTIONS

Are you interested in Plant-Microbe symbioses? Do you want to develop novel techniques to study species interactions in ecology and evolution? Plant tissues house some of the most diverse, yet vastly neglected, microbial communities on Earth. Exploring the untapped potential of these complex microbial communities remains one of the greatest scientific endeavors of our time.

The Department of Ecological Science at the Vrije Universiteit Amsterdam invites applications for a tenure-track position in Ecology and Evolution of Plant-Microbe Interactions. We are looking for an outstanding evolutionary biologist, with a research focus on plant-microbe interactions in a broad sense. The successful candidate will work to disentangle the complexity, and functionality of plant-associated microbes at various scales of biological organization. Potential areas of expertise might include, but are not limited to symbioses, plant-microbe phylogenetics /biogeography, rhizosphere interactions, plant-soil feedback, above- and below-ground ecology, agricultural ecology.

We are especially interested in candidates introducing new techniques and approaches to the department, including spatial and temporal mapping techniques, comparative methods, imaging techniques, modeling, and computation methods. Candidates in both applied and fundamental research fields are encouraged to apply. Several staff members of the department are part of a unique international team studying the ecology and evolution of the root microbiome dynamics of 100 wild and cultivated plant species (https://www.microp.org/), and the new Assistant Professor will be invited to join this consortium.

YOUR DUTIES - develop a strong, independent, extramurally funded research program - teach bachelor and master level courses in Biodiversity, Plant-Soil interactions, Plant (eco-)Physiology or related subjects - provide high quality training and supervision to PhD-students and postdocs - engage in professional development activities related to teaching and academic leadership

REQUIREMENTS - Ph.D. in Plant-Microbe Interactions or a related discipline in Ecology & Evolution, with at least 2 years of postdoc experience - strong track record of publication and successful acquisition of external funding - demonstrated skills in activating teaching methods for BSc and MSc level courses - excellent communication skills (written and spoken English) and motivation to work in a team - demonstration of outreach and communication with diverse audience - proficiency in Dutch is not required, but the successful candidate would be expected to develop at least a passive proficiency in the first three years after appointment.

ABOUT THE DEPARTMENT The Department of Ecological Science (www.amsterdamecology.nl) offers a stimulating international research environment with world-class academic reputation, and excellent state-of-the-art facilities. We have a strong commitment to bachelor and master level teaching. Research in the department covers a wide range of fundamental and applied research topics, including stress ecology, species interactions and evolutionary adaptation, molecular evolution, climate change and ecosystem functioning. Our strength lies in the ability to integrate studies of adaptive changes across the entire range of biological organizational levels.

WHAT ARE WE OFFERING? We offer a tenure track position at the level of assistant professor, initially for the duration of 6 years. During the period, performance will be evaluated in terms of teaching, publication record, acquisition of project funding, and academic leadership. After a successful evaluation permanent employment will be granted. On full-time basis the remuneration amounts to a minimum gross monthly salary of Â3.746 (scale 11) and a maximum Â5.127 (scale 11), depending on your education and experience.

Additionally, Vrije Universiteit Amsterdam offers excellent fringe benefits and various schemes and regulations to promote a good work/life balance, such as: - a maximum of 41 days of annual leave based on full-time employment - 8% holiday allowance and 8.3% end-of-year bonus - good growth opportunities - possibility to save holiday hours, for sabbatical leave, good paid parental leave scheme

APPLICATION To apply, submit a cover letter, CV, research and teaching statement, and names and contact information for three references by January 8, 2021 via https://werkenbij.vu.nl/ad/assistant-professor-plant-microbe-interactions/7ne34b .The job interviews are planned for end of January 2021, please take this into account when applying for the position.

VACANCY QUESTIONS If you have any questions regarding this vacancy, you may contact:

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Other

AGA SpecialEventsAwards Deadline Jan31

The American Genetic Association grants awards each year to its members for support of special events that advance the mission of AGA, particularly to support students to attend the event.

Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGA's purpose will be considered, especially those that could lead to Journal of Heredity articles.

Awards are between $1,000-$15,000. Funding is competitive, and applications must follow the guidelines.

To apply, visit https://www.theaga.org/ Anjanette Baker, AGA Manager theaga@theaga.org

Anjanette Baker <theaga@theaga.org>

ASN JasperLoftusHill YoungInvestigatorAward

Applications for the 2021 Jasper Loftus-Hills Young Investigator Award of the American Society of Naturalists are due January 15, 2021: https://www.amnat.org/announcements/NomYIAforms.html The Jasper Loftus-Hill Young Investigator's Award of the American Society of Naturalists honors outstanding promise and accomplishments of young investigators who conduct integrative work in the fields of Ecology, Evolutionary Biology, Behavioral Ecology, and Genetics. Applicants working in any of these fields are encouraged to apply.

The award honors outstanding promise and accomplishments of young investigators (3 years post-Ph.D.*, or in the final year of their Ph.D) (see * below) who conduct integrative work in ecology, evolution, behavioral ecology, and genetics. The award commemorates Jasper Loftus-Hills (1946-1974), an Australian biologist of exceptional promise who died tragically during the course of fieldwork three years after receiving his degree.

Winners of this award will present a research paper in the Young Investigator's Symposium at the ASN annual meeting and receive a $700 prize, a travel allowance of $700, cost of registration for the meetings, and a supplement of $500 in case of intercontinental travel. Four awards are made annually. Recipients need not be members of the Society.

In order to apply for this award, applicants should go to the Google form: https://forms.gle/BJfjQN4xsvyHkmtf8 , where they will be asked to answer a few questions and upload their application (see ** below).

The application should consist of one pdf, with the following (in this exact order): - CV (no page limit) - Research statement (3 page limit, including figures) - 3 reprints

Additionally, two letters by individuals familiar with the applicant's work should be uploaded by referees to https://forms.gle/CMhhK9dKVAahJA948 (a Google form). (see ** below). Applicants are responsible for ensuring their letter writers submit their letters before the deadline (this can be done before submitting an application), as applications will not be considered complete without these two letters.

With questions please contact Committee Chair Robin Hopkins rhopkins@fas.harvard.edu

* The standard timeframe covers anyone who graduated in 2018, 2019, or 2020 or who plans to defend in 2021. Time since PhD degree can be extended by 1 year for each child born or adopted during this period if the applicant was a primary care giver. Other forms of exceptional care giving responsibility (e.g. partner, spouse, aged parent, etc.) will be considered on a case-by-case basis.

**Applicants and letter writers will be asked to sign into an account registered with Google (does not have to be a gmail address) to upload their applications and letters, respectively. If you or your letter writers do not have a google account, please send materials directly to Robin Hopkins (rhopkins@fas.harvard.edu).

rhopkins@fas.harvard.edu

InMemoriam FrankWright

I am very sad to pass on news of the death of Frank Wright of Biomathematics and Statistics Scotland. Frank's long struggle with health problems ended on the morning of 15th December.

Frank's contribution to research was immense, covering many topics including codon usage, phylogeny and recombination.

Many of us around the world also remember Frank's friendship, loyalty and humour, his kindness and enormous desire to help others.

Frank had a passion for training, informal and formal, and always had something insightful to say about any phylogenetic technique. Frank loved his work and was full of stories about his work and supportive colleagues. It was a privilege to know him and work with him.

Frank's family are planning a small family funeral soon, with a larger celebration of Frank's life when such things become possible.

Please feel free to pass the sad news on to others. If you would like to be in touch with Frank's family, please let me know.

Daniel Barker Daniel.Barker@ed.ac.uk

Dr Daniel Barker Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh Charlotte Auerbach Road The Kings Buildings Edinburgh EH9 3FL United Kingdom

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

BARKER Daniel <Daniel.Barker@ed.ac.uk>

LinneSys SystematicsResearchFund

The Linnean Society (https://www.linnean.org/) and the Systematics Association (http://www.systass.org/) jointly administer the LinnéSys: Systematics Research Fund that provides grants annually for small-scale research projects in the field of systematics.

The Systematics Research Fund has been renamed to the LinnéSys: Systematics Research Fund.

Typical activities supported include contributions to fieldwork expenditure, the purchase of scientific equipment or expertise (e.g. buying time on analytical equipment), specimen preparation (including the cost of temporary technical assistance), and contributions to publication costs. However, please note that it is unable to fund the cost of article publication charges. Projects of a more general or educational nature will also be considered, provided that they include a strong systematics component. Typical activities not supported include attendance at scientific meetings and contributions to student maintenance or tuition fees. The fund does not provide payments for Bench Fees. Projects already substantially funded by other bodies may be disadvantaged. Applications of all nationalities are welcome, but applicants must be a current member of the Systematics Association or Linnean Society of London.

Successful projects are selected by a panel of systematists who represent a wide range of conceptual interests and taxonomic groups. Generally, applications in the range of 500-1000 are preferred, the value of any single award will not exceed 1500.

Deadline: 23.59 GMT on Monday 15 February 2021.

More information on LinnéSys on the Systematics Association webpage: https://systass.org/grants-and-awards/srf/ Questions about the application procedure can also be sent to the LinnéSys Administrator (LinneSys@systass.org)

Dr Anne D. Jungblut Grants & Awards Secretary Systematics Association

Anne Jungblut <a.jungblut@nhm.ac.uk>

Mollusc FreeGenomeSequence

Dear colleagues

We are proud to announce a new joint venture between the Senckenberg Museum Frankfurt and Translational Biodiversity Genomics centre (TBG), and Unitas Malacologica: The 2021 Mollusc of the Year!

Anyone can nominate their favourite mollusc species (but you have to be able to provide a specimen). All mollusc species are eligible (marine, terrestrial, freshwater, from any country). Five finalists will be put forward for a public vote in January. The TBG will sequence of the complete draft genome of the Mollusc of the Year.

Please spread the word! We particularly want this initiative to reach people and countries that do not have ready access to genome sequencing technology. Rules and nomination form are here: http://bit.ly/molluscoftheyear Best wishes,

Julia

Julia Sigwart Head of Section, Mollusca Senckenberg Research Institute & Museum, Frankfurt julia.sigwart@senckenberg.de

bit.ly/SMFMalacology

new book! "What Species Mean: Understanding the Units of Biodiversity" https://www.crcpress.com/What-Species-Mean/Sigwart/p/book/9781498799379 Julia Sigwart <Julia.Sigwart@senckenberg.de>

SORTEE society

I am pleased to announce the formation of SORTEE < https://www.sortee.org/ > - The Society for Open, Reliable, and Transparent Ecology and Evolutionary biology. (https://www.sortee.org)

SORTEE is a service organization which brings together researchers working to improve reliability and transparency through cultural and institutional changes in ecology, evolutionary biology, and related fields broadly defined. Anyone interested in improving research in these disciplines is welcome to join, regardless of experience. The society is international in scope, membership, and objectives.

You can follow SORTEE on Twitter @SORTEcoEvo < https://twitter.com/sortecoevo >

Why join SORTEE? < https://www.sortee.org/join/ >

SORTEE membership for 2021 is free and we promise to not send you too many emails if you join.

SORTEE is a network of people with shared interests, spread out across many disciplines/subdisciplines. Join us to engage with this exciting network.

SORTEE will be a forum to discuss and develop practices that promote open, reliable, and transparent science. Join to contribute to this discussion.

SORTEE will host gatherings of various sorts. Join and stay informed about these opportunities.

SORTEE will be a center for information about open, reliable, and transparent science. Join and learn how to improve your science.

SORTEE can best help science and the scientists in these disciplines if we are a diverse organization that fosters and amplifies diverse perspectives. Please help us: * diversify across disciplines and subdisciplines * diversify geographically * diversify by welcoming members of underrepresented groups * diversify in terms of types of interests in open, reliable, and transparent science To join SORTEE, please go to our website < https://www.sortee.org/join/ >

Tim Parker on behalf of the SORTEE Executive Committee < https://www.sortee.org/people/ >

SouthAfrica VolFieldResAssist SocialMoleRats

SouthAfrica.VolFieldResearchAssistant.SocialMoleRats

We are looking for 2-3 voluntary field research assistants to get involved with our research on a wild populations of social Damaraland mole-rats (Fukomys damarensis)in the Kalahari (South Africa). We are conducting a long-term capture-mark and recapture study, based at the Kalahari Research Centre, to investigate the life-history and social behaviour of Damaraland mole-rats (http://kalahari-meerkats.com/kmp/research-publications/damaraland-molerats-group/). Entire groups of mole-rats will be captured and individually marked. Some individuals may be fitted with a collar to measure behavior. Morphological measurements and tissue samples will be collected before the release of the animals. The field work is physically demanding, and weather conditions are challenging(heat during the day, cold during the night). Trapping also takes place during the night. The assistants will mostly be working in teams of two or three but will be embedded in a large research community.This position requires working in a small team in a remote location on free ranging animals.

Required qualifications:

Keen interest in ecological and/zoological field research

Commitment to 3-12 months at the project site

A valid driver's license

A BSc degree in biology, zoology, ecology or a wildlife related program is considered an asset

All assistants are reimbursed for travel expenses within South Africa, accommodation and food. Qualified assistants that commit to periods of more than 6 months can receive a stipend to cover additional expenses. Field work will start March 2021 and will be running for 12 months.

Please apply by email or contact for further information:hanna.bensch@lnu.se Application should include a cover letter explaining why you are interested in getting involved in this research project and a CV.We will review applications as they arrive.

Hanna Bensch, PhD candidate, Linnaeus University

Hanna Bensch <hanna.bensch@lnu.se>

PostDocs

AMNH NewYork Evolution

We are pleased to announce that we are accepting applications for our Postdoctoral Research Fellowships Program at the Richard Gilder Graduate School at the American Museum of Natural History.— Updated Deadline: January 8, 2021.

he Postdoctoral Research Fellowship Programs of the AMNH are designed to advance the training of each participant by having them pursue a specific, time-limited project in association with Museum professionals in the Museum setting. The applicant's project must fit into one or more of the main research areas of interest in the Museum's Scientific Divisions: Anthropology, Invertebrate Zoology, Paleontology, Physical Sciences (Astrophysics and Earth & Planetary Sciences), or Vertebrate Zoology.

Postdoctoral Fellows are expected to conduct their work at the Museum. Applicants are encouraged to contact potential curatorial sponsor(s) prior to applying. Appointments are typically made for two years. In addition to a competitive salary and benefits, limited relocation, research and publication support is provided. Newly graduated or soon-to-graduate PhDs may apply.— Fellows must have received their degrees or deposited their dissertations before they can begin their appointments. There are no citizenship or geographic requirements to apply.

Details about the Postdoctoral Research Fellowships Program can be found on https://www.amnh.org/-research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/-postdoctoral-research-fellowship-program . The UPDATED DEADLINE is Friday, January 8, 2021 for this cycle.

Please contact us (mailto:info-rggs@amnh.org) if you need any further information. — Richard Gilder Graduate School American Museum of Natural History https://www.amnh.org/research/richard-gilder-graduate-school

Anna Manuel <amanuel@amnh.org>

ArizonaStateU PopulationGenetics

The Jensen Lab is searching for a postdoc in the area of statistical and computational population genetics, for an NIH-funded project concerning the (joint)-inference of selection and demography from genomic data. The precise research questions and possible empirical applications are flexible, though the lab webpage summarizes our primary interests. Please see: jjensenlab.org

The Jensen Lab is in the School of Life Sciences, the Center for Evolution & Medicine, the Center for Mechanisms of Evolution, and is part of an excellent and interactive Population Genetics community at Arizona State University. Please see: asupopgen.org

Interested applicants should send a CV and a statement of interest by January 29, 2021, to: jeffrey.d.jensen@asu.edu

Jeffrey Jensen <Jeffrey.D.Jensen@asu.edu>

Barcelona ComparativeGenomics

Postdoc position in Comparative and Structural Genomics

Ruiz-Herrera's lab is looking for a highly motivated candidate that can apply for a "Juan de la Cierva" postdoctoral fellowship from the Spanish Government.

For more information see:

https://www.ciencia.gob.es/portal/site/MICINN/-menuitem.dbc68b34d11ccbd5d52ffeb801432ea0/-?vgnextoid=056fe027b89f5710VgnVCM1000001d04140aRCRD The aim of the project is to study the high-structural organization of mammalian genomes combining HiC, ChIP-seq and RNA-seq data. Applicants should have a PhD in a relevant area (evolutionary biology, genomics or genetics). We are seeking for someone with a vivid interest in evolution research and a background in bioinformatics and or population genetics/ statistical genetics.

Requirements:

PhD degree obtained before the 31st december 2018.

Competitive publication record.

Skills in bioinformatics and/or programming.

What we offer: - Three years contract. - The total annual amount stipend will be between euro 26,000 and euro 30,000 gross, depending on experience. - Additionally, the grant includes a complementary amount of euro 6,300 aimed exclusively at educational and training activities and attendance to meetings.

Ruiz-Herrera's lab is set at Universitat AutÃ²noma de Barcelona (UAB). The long-term research goal of our research group is to provide a unified and encompassing view of how genomes are organized and regulated in mammalian cells. Within this framework, the candidate will develop a project on the evolution and function of the higher-structural organization on mammalian genomes. For further information please see:

http://grupsderecerca.uab.cat/evolgenom/ .Likewise, UAB is located close to the city of Barcelona and is one of the major public universities in Spain. The UAB is internationally acknowledged for its quality and innovation in research. It coordinates a potent scientific and technological centre, which comprises all the departments, science and technology services, research centres, institutes and university hospitals affiliated with the UAB. Complete application packages, including a CV, a brief (1-page) statement of research interests, and the names and e-mail addresses of two referees should be sent to: Dr. Aurora Ruiz-Herrera. Email: aurora.ruizherrera@uab.cat Application deadline: 10th January 2021.

"A. Ruiz-Herrera" <aurora.ruizherrera@uab.cat>

Berkeley GlobalChangeBiodiversity

I would like to have this postdoc opportunity posted to the evoldir : https://aprecruit.berkeley.edu/JPF02804. It is for an independent postdoc in data science to explore how global change affects biodiversity.

Best, Ciera

Ciera Martinez <ciera.martinez@gmail.com>

Brno FishBroodParasitism

POSTDOCTORAL RESEARCH POSITION FOR 1-3 YEARS

TOPIC: Fish Evolutionary Ecology: Brood parasitism, Coevolution

REICHARD LAB (reichardlab.eu)

Institute of Vertebrate Biology, Czech Academy of Sciences, Brno

Two full-time postdoctoral positions are available at the Institute of Vertebrate Biology, Czech Academy of Sciences, located in Brno, Czech Republic. Positions will start when filled (February 2021 or later)

The positions are intended for experimental or laboratory work on brood parasitism, primarily on the cuckoo catfish and their cichlids hosts and/or bitterling fishes and their mussel hosts.

The work focus is negotiable within a broader theme (coevolutionary dynamics, phylogenomics). We would particularly welcome a candidate with focus on NGS techniques and associated bioinformatics pipelines (parentage, amplicon sequencing - MHC, phylogenetics), phylogenetic comparative methods, or experimental work with live fish.

For experimental work, access to well-equipped fish breeding facility and outdoor mesocosm system is granted. Applications from candidates with a background in ecology and evolution, ideally with a previous track record of working with fish models are especially welcome.

For molecular laboratory work, methodological expertise rather than a previous track of work on a related taxon is preferred.

Developing an independent project within a broader scope of our 5 year project on coevolution and brood parasitism in fish is possible.

QUALIFICATIONS - PhD in Biology

SALARY - 40 000 CZK, c. 1650 EUR per month (well above average for Czech living expenses)

APPLICATION PROCEDURE

For formal applications, please submit a CV and explain your previous work and motivation to apply for this position in a Cover Letter (single page is sufficient). Email your application to reichard@ivb.cz

All applications submitted until 15 January 2020 will be fully considered. Selected candidates will be interviewed by Skype.

For informal enquires and more details, feel free to email reichard@ivb.cz

Martin Reichard <reichard@ivb.cz>

BrookhavenNatlLab PlantMicrobeBioinformatics

Research Associate Biology - PlantMicrobeBionformatics

Job ID 2467

Position Description

We are seeking a bioinformatician to analyze genome wide transcriptomic responses to stress in plants and microbes for functional genomic studies. The post doc will be involved in many exciting projects using newly assembled reference genomes of host plants and nitrogen-fixing symbiotic microbes. We are particularly interested in the role of gene duplications that can enhance tolerance to stress or toxic environments, and how stress tolerant microbes provide benefits for host plants. Incorporation of evolutionary and/or ecological aspects and analyses into this research is highly encouraged. The research is essential to meet the DOE'Âs Biological and Environmental Research (BER) mission to use genome-enabled approaches to understand the relationship between soil biogeochemistry, nutrient cycling by plants, and the movement or transport of metals ions from soils into plant biomass (https://www.energy.gov/science/ber/-biological-and-environmental-research). This position has a high level of interaction with an international and multicultural scientific community, including the Joint Genome Institute (JGI) and the Environmental Molecular Sciences Laboratory (EMSL), both DOE run facilities. The research will support two JGI funded community science awards (New Investigator and Functional Genomics). Because this position is entirely computational, opportunities for working remotely are possible.

Position Requirements

Essential Duties and Responsibilities:

- Quantify gene expression changes in response to stress treatments such as heavy metals, temperature, drought.
- Assess the role of gene duplications on expression level.

- Identify candidate genes that provide greater tolerance to stress. - Develop statistical pipelines to identify differentially expressed genes and co-expression networks. - Integrate genome wide association study (GWAS) candidates with transcriptomics data to identify target genes for functional studies. - Required Knowledge, Skills, and Abilities:

- Requires a Ph.D. in bioinformatics with focus on genomics, or computational biology, evolutionary genomics, plant genomics/agricultural genomics or related field. - Experience mapping and analyzing RNA-seq data, including differential expression analysis (e.g. DeSEQ, edgeR). - Ability to install and use bioinformatics software (i.e., samtools, BWA, GATK, plink) in a Linux framework. - Proficient in one or more programming languages such as python or perl, and ability to write and modify scripts in R. - A proven track record of experimental design, execution and data analysis as reflected in manuscript writing and successful publication in peer-reviewed journals. - Demonstrated track record of poster presentations and/or oral presentations at scientific meetings. - Preferred Knowledge, Skills, and Abilities:

- Standard genome annotation software experience with genome assembly and annotation using RNA-seq data. - Gene co-expression network analysis using WCGNA or other tools. - Single gene alignment software and PCR primer design.

Other information:

Review of applications begins immediately. Applications will be accepted until the position is filled. Competitive salary will be commensurate with relevant experience and qualifications. Initial 1-year appointment subject to annual renewal contingent on performance and funding. Research is under the direction of Dr. Tim Paape. BNL policy requires that research associate appointments may be made to individuals who have received their doctorate within the past five years. Brookhaven National Laboratory is an equal opportunity employer committed to building and maintaining a diverse workforce. At Brookhaven National Laboratory we believe that a comprehensive employee benefits program is an important and meaningful part of the compensation employees receive. Our benefits program includes, but is not limited to:

Brookhaven National Laboratory (www.bnl.gov) delivers discovery science and transformative technology to power and secure the nation'Âs future. Brookhaven Lab is a multidisciplinary laboratory with seven Nobel Prize-winning discoveries, 37 R&D 100 Awards, and more than 70 years of pioneering research. The Lab is primarily supported by the U.S. Department of Energy'Âs (DOE) Office of Science. Brookhaven Science Associates (BSA) operates and manages the Laboratory for DOE. BSA is a partnership between Battelle and The Research Foundation for the State University of New York on behalf of Stony Brook University.

Organizational Overview

Researchers in the Biology Department at Brookhaven National Laboratory seek to unravel and fully describe the complexities of biological systems'Xfrom how plants make oils and other products to

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CAS Czech CanopyAntCompetition

A position for Postdoctoral Researcher is available to work on the project

Does competition really structure ant communities in tropical forest canopies?

A highly motivated Postdoctoral Researcher is sought to join a project that aims to explore the relative contribution of biotic (interspecies competition, forest structure) and abiotic effects (climate) on the structuring of canopy ant communities in tropical rain forests. The successful candidate will co-design, and conduct field surveys, and experimental transplants of ant colonies across different forest systems and between dominant species territories in New Guinea, a region with globally high insect and plant diversity. In addition to innovative manipulations of species composition, the project will include functional and phylogenetic measures of ant diversity, and behavioural and thermal-tolerance experiments. He/she will have opportunities to develop the project, as well as to build upon existing plot-based datasets on the ants living in trees. Duties will include conducting and supervising the field work in Papua New Guinea, and working in our laboratory in the Czech Republic.

The successful applicant will join the Ant Research Group (http://antscience.com/) at the Institute of Entomology, Biology Centre CAS, Czech Republic, under the leadership of Dr. Petr Klimes. The research facility is in Ceske Budejovice, a charming historical city in the south of the country, within easy reach of Prague and

Vienna. The laboratory is a dynamic, multinational group studying ant ecology. It is embedded within the Department of Ecology and Conservation Biology of Prof. Vojtech Novotny (the head), a world-class centre for tropical ecology research that publish in leading journals (e.g. Ecology Letters, Ecography, Science). The applicant will also collaborate with New Guinea Binatang Research Centre and the Laboratory of Behavioural Ecology at Johannes Gutenberg University of Mainz.

The deadline for applications is January 15th 2021, with expected start date of April 1st 2021 (negotiable). The successful applicant will receive the full time employment with salary CZK 40,000 per month (approx. EUR 1500 pre-tax). Note that living costs in Czech Republic are substantially lower than in many other EU countries, and the salary is competitive (e.g. http://bit.ly/-1NCkQKJ). The position is funded by a Czech Science Foundation grant until Dec 31st 2023. Applicants from all countries are eligible.

Required - A PhD degree in ecology or a related field. - Interest in the ecology of insects. - Ability to work independently and manage small team of assistants in the field, as well as collaborate with other senior and junior team members (i.e. co-supervise PhD students). - Fluency in spoken English, and skills in academic writing in this language - Good publication record for career stage - Experience with ecological analyses on the species-rich communities

Desirable - Previous experience in the tropics, particularly in canopy ecology or manipulative experiments - Research experience with ant ecology & entomology - A strong publication record in the above fields - Advanced analytical skills in R for the community ecology discipline

To apply, please send a CV, contact details for three references, and cover letter stating qualifications, previous work and motivation for the position to Jana Liparova (slancarova@entu.cas.cz). If you would like to discuss the project further, please feel free to contact Petr Klimes (peta.klimes@gmail.com).

Tom Fayle <tmfayle@gmail.com>

CGRU Texas CottonGenomics

A post-doctoral research position is available immediately at the Crop Germplasm Research Unit (CGRU) of the USDA-Agricultural Research Service in College Station, Texas. Work will focus on development of a practical haplotype graph of cotton (*Gossypium hirsutum* and *G. barbadense*), and development of a tool for imputation with low-pass sequencing. Within the haplotype data, the postdoc will also investigate important biological questions of the cotton genome including reciprocal introgression between species, polyploidy, genetic diversity, and/or recombination. There will also be significant interactions with the GRIN-Global and CottonGen database. The work will also utilize the resources of the U.S. National Cotton Germplasm Collection which is housed at College Station and managed by the CGRU. Applicants with backgrounds in one or more the following fields are encouraged to apply: bioinformatics, genetics, evolutionary biology, and quantitative or population genetics.

The position is available now and the start date is flexible. Potential candidates graduating in Dec. 2020 or even May 2021 are encouraged to apply. The position is available for two years (contingent upon review/renewal after year 1). Salary is at the GS-11 level (~$64.000/year). Standard federal employee benefits will be offered including participation in the Thrift Savings Plan (equivalent to a 401K), with government matching of up to 5% of salary contributed to the Plan.

This position is open only to U.S. citizens.

Submit application materials (1-page cover letter, CV, contact information for 3 references) to Joshua Udall, CGRU-ARS; joshua.udall@usda.gov. Applications will be considered until the position is filled.

jaudall1@gmail.com

ClemsonU ArthropodMetabarcoding

Postdoctoral Fellowship in Arthropod Biodiversity

The Caterino Arthropod Biodiversity Lab at Clemson University (South Carolina, USA) is seeking a postdoctoral researcher to conduct integrative research on arthropod biodiversity in the southeastern United States. As part of the NSF-funded project, 'Litter Arthropods of High Appalachia', we are collecting arthropods from leaf litter at high elevation sites across the southern Appalachians, and using metabarcoding to document and analyze patterns of diversity and endemism across these sites. Some lineages have shown high levels of local endemicity in the region, but few have previously been analyzed in detail. The postdoc will work as part of a collaborative team involving the Clemson PI, co-PI Paul Marek at Virginia Tech University, and graduate and undergraduate students at both institutions.

For more information on work going on in the Caterino Lab visit: https://sites.google.com/site/caterinolab/ RESPONSIBILITIES The postdoc will participate in fieldwork, molecular lab work, data analysis, manuscript preparation, mentoring graduate and undergraduate students, presentation at national/international meetings, and outreach.

QUALIFICATIONS: Candidates must have a Ph.D. in Systematic Biology, Entomology, or a closely related field, and have direct experience with wet lab procedures commonly used in molecular systematics (DNA extraction, PCR, etc.), as well as phylogenetic data analysis. Candidates with experience in next-generation sequencing techniques, especially metagenomic procedures, will be preferred. Additionally, desired expertise would include arthropod taxonomy, entomological fieldwork, and morphological and molecular character development. Ideal candidates will have particular expertise in the systematics of some group of terrestrial arthropods prominent in leaf litter.

PAY & WORK SCHEDULE: Standard hrs: 40/wk. Annual starting salary is USD$47,486, with annual cost-of-living adjustments. The position will be renewable annually for up to two years, contingent on satisfactory performance.

HOW TO APPLY: To apply, please prepare a cover letter describing applicable experience, C.V., contact details for three references, and unofficial transcripts. The application must be submitted through http://apply.interfolio.com/82020. If a Ph.D. degree has not yet been earned, please indicate anticipated graduation date. Any additional questions about the position may be directed to the PI at mcateri@clemson.edu.

Review of materials will begin immediately and will continue until the position is filled. To ensure full consideration, please submit materials by January 15, 2021. Start date is negotiable, but the position is open now.

JOB LOCATION: Poole Agricultural Center - Clemson Main Campus, Clemson, SC 29634

The Jeanne Clery Disclosure Act requires institutions of higher education to disclose campus security information including crime statistics for the campus and surrounding areas. As a current or prospective Clemson University employee, you have a right to obtain a copy of this information for this institution. For more information regarding our Employment, Campus Safety and Benefits, please visit the Human Resources-Prospective Employees web page: http://www.clemson.edu/cao/humanresources/prospective/ Clemson University is an Affirmative Action/Equal Opportunity employer and does not discriminate against any individual or group of individuals on the basis of age, color, disability, gender, national origin, race, religion, sexual orientation, veteran status or genetic information.

Michael S. Caterino Morse Chair of Arthropod Biodiversity Director, Clemson University Arthropod Collection Department of Plant and Environmental Sciences (PES) MAIL: 277 Poole Agricultural Center OFFICE: E-254 Poole Agricultural Center Clemson University Clemson, SC 29634-0310 mcateri@clemson.edu Office phone: (864) 656-3105 LAB: sites.google.com/site/caterinolab/ MUSEUM: sites.google.com/site/clemsonarthropodcollection/

Michael S Caterino <mcateri@clemson.edu>

CNRS Perpignan EpigeneticsEcolEvolution

Postdoc: Perpignan_CNRS_ERC_EpigeneticsEcologyEvolution

—A postdoctoral research associate position is available in the research group of Benoit Pujol at CNRS in Perpignan (France) to study epigenetics in ecology and evolution.

—The postdoctoral associate will participate to the ERC-funded ANGI project aiming at a better understanding of the adaptive potential of populations. The post-doc will use epigenomic data to test hypotheses on the adaptive significance of epigenetic variation in plants.

Start date: February, with preference for earlier dates that month.

—The post-doc will also participate to collective research actions conducted by the group to make our knowledge on the adaptive potential of wild populations progress (fieldwork, collaborative work, discussion, paper preparation and outreach, etc.).

—Some data is currently available and ready for analysis; thus the postdoctoral associate can expect to begin working on analyses for publication during the first six months of their appointment. There will be scope for collaboration on other projects underway in the team.

—A Ph.D. in epigenetics, and expertise in bioinformatic and biostatistical analyses with knowledge in evolutionary ecology and on mobilome. Postdoctoral research experience is not required. Proficiency in bioinformatic analyses in the domain of epigenetics is required (database management, coding, NGS bioinformatics pipelines, mapping on genome, post-genomic analysis, browser visualisation, genome functional annotation, etc.). Experience in wild plant population study is not required. The initial appointment is for six months, with a possible contract extension of six months conditional on performance.

—French is not mandatory.

—To apply, please prepare a short cover letter (one page maximum) explaining your interest in the position, a CV, and contact information (phone number and email) for two references and submit your application via the CNRS employment portal: https://bit.ly/3rjRu0S — Closing date for application: 11/01/2021

—SALARY (depending on experience):

Wage: monthly salary before tax between 2560 and 3509 euros monthly depending on experience

Benoit PUJOL Researcher in evolutionary ecology at CNRS, France Quantitative genetics and adaptive potential of wild populations Want to follow my group's research, see twitter: @BenoitPujol

Centre de Recherches Insulaires et Observatoire de l'Environnement (CRIOBE) Centre de Biologie et d'Ecologie Tropicale et Méditerranéenne Universite de Perpignan, 52 Av. Paul Alduy - 66860 Perpignan cedex, France Mail: benoit.pujol[AT]univ-perp.fr

Benoit Pujol <benoit.pujol@univ-perp.fr>

ColoradoStateU MolecularEvolution

The Sloan lab at Colorado State University is recruiting a postdoctoral researcher who is broadly interested in molecular evolution to work on cellular integration of mitochondrial and nuclear protein synthesis. With the support of a new NSF grant, the lab will be investigating how the dynamic history of plant mitochondrial tRNA populations affects interactions with the nuclear-encoded enzymes responsible for tRNA editing and charging. In particular, we will investigate the ongoing loss of tRNA genes from the mitochondrial genomes of certain plants and how they are functionally replaced by importing cytosolic (nuclear) tRNAs that are separated by billions of years of evolution.

The project will include both comparative genomic and molecular genetic wet-lab components. A postdoc would have the opportunity to contribute to either or both of these areas depending on their skills and interests. Relevant areas of experience could include one or more of the following: protein sequence evolution, mitonuclear interactions, gene duplication, subcellular targeting, protein import, protoplast transformation, fluorescence microscopy, and both short-read and long-read sequencing technologies.

Our lab is in the Department of Biology, which is housed in a state-of-the-art research facility that opened in 2017. The department includes numerous labs in the fields of both plant molecular biology and evolutionary biology, so there are ample opportunities for collaboration outside the lab group. The university is in Fort Collins, Colorado, which routinely ranks among the top locations in the country in terms of overall quality of life. More information about our lab is available at our lab website: https://sites.google.com/site/danielbsloan/ We will be looking for a highly motivated postdoctoral researcher who is excited about addressing evolutionary questions at the molecular level and wants to contribute to a positive and collaborative intellectual environment. Start date is flexible, but we envision someone joining the lab in spring, summer, or early fall 2021. Inquiries can be e-mailed to Dan Sloan (dbsloan@rams.colostate.edu) and should include a CV and a brief statement of research/career goals. Evaluation will begin January 1, but inquiries are still highly encouraged after that point.

Dan Sloan <dbsloan@rams.colostate.edu>

CRG Barcelona ModelingSequenceEvolution

Postdoctoral position at the Centre for Genomic Regulation (CRG), Barcelona, Spain

The "Evolutionary Processes Modeling" group at the Centre for Genomic Regulation invites applications for a postdoc position to study genetic variation in human genomes (healthy or cancerous) using population genetics, computational and statistical methods.

Read more and apply here:

https://recruitment.crg.eu/content/jobs/position/-postdoctoral-researcher-group-evolutionary-processes-modeling-0 Deadline: 15 January 2021

About the institute

The Centre for Genomic Regulation (CRG) is an international research institute of excellence, based in Barcelona, Spain, with more than 400 scientists from 44 countries. The CRG shares principles of an interdisciplinary, motivated and creative scientific team that is supported by high-end and innovative technologies and a flexible and efficient administration.

In 2013, the CRG received the 'HR Excellence in Research' logo from the European Commission. This is a recognition of the institute's commitment to developing an HR Strategy for Researchers designed to bring the practices and procedures in line with the principles of the European Charter for Researchers and the Code of Conduct for the Recruitment of Researchers.

For further information, see https://www.crg.eu/ . About the group

Our group is particularly interested in how the evolution and survival of cancer cell populations relies on mutation influx as well as in the selection inference from allele frequency information. To this end, we develop mathematical and computational approaches to estimate mutation rates and selection. Estimates of the strength of selection in cancer allow for a prioritization of genes and non-coding regions by their disease relevance, with the ultimate goal of promoting therapeutic advances.

Cancer is a genetic disease, subject to population genetics forces like mutation, selection and stochasticity. We have recently demonstrated that coding sequences of cancer tumors not only exhibit positively selected mutations that drive cancer (www.nature.com/articles/-s41588-019-0572-y), but that there exist genes that the tumor cannot afford to lose to the mutational pressure (www.nature.com/articles/ng.3987). In addition to genes, we have also identified cancer driver loci in the non-coding part of the genome (www.nature.com/-articles/s41467-017-00100-x), which is another active ongoing research effort in the group.

We have also studied mutation and selection in the framework of human polymorphisms (www.nature.com/-articles/ng.3831; academic.oup.com/mbe/article-abstract/36/8/1701/5475505) and de novo variants (www.nature.com/articles/s41467-020-17162-z). Here, a particular focus of the group lies on the description of purifying selection in humans and across species, accounting for mutational processes as well as the effects of genetic drift.

The Evolutionary Processes Modeling lab was established in October 2018 and is part of the "Bioinformatics and Genomics" program at the CRG. Further information can be found at https://weghornlab.net/ and at www.crg.eu/en/programmes-groups/weghorn-lab . Candidate profile

- PhD degree in population genetics, physics, statistics, genetics, bioinformatics, computer science or a related discipline. - Familiarity with the principles of population genetics and statistical analysis. - Experience with computational analysis of sequencing and other biological datasets.

The ideal candidate should be highly motivated and eager to work on evolutionary and biological problems through the use and development of theoretical and computational approaches.

The offer

Contract duration: 1 year (with possibility of extension). Estimated annual gross salary: Salary is commensurate with qualifications and consistent with our pay scales.

Target start date: First quarter of 2021.

We provide a highly stimulating environment with state-of-the-art infrastructure and unique professional career development opportunities. We offer and promote a diverse and inclusive environment and welcome applicants regardless of age, disability, gender, nationality, race, religion or sexual orientation. The CRG is committed to reconcile a work and family life of its employees and offers extended vacation period and the possibility to benefit from flexible working hours.

Application procedure

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DTU-Aqua Denmark ComparativeGenomics

Postdoc in comparative genomics

We are looking for a highly motivated researcher for an 18 month postdoctoral position collaborating in an exciting project on comparative genomics of marine fish and shellfish species. In the project, we use genome resequencing data from a range of species to reconstruct the demographic history and characterize genomic signals associated with population divergence and local adaptation in high gene flow scenarios. The work will improve our understanding of interacting evolutionary processes and provide valuable data for securing sustainable management and conservation of exploited resources. Applicants are encouraged to develop their own research ideas within this framework.

The fellowship is part of a larger Nordic collaborative project, MarGen_II, financed by the EU Interreg Ãresund-Kattegat-Skagerrak Programme, the Danish Rod and Net License Funds and the National Institute of Aquatic Resources (DTU Aqua). The project will primarily be carried out in the population genetics group, Section for Marine Living Resources, situated in Silkeborg, Denmark. DTU Aqua is an institute at the Technical University of Denmark. In addition, the position offers many opportunities for collaborating with Nordic and other European colleagues in the field.

Qualifications: The position involves bioinformatic analyses of already available genome resequencing data from a range of species with high quality reference genomes. The overall aims are to combine information about demographic history with genome scans to understand the interacting effects of demographic and evolutionary processes during population divergence, with a particular focus on populations in the environmental transition zone between the marine North Sea and the brackish Baltic Sea. As such, a strong background in evolutionary biology, population genetics and bioinformatics is important.

In addition, we are looking for candidates who have - Keen interest in research and the field of marine and aquatic sciences - Good collaborative skills - Proficiency in written and spoken English

Candidates must hold a PhD degree (or equivalent).

Salary and appointment terms: The appointment will be based on the collective agreement with the Danish Confederation of Professional Associations. Starting date is 01 March 2021 and duration of employment is 18 months.

Application: Apply online at https://www.dtu.dk/english/About/JOB-and-CAREER/vacant-positions/job?id=d198fd80-4856-4a56-943d-485106026504 .The deadline is 4 January 2021. For further information, please contact Senior Researcher Jakob Hemmer-Hansen, jhh@aqua.dtu.dk.

You can read more about DTU Aqua at www.aqua.dtu.dk and the population genetics group at https://www.aqua.dtu.dk/english/research/population_genetics . All interested candidates irrespective of age, gender, race, disability, religion or ethnic background are encouraged to apply.

Jakob Hemmer Hansen <jhh@aqua.dtu.dk>

DukeU EvolutionaryBiomechanics

Postdoctoral Researcher in Evolutionary Biomechanics

Join an interdisciplinary team examining the evolution and scaling of muscle and elastic systems. Based at the Patek Lab in the Biology department at Duke University, and collaborating closely with the Physics of Soft Matter Lab in the Physics Department at Harvey Mudd College, the broad goal of this research is to establish the principles by which biological systems navigate physics-based limits and transitions through scaling and evolutionary processes.

Requirements:

* Ph.D. in Biology or related field * journal publication record * experience working with live organisms, ideally in the field * previous experience in at least one of the following areas: comparative biomechanics, comparative physiology, or phylogenetic evolutionary analysis

The candidate should demonstrate:

* Interest in physiological and mechanical principles of biological movement in an rigorous evolutionary framework * Ability to lead productive research initiatives with creativity, self-sufficiency and motivation * Interest in conducting marine fieldwork * Interest in integrating biomechanical and physiological data with mathematical modeling and phylogenetic comparative analyses * Commitment to mentor and collaborate with students in the Physics of Soft Matter Lab at Harvey Mudd College (led by Prof. Mark Ilton). Option to spend summers guiding the group, with support provided to develop mentoring, leadership and scientific management skills. * Commitment to engage broader communities in research and develop broader impact skills through working with high school teachers and implementing structural changes in academic research to enhance inclusiveness through the Muser program.

APPLICATIONS DUE JANUARY 22, 2021 Become part of a diverse and inclusive research team and university, with outstanding job benefits in a culturally diverse and affordable geographic region. The position is available immediately with the start date ideally no later than late spring or early summer 2021. 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 and questions about the position. The job application must be submitted to Academic Jobs Online (job #17817) and should include:

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

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

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

Billy Ray <william.ray@duke.edu>

GeorgiaTech EvolutionSocialBehaviour

Postdoctoral position studying social behavior, epigenetics, and living-systems physics

The Goodisman Lab at the School of Biological Sciences at Georgia Tech seeks a postdoctoral fellow interested in studying questions at the intersection of social behavior, evolution, epigenetics, and living-systems physics. The successful candidate would study the consequences of the built environment on social behavior. The built environment, constructed by collectives of individuals, has been fundamentally important to the success of biological societies. This research program investigates the link between cognition, social behavior, epigenetic information, and the built environment in insect societies.

This is a collaborative investigation which combines expertise in genetics, insect behavior, granular media physics, epigenetics, and the dynamics of collective actions. Students would work jointly in the labs of Michael Goodisman (https://www.goodismanlab.biology.gatech.edu/), Soojin Yi (https://yilab.gatech.edu/), and Dan Goldman (https://crablab.gatech.edu/). The research program is interdisciplinary by nature. Thus candidates with experience in genomics, evolution, behavior, epigenetics, insect science, computational biology, or physics may be appropriate. The candidate would be encouraged to develop an independent research direction that aligns with general research programs in the labs.

Interested applicants are encouraged to contact Dr. Goodisman at mg225@gatech.edu. Applicants should submit applications for Job ID 222494 through the site

https://careers.hprod.onehcm.usg.edu/-psp/careers/CAREERS/HRMS/c/-HRS_HRAM_FL.HRS_CG_SEARCH_FL.GBL?Page=-HRS_APP_JBPST_FL&Action=U&FOCUS=-Applicant&SiteId=3000&JobOpeningId=-222494&PostingSeq=1 Applications should include: (1) A cover letter describing relevant experience, qualifications, and interests (2) A CV (3) The names and contact information of three references. Review of applications will begin January 21, 2021 and continue until a suitable candidate is identified.

Michael A D Goodisman, Associate Professor

School of Biological Sciences, Georgia Institute of Technology Cherry Emerson Bldg A124, 310 Ferst Drive Atlanta, GA 30332-0230, United States Email: michael.goodisman@biology.gatech.edu Lab webpage: http://www.goodismanlab.biology.gatech.edu/ "michael.goodisman@biology.gatech.edu"

IOW Warnemuende ResurrectionEcology

Postdoc and PhD opportunities in the PHYTOARK project

Dear all,

We currently have three openings in the multidisciplinary team of researchers in the "PHYTOARK" project funded by the Collaborative Excellence Program of the Leibniz Competition, one postdoc and two PhD positions (see separate posting for the PhD positions).

Background. PHYTOARK - "Predicting the future from signatures of the past: using living sediment archives and ancient DNA to understand responses of marine primary producers to environmental changes" - is an interdisciplinary collaborative project that looks into the Holocene history of the Baltic Sea to investigate past patterns of phytoplankton biodiversity change on the levels of communities and populations and integrates this change with Holocene and Anthropocene climate warming. The results are used in ecosystem models to develop novel tools for the assessment and prediction of ecosystem functioning under global change. The project will be carried out by a network of German and international partners. Network partners within Germany are located at the Institute of Baltic Sea Research Warnemuende (IOW), Senckenberg Research Institute (SGN), University of Hamburg and University of Konstanz.

Postdoc - Resurrection Ecology This sub-project will investigate intraspecific changes and potential evolutionary adaptation within and among populations of key phytoplankton species using resurrection ecology approaches. The postdoc will be based at the Institute of Baltic Sea Research Warnemuende (IOW), with Dr. Anke Kremp. Application deadline January 8th, 2021 - complete advert here - https://bit.ly/2KGXCiR For scientific enquiries please contact anke.kremp@io-warnemuende.de

Best regards, the PHYTOARK team

– Prof. Dr. Laura Epp University of Konstanz Limnological Institute Junior Professor for Environmental Genomics in Aquatic Systems Mainaustraße 252 78464 Konstanz / Egg Germany

Office Phone: 0049 7531 88 3391 Mobil Phone (frequent home office): 0049 176 6477 6818 laura.epp@uni-konstanz.de https://www.researchgate.net/profile/-Laura_Epp https://www.limnologie.uni-konstanz.de/-en/ag-epp-environmental-genomics/ Laura Epp <laura.epp@uni-konstanz.de>

MaxPlanckInst Tubingen EvolutionaryGenomics

TheMaxPlanck Institute for DevelopmentalBiology in T??bingen isaworld-renowned research institute and part of the German Max Planck Society. The Algal Development and Evolution Department is seeking a full timePostdoctoral Associate(f/m/d) with excellent skills and knowledge in the field of Next Generation Sequencing technologies and evolutionary genomics to work on large scale brown algal genomic data in the context of the ERC consolidator grant TETHYS. The successfulcandidateisexpectedtodevelopand applycomputational toolsforthe analysis of high-throughput sequencing data, like the analysis of DNAseq, RNAseq, ChipSeq or HiC data. The successful candidate will be involved in various studies using brown algae as a model system, focused on comparative genomics, sex chromosome evolution, epigenetic analysis. General responsibilities also include data and pipeline management as well as participating in the writing of resultant manuscripts. The successful candidate is expected to interact closely with experimental biologists. The ideal candidate will have:

a PhD in bioinformatics, computer science, data science, biology or related discipline with focus on computer science, in particular with regard to high throughput genomic data analysis

A demonstrated track record in next generation sequencing data analysis is required experiences in programming, preferably in R, C/C++, Python good interpersonal and communication skills, as well as the ability to work well both independently and as part of a team. good command of English, both written and spoken

The payment level is based on the German state public service salary scale (TV??D-Bund) according to the training, qualifications and professional experience. The benefits correspond to the regulations of the public service. The position is available from January 2021, and will remain opened until a suitable candidate is found. Informal enquiries can be made to susana.coelho@tuebingen.mpg.de.The initial contract is for one year potentially renewable for 3 years.Send your application to office_coelho@tuebingen.mpg.de. Applications must include a cover letter, curriculum vitae, and names and contacts of a least two reference persons. The Max-Planck Society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals. The Max-Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

Susana Coelho, PhD Department of Algal Development and Evolution Max Planck Institute for Developmental-Biology Max-Planck-Ring 5 72076 T??bingen Tel.: +49 7071-601-1307 E-mail: susana.coelho@tuebingen.mpg.de

Susana Coelho <susana.coelho@tuebingen.mpg.de>

NorthDakotaStateU PDF PhD HouseSparrowEvol

PhD student

The Heidinger Lab seeks to recruit an enthusiastic and motivated Ph.D. student to contribute to an NSF funded study examining the physiological mechanisms that underlie the rapid phenotypic diversification of body size and other life-history traits in house sparrows (Passer domesticus). This project is highly integrative and will include experimental fieldwork, hormone assays, qPCR and transcriptomics, and the measurement of contemporary and historical museum specimens and there is large scope to develop projects related to this general theme.

The Heidinger Lab is located at North Dakota State University (NDSU) in Fargo, ND. Students would join a vibrant department with several other researchers with expertise in integrative organismal biology including: Drs. Tim Greives, Julia Bowsher, Kendra Greenlee, and Ned Dochtermann. Ideally the position will begin in August 2021 and students should enroll in either the Biological Sciences or Environmental and Conservation Sciences graduate program at NDSU. Competitive stipend funding and tuition waivers via teaching and/or research assistantships are available.

If you are interested in this position, please contact Dr. Britt Heidinger at britt.heidinger@ndsu.edu. Please include the following information in your email: 1) your research interests and experiences, 2) a curriculum vitae, 3) your GPA and GRE scores (if available), and 4) contact information for three potential references.

Post-doc position

An enthusiastic and highly motivated post-doctoral researcher is sought to join the lab of Dr. Britt Heidinger (britt.heidinger@ndsu.edu) in the Department of Biological Sciences at North Dakota State University (NDSU). This is a 12-month, NSF funded position (with the possibility of renewal) to study the mechanisms (physiological and transcriptomic) that underlie the rapid phenotypic diversification of body size and other life-history traits along a latitudinal gradient in house sparrows (Passer domesticus). This project is highly integrative and will include experimental fieldwork, hormone assays, qPCR, transcriptomics, and the measurement of contemporary and historical museum specimens. The post-doc will reside in Fargo, ND, but will also help coordinate and conduct fieldwork along a latitudinal temperature gradient including sites in Lawrence, KS, and Baton Rouge, LA. During this position, the post-doc will gain valuable experience in research design, endocrine and molecular techniques, and mentoring graduate and undergraduate students. The post-doc is also encouraged to pursue independent lines of research related to this general theme, which may include analyses of a unique collection of museum specimens. The start date is somewhat flexible, but ideally will begin before March 1st, 2020.

Candidates must 1) have a Ph.D. degree in biological sciences or a related discipline from an accredited institution; 2) have a demonstrated interest in research in evolutionary and physiological ecology; and 3) have strong oral and written communication skills, including an ability to coordinate and work as part of a research team.

Preference will be given to candidates with demonstrated experience in 1) field research; 2) transcriptomics; 3) qPCR; 4) hormone assays; and 5) avian systems.

Applicants must submit a cover letter; a curriculum vitae; a description of research experience (2 pages maximum); and contact information (including telephone numbers and e-mail addresses) for three professional references. All application materials must be submitted online at:

https://adminsys.ndus.edu/psc/-recruit/EMPLOYEE/HRMS/c/-HRS_HRAM_FL.HRS_CG_SEARCH_FL.GBL?Page=-HRS_APP_JBPST_FL&Action=U&FOCUS=-Applicant&SiteId=1&JobOpeningId=-2922683&PostingSeq=1 Review of applications will begin in December and continue until the position is filled.

Questions regarding the search may be sent to britt.heidinger@ndsu.edu

Britt J. Heidinger, Ph.D. (she/her/hers)

Associate Professor Department of Biological Sciences NDSU Dept 2715 PO Box 6050 North Dakota State University Fargo, ND 58108-6050

Email: britt.heidinger@ndsu.edu

Phone: 701-231-5377

"Heidinger, Britt" <britt.heidinger@ndsu.edu>

NRC Maryland ResAssoc MutationEvolution

The US National Research Council (NRC) offers competitive Research Associateships for post-doctoral and senior scientists to conduct research in participating federal labs. The awards include a generous stipend as well as benefits (health insurance, travel, relocation), as explained on the program web site (http://sites.nationalacademies.org/pga/rap/).

To apply, you must write a brief research proposal that reflects a plan of your own, or a plan that we develop together, involving some computational approach to molecular evolution. Especially welcome are proposals for empirical or theoretical work on biases in the introduction of variation as a dispositional factor in evolution, building on work such as Yampolsky and Stoltzfus (2001), Stoltzfus and McCandlish (2017) or Stoltzfus and Norris (2016).

The upcoming deadline for proposals is February 1, 2021 (there is another deadline August 1). If you are interested, contact me with a brief introduction, and we'll go from there. Updated information may be available at

http://www.molevol.org/nrc-research-associateship-mutation-and-evolution/.

Arlin Stoltzfus (arlin@umd.edu)

Data Scientist, Office of Data & Informatics, NIST Fellow, IBBR; Adj. Assoc. Prof., UMCP; IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org Stoltzfus A, McCandlish DM. 2017. Mutational biases influence parallel adaptation. Mol Biol Evol 34:2163-2172 (http://doi.org/10.1093/-molbev/msx180)

Stoltzfus A, Norris RW. 2016. On the Causes of Evolutionary Transition:Transversion Bias. Mol Biol Evol 33:595-602. http://mbe.oxfordjournals.org/-content/33/3/595.abstract Yampolsky LY, Stoltzfus A. 2001. Bias in the introduction of variation as an orienting factor in evolution. Evol Dev 3:73-83. https://onlinelibrary.wiley.com/doi/epdf/-10.1046/j.1525-142x.2001.003002073.x Arlin Stoltzfus (arlin@umd.edu) Office of Data and Informatics, NIST;Fellow, IBBR; Adj. Assoc. Prof., UMCP IBBR, 9600 Gudelsky Drive, Rockville,MD, 20850 tel: 240 314 6208; web: www.molevol.org Arlin Stoltzfus <arlin@umd.edu>

OxfordU MolecularBasisOfAvianFertility

Oxford University.Molecular basis of avian fertility.

A Postdoctoral Research Assistant position is available to work in Professor Tom Pizzari's group on a BBSRC-funded project entitled "Interrogating the seminal fluid proteome to resolve the molecular basis of fertility in poultry".

The postholder will conduct experimental research investigating compositional variation in the seminal fluid proteome associated with sperm fertilising efficiency, in both red junglefowl (Gallus gallus) and commercial broiler breeders (G. domesticus). This will entail planning and conducting experiments, data collection and analysis, leading in disseminating results and in the writing of scientific articles. The postholder will liaise regularly with the PI and project partners (Dr. S. Dorus - academic project partner; Moy Park Ltd, industrial project partner). The postholder will visit Dr. S. Dorus at Syracuse University for training in relevant bioinformatic and proteomic approaches. Finally, the postholder will be actively involved in the running of different engagement, dissemination and outreach activities as outlined in the pathways to impact, and will be responsible for data archiving, dataset curation and the implementation of data management plan.

The successful candidate will have: a relevant PhD/DPhil, expertise in reproductive physiology, demonstrable experience of managing own academic research, and in the dissemination of scientific results through publications and presentations. The successful candidate will have excellent communication skills, including the ability to write for publication, present research proposals and results, and represent the research group at meetings. They will also have the ability to contribute ideas for new research projects and research income generation.

Committed to equality and valuing diversity. The closing date for applications is 12:00 noon on the 8th January 2021.

For more information contact Prof Tom Pizzari at:

tommaso.pizzari@zoo.ox.ac.uk

Apply online at https://my.corehr.com/pls/uoxrecruit/erq_jobspec_version_4.display_form?p_recruitment_id=8673&p_form_profile_detail=&p_company=&p_display_apply_ind=Y&p_display_in_irish=N&p_refresh_search=Y&p_applicant_no=&p_internal_external=E&p_process_type Job Details - my.corehr.com

Postdoctoral Research Assistant Department of Zoology, 11a Mansfield Road, Oxford, OX1 3SZ 32,817 - 35,845 A Postdoctoral Research Assistant position is available to work in Professor Tom Pizzari's group on a BBSRC-funded project entitled "Interrogating the seminal fluid proteome to resolve the molecular basis of fertility in poultry".

my.corehr.com

Tommaso Pizzari <tommaso.pizzari@zoo.ox.ac.uk>

PennStateU EvolutionaryBiology

We are extending the deadline to *December 18* for initial pre-applications (nominations) for Eberly Fellows seeking to work in the Dept of Biology at Penn State

https://science.psu.edu/research/eberly-postdoctoral-research-fellows The Penn State Eberly College of Science invites nominees for the Eberly Research Fellowship program.

Eberly Fellowships are designed to attract exceptional early career scientists to Penn State to enhance their career goals in the vibrant, highly collaborative environment of the Eberly College of Science and the broader STEM community at Penn State. The Eberly College of Science'Xincluding the Departments of Astronomy and Astrophysics, Biology, Biochemistry and Molecular Biology, Mathematics, Physics, and Statistics'Xranks in the top 10 universities in the United States and has annual research expenditures exceeding $125 million. Each of these six departments expects to appoint one or more Eberly Fellows. Nominations of early career scientists with exceptional promise in basic research in physics, biology, molecular biology, astronomy, mathematics, and statistics, and/or applied research in health, energy, materials, or the environment, are encouraged. Interdisciplinary as well as traditional disciplinary research is encouraged. Fellows who wish to also gain training and experience in teaching may elect to receive mentored teaching experience. Eberly Fellow advisers must hold their primary appointment in one of the seven departments of the Eberly College of Science. Coadvisers and cross-disciplinary research are also supported.

Department of Biology Pennsylvania State University

"Jesse R. Lasky" <jrl35@psu.edu>

PortlandStateU SomaticMutation

Postdoc position: Genomics of Somatic Mutation Accumulation and Clonal Evolution in /Mimulus/

A postdoctoral position is available in the Cruzan lab at Portland State University as part of a collaborative

NSF-funded project focused on understanding the consequences of clonal evolution and natural selection on somatic mutation accumulation in plants. Mutation accumulation is intrinsically different in plants compared to animals, because the same germ cells that subtend vegetative growth are responsible for gamete production. Somatic mutations can occur with each mitotic division during stem growth; consequently, plants have enormous potential to accumulate mutations, but the effects of these mutations on adaptation is unknown. This project will use genomic and greenhouse experiments to identify the fitness consequences of somatic mutations for plants in the next generation, using /Mimulus/ as a model system.

A PhD in evolutionary genetics or a related field is required. We seek an individual with experience and expertise in at least two of the following: genomics, bioinformatics, and plant biology. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds.In addition, the successful candidate will have an excellent understanding of experimental design and a proven publication record, and they will have intellectual purview over the design and implementation of experiments. This work will be conducted in collaboration with PIs, graduate, and undergraduate students at Portland State University (Cruzan lab) and the University of Oregon (Streisfeld lab).

Interested individuals should send a letter of introduction to Mitch Cruzan (Cruzan@pdx.edu) that includes a brief statement of your background.Please include an essay outlining your research interests and a recent copy of your CV.

Mitch Cruzan, Department of Biology, Portland State University, Portland, OR

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

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

cruzan@pdx.edu

SLU Alnarp EvolutionaryEcology

Postdoctoral position in evolutionary ecology: herbivory and tritrophic interactions under climate change

We are recruiting a postdoc to a BiodivERsA project will partners in Sweden, Finland, Belgium and Spain. The aim of the project is to generate fundamental new insights into the mechanisms of climate adaptation in plants, using wild strawberry as model plant. The project connects genetic and evolutionary mechanisms to biodiversity patterns, and interlinks abiotic with biotic selection.

More information and link to online application system here: https://www.slu.se/en/about-slu/work-at-slu/-jobs-vacancies/?rmpage=job&rmjob=4319&rmlang=-UK Johan A. Stenberg Professor

Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

Department of Plant Protection Biology PO Box 102, SE-230 53 ALNARP Visiting address: Sundsvägen 14 Tel: +46 40 41 53 78 johan.stenberg@slu.se, www.slu.se/stenberg — När du skickar e-post till SLU sÃ¥ innebär detta att SLU behandlar dina personuppgifter. För att läsa mer om hur detta gÃ¥r till, klicka här < https://www.slu.se/om-slu/kontakta-slu/-personuppgifter/ >

E-mailing SLU will result in SLU processing your personal data. For more information on how this is done, click here < https://www.slu.se/en/about-slu/contact-slu/personal-data/ >

Johan A Stenberg <Johan.Stenberg@slu.se>

TU Munich PopulationGenomicsPlantPathogens

The Chair of Phytopathology at the Technical University of Munich, TUM School of Life Sciences, hires a

Postdoc in the field of Population genomics of plant pathogens

We are interested in understanding the diversity and evolution of plant pathogens. To understand various factors involved, we study both wild plant pathosystems as well as agricultural systems. In the lab we work with various cereal pathogens and several pathogens on wild and domesticated Solanum species. We apply comparative genomics and population genomics approaches to understand the biology of the host and the pathogens and the factors that govern their evolution.

For this project, we are looking for a postdoctoral researcher to investigate the genetic diversity of a crop pathogen. The applicant must have a PhD and have an interest in ecological modeling and/or population genomics. Experienced with NGS data analysis is an advantage. Excellent English skills, both written and spoken, are essential.

The project will be carried out in the group of Dr. Remco Stam at the Chair of Phytopathology (Prof. Dr. Ralph Hückelhoven). The chair hosts several research groups studying the biology of plant pathogen interaction and is well equipment to study defence responses on different levels. The project is in collaboration with a leading company in plant breeding and agrochemistry and benefits from access to their genetic resources as well as many active collaborations in the field of population genetics and genomics and access to state-of-the-art resources on the TUM Life Science Campus in Freising-Weihenstephan.

The Technical University of Munich wishes to increase the percentage of employed women. Women are therefore explicitly encouraged to apply. Handicapped persons with equivalent qualification will be given preference. The salary is according to German income level TV-L E13. The position is initially for one year, with the possibility for extension.

Please send your comprehensive application including a letter of motivation (1 page), your CV, certificates, list of publications, and names of 2 potential referees as a single pdf file by email to:— remco.stam@tum.de Informal inquiries can be made on the same address.

The position is to be filled from February 2021. Reviewing applications will start 21 December 2020, Interviews will start in January, until a suitable candidate has been found.

Website of the lab: www.remcostam.com Related publications The current epidemic of the barley pathogen Ramularia collo-cygni derives from a recent population expansion and shows global admixture. R. Stam*, H. Sghyer, A Tellier, M.Heß and R. Hückelhoven (2019)— Phytopathology 109:2161-2168 A new reference genome shows the one-speed ——— genome structure of the barley pathogen Ramularia collo-cygni. R. Stam*, M. Münsterkötter, S. Pophaly, L. Fokkens, H. Sghyer, U. Güldener, R. Hückelhoven and Heß, M. (2018). Genome Biology and Evolution 10 (12) 3243-3249 L. Fokkens, S. Shahi, L.R. Connolly, R. Stam, S. M. Schmidt, K. M. Smith, M. Freitag and M. Rep The multi-speed genome of Fusarium oxysporum reveals association of histone modifications with sequence divergence and footprints of past horizontal chromosome transfer events; bioRxiv 465070

Remco Stam <stam@wzw.tum.de>

UBern EvolutionHybridization

Dear EvolDir Community,

The Division of Theoretical Ecology and Evolution at the University of Bern, led by Claudia Bank, is looking for an

Advanced Postdoc in Ecological and Evolutionary Modeling of Hybridization (50-100%)

to be part of a team working on the collaborative HFSP-funded project “Chance or curse? The consequences of hybridization in a changing world” (see also the simultaneous postdoc opportunity in Vitor Sousa’s lab at the University of Lisbon, https://bit.ly/OpenCall-EG-cE3c-Dec2020).

Once thought to be rare, we now know that hybridization is quite common. There has been a longstanding debate about the importance of hybridization because it can have both beneficial and harmful effects. By creating new phenotypes, hybridization can help organisms adapt, but it can also drive extinction by generating harmful combinations of genes. Past work has proposed that in stressful environments, the benefits of hybridization may outweigh the costs, but this idea has not been clearly tested. Understanding these dynamics has become more pressing as rates of hybridization have increased due to the stresses of rapidly changing environments. In collaboration with Drs. Molly Schumer, Chelsea Rochman, and Vitor Sousa, we will combine diverse and multidisciplinary expertise to tackle fundamental questions about the consequences of hybridization via field observations, laboratory experiments, computational tools, and mathematical models.

We are looking for a postdoc with proven expertise in ecological/eco-evolutionary modeling, preferably with at least 2 years of postdoctoral experience. They will develop models and approaches to predict the outcomes of hybridization by incorporating interacting and selected genetic loci into ecological models of hybrid populations in isolation or in a spatial environment. The ideal candidate is open to exploring both mathematical approaches and large-scale simulations that take into account ecological variables in order to quantify extinction probabilities and other evolutionary outcomes. In addition to independently developing this project, the desired candidate is keen to contribute their expertise to other projects in the lab (and in the collaborative team) and open to mentoring occasional undergraduate and Masters students with interest in the topic.

We provide a dynamic and interdisciplinary work environment within the research group (Division of Theoretical Ecology and Evolution, former Evolutionary Dynamics Group), within the Institute of Ecology and Evolution in Bern (https://www.iee.unibe.ch/), and within the collaborator team (Molly Schumer, Stanford University, https://schumerlab.com/; Chelsea Rochman, University of Toronto, https://rochmanlab.com; and Vitor Sousa, University of Lisbon, https://ce3c.ciencias.ulisboa.pt/member/vitorsousa). If desired by the candidate, short or mid-term visits of the collaborator labs are encouraged, and the candidate is expected to present and discuss their work at international workshops and conferences. The salary will be commensurate with qualifications and experience, according to the University of Bern statutes. Funding for this position is currently available for 3 years. Our lab philosophy includes open communication, regular individual meetings and evaluation of mentoring and career development needs, and prioritising the well-being of all lab members.

Contact and Application

If interested, please send a complete CV, a motivation letter explaining the fit for the position, and the desired starting date (<1 page), a statement of research interests and approaches (<1 page), and names of 3 referees by email as a single pdf file to claudia.bank@iee.unibe.ch. Evaluation of the applications will begin immediately and continue until the position is filled, with a desired starting date as early as possible. Following the University of Bern's policy, it is expected that the candidate relocates to Switzerland in time for the starting date of the position.

Best wishes, Claudia Bank

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Prof. Dr. Claudia Bank

Head of Division, Theoretical Ecology and Evolution
Institute of Ecology and Evolution, University of Bern
Bern, Switzerland

Group Leader, Evolutionary Dynamics Group Gulbenkian Science Institute Oeiras, Portugal

Website: https://banklab.github.io/ Claudia Bank <evoldynamics@gmail.com>

UBritishColumbia CiliateEndosymbionts

Research Associate Position in Genome Evolution of Ciliate Endosymbionts

The Keeling lab in the Department of Botany at UBC seeks a well-trained highly motivated and enthusiastic individual interested in exploring the evolutionary biology of complex microbial life and their endosymbionts using genomics and single cell genomics methods coupled with phylogenomic analyses, as a Research Associate.

The applicant must have a PhD or equivalent and at least three additional years of research experience. Expertise in eukaryotic biodiversity and evolutionary history, and the application of single cell genomics methods (genomic and transcriptomic datasets) and phylogenic analyses are essential, as is expertise in lab maintenance and manipulation of ciliated protists. The applicant must have excellent written and oral communication skills and be highly organised. Molecular biology and analyses techniques are also highly desirable. The candidate must have a proven record of publication in significant journals in the field.

The position is available starting April 20, 2021 for an initial period of one year with a possibility for extension subject to a satisfactory performance and funding. To apply, please send a cover letter outlining research experience and interest, a curriculum vitae and the names and contact information for 3 referees by E-mail to Patrick Keeling, Department of Botany, University of British Columbia. E-mail pkeeling@mail.ubc.ca. Use the Subject line "CILIATE ENDOSYMBIONT GENOMICS". Closing date is Jan 4, 2021.

UBC hires on the basis of merit and is strongly committed to equity and diversity within its community. We especially welcome applications from visible minority group members, women, Aboriginal persons, persons with disabilities, persons of minority sexual orientations and gender identities, and others with the skills and knowledge to productively engage with diverse communities.

"Keeling, Patrick" <pkeeling@mail.ubc.ca>

UCalifornia Berkeley HumanEvolGenetics

Post-doctoral position - University of California, Berkeley - Human Evolutionary Genetics.

Description: The Moorjani Lab (https://moorjanilab.org/) at University of California, Berkeley uses computational and statistical methods to investigate questions in human evolutionary genetics, in particular on mutation rate, demographic inference and archaic ancestry. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and disease. To this end, we use genetic data from ancient specimens and present-day species to learn about: (1) when key events (such as introgression and adaptations) occurred in human history, (2) how different evolutionary processes such as mutation rate evolve across primates, and (3) how we can leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Responsibilities: A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Required qualifications: Ph.D. or equivalent in genetics, genomics, computational biology or related fields and demonstrated record of productivity and publications. Experience with programming (e.g. C/C++, Python/ Perl, R or other programming languages), genomic data analysis and methods development.

Please contact Priya with your CV and a brief overview of research questions you are interested in pursuing. Please also request three recommenders to send a letter of reference on your behalf.

Salary: This is a multi-year postdoctoral position (initial appointment is for 12 months and renewable annually up to three more years). Salary is commensurate with qualifications and experience.

Contact: Priya Moorjani Assistant Professor Department of Molecular and Cell Biology Center for Computational Biology https://moorjanilab.org/ Email: moorjani@berkeley.edu

Priya Moorjani <moorjani@berkeley.edu>

UCambridge DrosphilaCoevolution

Applications are invited for a postdoctoral Research Associate to work with Professor Frank Jiggins in the Department of Genetics, University of Cambridge and Dr Ben Longdon, University of Exeter, on a Leverhulme Trust funded research project 'A new laboratory model to test the principles of host-parasite coevolution'. The successful candidate will be based in the Department of Genetics, University of Cambridge, and will conduct fundamental research aimed at understanding the evolutionary dynamics of coevolution.

Taking advantage of our detailed knowledge of the genes controlling the susceptibility of Drosophila to viral infection, the post holder will investigate the processes underpinning coevolution by tracking allele frequencies within laboratory populations. The post requires creative candidates who are enthusiastic about taking experimental approaches to understand the processes governing coevolution in nature. Successful candidates will have an advanced understanding of evolutionary processes and concepts. It will be advantageous to have previously worked on coevolution.

Applicants should hold, or are about to be awarded, a PhD in Evolutionary Biology.

Full details: https://www.jobs.cam.ac.uk/job/26935/ “F. Jiggins” <fmj1001@cam.ac.uk>

UCLouvain Belgium EvolutionaryEcology

UCLouvain_Insect Learning for Rapid Adaptation to changing habitats

Postdoc position in Evolutionary Ecology

We are looking for highly motivated candidates to apply for a 2 to 4-year postdoctoral position, funded through

UCLouvain university ("Action de recherche concertée"), in the laboratory of Prof Caroline Nieberding (https://nieberdinglab.be/, UCLouvain, Belgium).

Animals were long thought not to learn. Over the years research has, however, revealed that most animals do learn to some extent. This paradigm shift has led to the hypothesis that learning is a form of behavioural plasticity that participates to rapid adaptation of natural populations in nature, in response to human induced habitat degradations. Yet, the adaptive value of learning remains rarely quantified so far. This project will quantify the adaptive value of learning in the field in a number of butterfly species facing increasing reduction and fragmentation of suitable habitats. Butterflies are flagship and bioindicator species of the quality of European natural habitats, and we have occurrence data spanning several decades. This project aims at providing one of the first field-based estimates of the selective value of learning for a key behavioural trait, oviposition site selection ("OSS" hereafter). OSS is key to colonisation of suitable habitats in butterflies, the larvae of which have only a low mobility. As learning is costly, we expect that increased learning and memory skills are correlated to reduced survival and/or egg production and we will quantify potential trade-offs associated with learning and memory.

The postdoctoral research will include experiments in the field in Belgium and ecologically-relevant experiments in the laboratory, where field-caught animals can be monitored. The ideal candidate for this position will have a strong background in behavioural ecology, statistical analyses, expertise in butterfly ecology and a capacity for creative and critical thinking. The candidate will have opportunities to learn some of the specific skills required for the project by our network of national and international collaborators. Applicants should hold a PhD diploma. The deadline for applications is December 15th, or until the application is filled.

The salary will be around 2000 euro netto per month plus benefits (health insurance,...) which are included in the Belgian system. Our University is an Equal Opportunity/Affirmative Action Employer, and is in a French-speaking region of Belgium, but the language for meetings and scientific interactions is English. For background information about our university, see https://uclouvain.be/en/index.html . Applications should be sent to Prof. C. Nieberding (caroline.nieberding@uclouvain.be). Applications will include: 1) a motivation letter including a statement of interests; 2) full CV including list of publications; 3) Contact details of at least 2 referees. Informal inquiries are welcome. More info on the duration of the project can be obtained by contacting C. Nieberding directly. We will start reviewing applications as they arrive until the appropriate candidate is selected, and the project will be starting in Spring 2021.

Prof. Dr. Caroline Nieberding

Evolutionary Ecology and Genetics Group Biodiversity Research Centre Earth and Life Institute University of Louvain (UCLouvain) Carnoy building, office b112 Belgium phone: +32 (0)10 47 34 88 website: https://nieberdinglab.be Parcel and mail deliveries at the secretary's office :

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UCrete Greece LanguageEvolution

Post-doctoral position-University of Crete, Greece, Language Evolution

Description:

The Department of Biology at the University of Crete seeks a Post- doctoral researcher to perform phylogenetic and statistical research in language evolution in the context of the H.F.R.I. funded interdisciplinary project "Modeling Glossogeny. Using biological tools in the study of genetic and areal stability of morpho- syntactic parameters" (PI: Elena Anagnostopoulou).

The post- doctoral researcher will analyze linguistic data in collaboration with the PI and the members of the research team of the project (Drs. Manolis Ladoukakis and Dimitris Michelioudakis). The analysis involves the use of phylogenetic and statistical tools adjusted to historical linguistic research. Candidates must have earned their Ph.D. degree recognized by D.O.A.T.A.P. (Hellenic NARIC; for the application it is sufficient for candidates to have proof that the process for the recognition has officially started via the registration/protocol number) and have specialized in Linguistics or Population Genetics or Phylogenetics.

Qualified linguistics candidates should possess: - Expertise in theoretical linguistics in the areas of parametric syntax and morphology - Experience in working with and analyzing typological and/or historical data - Preferred qualifications include familiarity with computational and statistical methods in linguistics and/or computational phylogenetics in historical linguistics

Qualified biology candidates should possess: - Experience in working with and analyzing phylogenetic data and/or population genetics data - Experience in statistical methods in biology

The details of the submission procedure as well as the documents required for application can be found at the application link provided below.

Application Deadline: 29-Jan-2021

Email Address for Applications: calls.elke-reth@uoc.gr Web Address for Applications: https://www.elke.uoc.gr/announcements/news/view.aspx?idI44 Contact Information: Manolis Ladoukakis Email: ladoukakis@uoc.gr

Emmanuel (Manolis) LADOUKAKIS, M.Sc., Ph.D.

Department of Biology University of Crete Voutes University Campus 70013 Heraklio Greece

Tel: +30 2810 394067

Manolis Ladoukakis <ladoukakis@uoc.gr>

UEdinburgh QuantitativeGeneticsGeneEditing

Research Fellow in Quantitative Genetics/Genome-Editing

To analyse sequence data on a huge pig data set. Closing: 5 January

We are looking for a post-doctoral researcher in quantitative genetics/genome-editing, to work on a project, led by Prof. Richard Mellanby in collaboration with our industrial partners PIC (part of Genus plc). In the past three years the project has generated one of the largest and most powerful livestock genetics data sets globally with accurate whole genome sequence information and phenotypes on hundreds and thousands of individuals. Plans are in place to utilise/interrogate this data to develop an Allele Testing platform, a large scale genome-wide experimental and computational framework, for identification of causal variants in livestock.

*The Opportunity: *This project has four aims: (1). Develop an “Allele Testing” framework using genomics analyses, grounded in quantitative genetics, population genetics and bioinformatics, to generate a ranked list of causal genomic variants from whole genome sequence data; (2). Use genome-editing to introduce putative causal genomic variants into an in vitro cell system for phenotypic interrogation; (3). Undertake such analyses in a very large dataset encapsulating phenotype and sequence data in pigs to make novel discoveries about animal genomics (4). Deploy this knowledge to develop novel strategies to apply genomic information in breeding.

Interviews will be held January 2021

If invited for interview you will be required to evidence your right to work in the UK. Further information is available on our *right to work* < https://www.ed.ac.uk/human-resources/demonstrating-rtw > webpages.

The University is able to sponsor the employment of international workers in this role.â€ If successful, an international applicant requiring sponsorship to work in the UK will need to satisfy the UK Home Office’s English Language requirements and apply for and secure a Tier 2/Skilled Worker Visa.

Informal enquires can be made to Richard Mellanby (Richard.Mellanby@ed.ac.uk) or Melissa Jungnickel (melissa.jungnickel@roslin.ed.ac.uk), while formal applications should be submitted through The University of Edinburgh website.

https://www.ed.ac.uk/roslin/work-study/opportunities/vacancies/research-fellow-in-quantitative-genetics-genome martin johnsson <sorill@gmail.com>

UFribourg Switzerland EvolutionaryPhysiology

Postdoc: UFribourg_Switzerland.EvolutionaryPhysiology

We are looking for a postdoc to join the—Social Fluids Lab (http://leboeuflab.com/) studying collective control of physiology from ***either a molecular or computational/physics perspective.***

The Social Fluids Lab Our lab takes an integrative approach to studying how behavior evolves. We study socially exchanged fluids and how they can be used for consensus building and be co-opted by evolution to influence physiology and behavior. We use social insects as a model system because many engage in a mouth-to-mouth fluid exchange called trophallaxis, wherein they transmit endogenously produced molecules that can influence receivers.——In many species that engage in this behavior, every individual in the colony is connected through this network of fluid exchange. The exchanged fluid is rich with proteins, hormones, RNA and small molecules (LeBoeuf et al. 2016 eLife). Some of these components, when fed to larvae by trophallaxis, can influence developmental fate and timing! This provides a means for how some social insect communities can collectively decide on the colony's developmental progression - by sending cues and signals over the social circulatory system.

Our lab uses machine learning approaches in both evolutionary proteomics and long-term automated tracking of behavior and fluorescence in ant colonies to answer our questions about the evolution of behavior. We are a relatively young research group building this field of socially exchanged materials.

Lab values Creativity, interdisciplinarity, collaboration, open source, open access, inclusiveness, team mentality.

You: We are looking for a primarily molecular and/or primarily computational postdoc to join our group. The ideal candidate is collaborative, committed and passionate about their research; they should fit (broadly) one of the two phenotypes detailed below.

Phenotype 1 (molecular):—How does the social circulatory system circumvent the longevity-fecundity tradeoff? You are comfortable with molecular and biochemical approaches (e.g. in situ hybridization, protein purification, developing assays, microscopy). You are interested in behavior, superorganismal physiology and how socially transmitted components can influence receivers.

Phenotype 2 (computational):—Quantitative behavioral tracking of different kinds of individuals different individuals (adults and larvae) in the same network and fluorescent tracking of flow over the social network. You are comfortable coding in python and have experience with image and/or network analysis. You might not be a biologist by training but rather an engineer, computer scientist or physicist. You are interested in collective behavior and distributed problem-solving.

Your specific project will depend on your interests but will certainly focus on socially exchanged fluids and collective developmental control in social insects. If you think you have yet another phenotype that would fit well with the Social Fluids labor for another type of position, write to Adria.

Positions Start dates are flexible, aiming at first half of 2021. Position is currently funded for 2 years but could be extended depending on circumstances, for example, a candidate coming with or applying for their own funding.

Submission Applications (in English) should include a statement on your background and motivation to join our research group*, CV (including—an annotated list of publications (preprints included) wherein you describe your contribution to the works), and the names and contact details of two references.

Applications should be sent as a single pdf to—adrialeboeuf AT gmail DOT com.

DEADLINE: February 1st, 2021.—Applications will be reviewed until positions are filled.

*This part is absolutely key to your application: What sparked your interest in our group? What scientific questions are you motivated by that align with ours? What research skills would you bring?

All the best, Adria

Dr. Adria LeBoeuf Group Leader, Lab of Social Fluids Department of Biology University of Fribourg http://leboeuflab.com/ Adria LeBoeuf adrialeboeuf@gmail.com

Eric Grenier <sanjoaquin@tornicentro.la>

UGuam CoralPopGenomics

Post-Doctoral Researcher in Coral Population Genomics (JOB # RC-21-17)

The Island Evolution Lab (www.uog.edu/ml/labs/-combosch) at the University of Guam Marine Laboratory seeks to recruit a postdoctoral research associate (Postdoc). The position is initially funded for 2 years, with the possibility of further extension, and is scheduled to be filled as soon as possible (i.e. ideally by in February/March 2021). It is funded by the National Science Foundation's (NSF) Established Program to Stimulate Competitive Research (EPSCoR) project Guam Ecosystems Collaboratorium for Corals and Oceans (GECCO). The selected candidate will join a vibrant lab and have the opportunity to contribute to a variety of projects in the fields of population genetics and evolutionary genomics. The Island Evolution Lab is committed to promoting diversity, equity and inclusion. We believe that a more diverse and interesting workplace generates more diverse and interesting outcomes in terms of ideas, experiences, people and publications. Guam and UOG are small but very diverse places, where people from many different, distant backgrounds interact within the local Chamorro culture. We try to actively contribute to this rich and inspiring diversity.

The postdoc will be responsible for: - Leading studies within a large-scale population genomics research project, aimed at the distribution of genetic diversity within and among Micronesian Islands to quantify connectivity among reefs and identify local adaptations. - Applying new methods and analytical tools to investigate population genomic patterns among scleractinian corals across oceanic islands. - Writing publications and assisting with other projects in the laboratory, depending upon skills and research interests. - Mentoring graduate and undergraduate students. - Other duties assigned.

Minimum qualifications: - PhD or postdoctoral experience in genetics, genomics, marine biology or related field. - Experience in analyzing large genetic/genomic datasets. - Proficient in Bash, R and command-line tools and scripting. - Scientific field work experience, ideally marine, including diving experience.

Minimum knowledge, skills and abilities: - Organized. - Team science oriented and interested in mentoring. - Highly motivated and pro-active. - Excellent writing and good communication skills.

Preferred qualifications: - Experience with population genomic datasets and analysis. - Proficient in Python, GitHub etc. - Scientific dive certification (AAUS), ideally with experience working on tropical reefs. A scientific dive certification (AAUS) can also be obtained at the Marine Lab. - Basic knowledge of coral biology and taxonomy and/or experience working with corals. - Interest in contributing to website content, social media and other outreach efforts. - Experience working in an island setting.

Salary & Benefits: - Grade N, Step 1, $21.64/h. Temporary, Full-Time, 40 hours per week. - Social Security, Medical and Dental Insurance, 4 hours annual leave and 4 hours sick leave per pay period, holiday pay, up to 3% 403(b) match based upon employee contribution of 3%.

Application process: Deadline: Position Open Until Filled. The initial review of applications will occur on January 07, 2021 (Chamorro Standard Time/UTC+10). To apply, please 1) fill out the online application form at www.uog.edu/rcuog/employment- application and email the following documents to the Research Cooperation of the University of Guam (RCUOG) at rcuoghr@triton.uog.edu: 2) A cover letter, outlining your interests in the job, addressing the requirements listed above and summarizing your past academic accomplishments. 3) CV, including a list of three references with contact information. Letters will be requested directly, as needed. 4) University transcripts.

Questions and inquiries should be sent to David Combosch (comboschd@triton.uog.edu). Formal job announcement: https://www.uog.edu/rcuog/job-announcements.php Si yu'os ma'Ã¥se,

Dr. David Combosch (he/his), Associate Professor Island Evolution Lab, https://www.uog.edu/ml/labs/-combosch Marine Laboratory, University of Guam

The University of Guam is an equal opportunity provider and employer.

"comboschd@triton.uog.edu"
<comboschd@triton.uog.edu>

UKansas TE Regulation GenomicShock

An NSF-funded postdoctoral research position is available in the Department of Ecology and Evolutionary Biology at the University of Kansas in the laboratory of Justin Blumenstiel. The primary goal of the project is to determine how DNA damage and the DNA damage response shape the profile of heritable transposition in the male and female germline during hybrid dysgenesis. Using pooled long-read sequencing, we have recently found that DNA damage in the female germline caused by the excision of DNA transposons is associated with the activation of LTR class elements. Whether this is also the case in the male germline is not known. Thus, one goal of the project is to compare patterns of germline transposition between males and females where natural selection may act differently on the mutation rate. Using a combination of CRISPR and long-read pooled genome sequencing (either Oxford Nanopore or PacBio), the postdoctoral scientist will lead a project aimed at a genetic analysis of genome-wide transposition during hybrid dysgenesis. The researcher will also contribute to other projects in the lab that are focused on the evolution of piRNA silencing, epigenetic inheritance and how transposable elements and the meiotic machinery jointly shape recombination landscapes.

The Blumenstiel lab incorporates genomics, population genetics, molecular evolution and genetics to understand how genetic conflict shapes the mechanisms of genetic and epigenetic inheritance. The integrative nature of research in the laboratory makes this position well suited for a molecular biologist interested in incorporating evolutionary approaches or an evolutionary biologist seeking training in molecular genetics and genomics. More information about the lab can be found at http://www.blumenstiellab.org/ . The KU Department of Ecology and Evolutionary Biology and sister department of Molecular Biosciences offer a collegial and collaborative environment in Lawrence, Kansas. Lawrence, Kansas is a vibrant community and is frequently cited as a top college town. There are many great places to eat and extensive cultural venues including the Lawrence Arts Center and the Spencer Museum of Art. The cost of living is excellent and we are a 45-minute drive from Kansas City.

A Spring/Summer 2021 start date is anticipated, but this is flexible. The position may also be initially performed remotely, if needed, for a period of about six months. To apply for the position, please submit an application to the Department of Ecology Pool Postdoctoral Scientist general job announcement and contact Justin Blumenstiel to indicate that you have applied (jblumens@ku.edu). A complete application will include a cover letter, curriculum vitae and contact information for three references. Please do not hesitate to contact Justin Blumenstiel if you have any questions.

For a complete announcement and to apply online, go to: https://employment.ku.edu/staff/17818BR The University of Kansas prohibits discrimination < http://policy.ku.edu/IOA/nondiscrimination > on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university's programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, Room 1082, Dole Human Development Center, 1000 Sunnyside Avenue, Lawrence, KS 66045, 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).

Justin Blumenstiel Associate Professor Chair, Graduate Admissions Committee Department of Ecology and Evolutionary Biology University of Kansas Lawrence, KS 66045

jblumens@ku.edu

"No Drosophila female could conceivably lay two billion eggs in her lifetime". Lewontin and Hubby. 1966.

"Blumenstiel, Justin P" <jblumens@ku.edu>

UKoblenz PopulationGenetics

Job announcement

University of Koblenz-Landau, Institute for Integrated Natural Sciences Postdoctoral Research Assistant in Animal Ecology / Population Genetics

Application deadline: 15th January 2021

The Department of Zoology, Institute for Integrated Natural Sciences, at the University of Koblenz-Landau, Campus Koblenz, invites applications for a

Postdoctoral Research Assistant.

Starting date: April 1st 2021 Duration: 3 years (with the possibility of extension for another 3 years) Salary: German salary scale (TV-L 13, 100%) Teaching obligation (in German or English): 6 hours per week

We invite applications from highly motivated and productive candidates who are interested in and capable of developing his / her own independent research profile. We will consider a wide spectrum of candidates working in the fields of animal ecology, animal biodiversity research, and / or population genetics. Applicants working on timely questions in biodiversity research or population / landscape genetics with state-of-the-art approaches are particularly encouraged to apply. Areas of interest include, for example, organismal and community responses to environmental change, conservation biology, and dispersal / movement ecology.

The successful candidate will hold a Ph.D. in animal ecology / population genetics and will have a strong publication record and background in ecology. He / she will have broad experience in either (1) molecular genetic methods (e.g. ddRADseq, PCR, SNP calling, analyses of relatedness, isolation by distance, resistance, and environment, dbRDA) or (2) biodiversity research in a more narrow sense (in depth knowledge on at least one animal group, conservation biology, multivariate statistics, GLMM, model averaging, structural equation modelling, PCA, NMDS). Excellent English communication skills are essential.

Our department works mainly in the fields of evolutionary ecology and conservation biology. For further information please visit:

https://www.researchgate.net/profile/Klaus_Fischer . The University of Koblenz-Landau is an equal opportunity employer.

Applications should include (1) a cover letter with short statements of motivation and future research plans, (2) scientific CV with degree certificates, (3) list of publications, (4) list of externally acquired funds (if any), and (5) contact details of two academic referees. Applications should be submitted electronically as a single PDF file to bewerbung@uni-koblenz-landau.de before January 15th 2021. Please mention your name and the call number (92-2020) in your application and in the header of your email.

For any enquiries please contact Prof. Dr. Klaus Fischer via e-mail:

klausfischer@uni-koblenz.de

Prof. Dr. Klaus Fischer Institut für Integrierte Naturwissenschaften Abteilung Biologie Universität Koblenz-Landau Universitätsstraße 1 D-56070 Koblenz

klausfischer@uni-koblenz.de Phone: +49-261-287-2238

Klaus Fischer <klausfischer@uni-koblenz.de>

ULausanne Switzerland ExperimentalEvolutionMicrobiota

Postdoc in experimental evolution of gut microbiota

A postdoctoral position is available in Tadeusz Kawecki's research group at the Department of Ecology and Evolution, University of Lausanne, Switzerland (https://www.unil.ch/dee/kawecki-group). We are looking for a qualified and motivated researcher interested in using experimental evolution to study adaptation of ambient bacteria to life as Drosophila commensals and the consequences of this adaptation for the microbe and the host. The researcher will take the lead in establishing the microbiota evolution research project, with a considerable degree of autonomy, and at a later stage co-supervise a PhD student. The project will involve laboratory experiments in a controlled, highly simplified microbe-insect host system. The project is part of the new Swiss National Centre of Competence in Research (NCCR) "Microbiomes", a large interdisciplinary consortium using experimental and computational approaches to understand the dynamics of diverse microbiomes (https://nccr-microbiomes.ch/). This opens a lot of opportunities for interactions, collaborations, training and career development.

The position is at 100%, initially 1 year, renewable for 2 years; a further extension for 2 additional years may be possible depending on funding. Annual gross salary: about CHF 80,000, starting date in spring 2021 (negotiable).

We are seeking a candidate with a PhD degree, experience in experimental microbiology, interest in evolutionary biology of microbe-host interactions, and a drive for academic research. Experience with insect microbiota and basic bioinformatic skills would be an advantage. Good interpersonal skills and a considerable degree of independence are expected. No-preexisting knowledge of French is required (research-related discussions, seminars etc. and a part of teaching are in English), but learning basic French would make living in Lausanne easier.

For more information and the application process (which must occur via the University of Lausanne recruitment platform) see https://bit.ly/3gzYKAo (to apply, you may have to create an account first).

Contact: tadeusz.kawecki@unil.ch

Review of applications will begin on 27 December and will continue until a suitable candidate is found.

Tadeusz Kawecki <tadeusz.kawecki@unil.ch>

ULodz EvolutionaryAnthropology

POST-DOCTORAL FELLOW

The Department of Anthropology, University of Lodz, Poland invites applications for two 1-3 year post-doctoral fellowship positions in any area of evolutionary anthropology, with the possibility of the positions becoming permanent.

The Department of Anthropology has particular research strengths in clinical, dental and ontogenetic anthropology, and has an interest in developing expertise in human evolutionary genetics.

The selected candidate will be expected to develop their own area of research and to cultivate collaborations within the Department. Candidates will be expected to have excellent English verbal and written skills. To apply, please submit:(1) a two-page cover letter outlining your future research plans, (2) CV, and (3) contact information for two professional references, to Carl Smith (carl.smith@biol.uni.lodz.pl).

The sole criterion for selection will be scientific excellence.

The position is available immediately and will remain open until filled.

Carl Smith <carl.smith@biol.uni.lodz.pl>

ULodz Poland InsectEvolution

POST-DOCTORAL RESEARCHER

The Natural History Museum of the University of Lodz, Poland invites applications for a post-doctoral position in any area of evolutionary research relating to terrestrial insects.

The selected candidate will be expected to develop their own area of research and to cultivate collaborations within the Faculty of Biology and Environmental Protection. Candidates will be expected to have excellent English verbal and written skills.

To apply, please submit:(1) a two-page cover letter outlining your future research plans, (2) CV, and (3) contact information for two professional references, to Carl Smith (carl.smith@biol.uni.lodz.pl) as soon as possible.

The sole criterion for selection will be scientific excellence.

The position is available immediately and will remain open until filled.

Carl Smith <carl.smith@biol.uni.lodz.pl>

UOtago AntarcticMolEcol

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U_Otago_New_Zealand_Antarctic_MolecularEcology We are seeking a Postdoctoral Fellow to contribute to the Marsden-funded research project 'How vulnerable are Antarctica's coasts to colonisation'. In this role you will work on a project that will bring together interdisciplinary approaches in genomic, ecological, physiological, and oceanographic / sea ice modelling to build a comprehensive picture of the scale of biological incursions to Antarctica via macroalgal rafting.

This position represents an exciting opportunity to join one of the country's most research-intensive Universities and become part of a team helping to lead Antarctic research in New Zealand.

Your skills and experience The successful candidate will bring high-level computational skills in EITHER genomic (bioinformatic) analyses OR physical environmental modelling (oceanographic particle dispersal / modelling coastal polynya / habitat modelling with climate change).

In addition, the successful candidate will be expected to have: - A PhD in relevant field.

- Proven track record of high-quality research outputs such as peer- reviewed papers.
- Research experience in evolutionary biology, physical oceanography or habitat modelling.
- Good organisational skills and the ability to keep accurate records.
- Ability to work well as part of a team, as well as independently.
- Knowledge and respect for the Treaty of Waitangi and its relevance in a university setting.

Expertise in any of the following areas could be an advantage: - Molecular laboratory skills, especially Genotyping by Sequencing library preparation.

- Marine biology.
- Antarctic research.

Further details This is a fixed term (three years), full-time position available from March 2021 (mid-2021 at the latest) or a date to be mutually agreed with the successful candidate.

For more information, see https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=2002326 Applications will close on Sunday, 31 January 2021.

Ceridwen Fraser <ceridwen.fraser@otago.ac.nz>

UPadua EvolutionHumanMicrobiome

POST-DOCTORAL FELLOW

The Department of Comparative Biomedicine and Food

Sciences, University of Padua (Italy), invites application for 1 year post-doctoral fellowship position to work on the evolution of human microbiome.

The project focus on the analysis of ancient microbiome traces from of human dental calculus spanning from Paleolithic untill Bronze Age in Italy, through metagenomic and metaproteomic analysis. The selected candidate will be expected to analyse metaomics data and correlate them with archaeological, antropological and paleobotanical data. More details are available through: https://euraxess.ec.europa.eu/jobs/584299 To apply please check for this web-page: https://www.bca.unipd.it/bando-di-selezione-il-conferimento-di-n-1-assegno-lo-svolgimento-di-attivita%E2%80%99-di-ricerca-tipo-0 The criterion for selection will be scientific excellence. The position will expires the 18.12.2020 and it will starts in January 2021.

For information contact Andrea Quagliariello <andrea.quagliariello@unipd.it>

UppsalaU FungalGenetics

PostDoc Position at Uppsala University - Fungal Genomics

Systematic Biology, Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University, Sweden.

A two-year position on a Carl Tryggers post-doc stipend is available to research fungal accessory genomes with Dr. Aaron Vogan at Uppsala University.

Project description:

Species of the fungal plant pathogen *Fusarium* are responsible for major crop losses globally through direct disease and mycotoxin production. Management of *Fusarium* disease is difficult as pathogenicity is often conferred by non-conserved chromosomes referred to as accessory or lineage specific (LS) chromosomes. These chromosomes can be transferred horizontally between strains and their rapid evolution is important for the fungus to evade host resistance. We recently described a family of selfish genes known as *Spoks*. The *Spoks* are meiotic drivers, meaning they are capable of biasing their transmission from one generation to the next at frequencies above 50%, violating Mendel's law of equal segregation. In *Fusarium*, *Spok* homologs (*FuSpok*s) are present in high copy number on the LS chromosomes and one *FuSpok* has previously been indicated to have meiotic drive function. Together, these findings raise the hypothesis that the *FuSpok*s selfishly influence the spread of *Fusarium* LS chromosomes. The overall aim of this project is to characterize the *Fu**Spok* genes with the use of gene knock-ins in the model fungus *Podospora anserina*. This will provide key insights as to the role of the *Spok* genes on the LS chromosomes in *Fusarium*, and progress towards the long-term goal of using these genes to manage disease.

Requirements:

Applicants should possess a PhD degree in microbiology, molecular biology, fungal genomics, or a related field, and general molecular biology laboratory skills. Experience performing transformations on filamentous fungi are a plus. Candidates must have received their PhD from an institute other than the Institute of Organismal Biology at Uppsala University and cannot currently have employment at the Department of Organismal Biology. Proficiency in spoken and written English is required.

Application:

Please submit your CV, a letter describing your research interests and skills, and contact information for two references to Aaron Vogan (aaron.vogan@ebc.uu.se), Department of Organismal Biology, EBC, Norbyvägen 18D, SE 752 36 Uppsala, Sweden. Applications are due by February 12 2021.

Starting Date: As soon as possible.

Additional info:

The Evolutionary Biology Centre offers a superb interdisciplinary working environment located at the heart of Uppsala. Uppsala is located 40 minutes north of Stockholm by train, 20 minutes from Stockholm's international airport.

Aaron Vogan

Researcher Uppsala University Norbyvägen 18D Uppsala, Sweden 752 36

Aaron vogan <voganaa@gmail.com>

UppsalaU PopulationGenomics-SexSpecificAdaptation

A fully funded 2-year postdoc position is available within population genomics at the Department of Ecology and Genetics, Uppsala University, Sweden.

The aim of the project is to experimentally examine how sexually antagonistic and sex-limited selection affect the genetic architecture of a polygenic trait during the evolution of sexual dimorphism. The postdoc fellow will utilize replicated artificial selection lines in a seed beetle Callosobruchus maculatus to test for allele frequency changes in a time series associated with an increase or decrease in sexual size dimorphism.

The duties for the postdoc will include preparing DNA extractions for sequencing from available material, bioinformatic analysis of DNA and RNA-seq data. Analysis and writing of manuscripts based on the goals of the project.

For this position the candidate must hold a PhD degree (obtained within the last three years) in evolutionary biology, genetics/genomics or bioinformatics. Experience in analyses of next-generation sequencing data is necessary, as is a background in population genetics/genomics.

Please see here for further information about the project: https://www.uu.se/en/about-uu/join-us/details/?positionId=370632 The position is available in the group of Assist. Prof. Elina Immonen (https://immonenelina.wordpress.com)

N?r du har kontakt med oss p? Uppsala universitet med e-post s? inneb?r det att vi behandlar dina personuppgifter. F?r att l?sa mer om hur vi g?r det kan du l?sa h?r: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy
Elina Immonen <elina.immonen@ebc.uu.se>

UToronto Mississauga PlantEvolutionaryGenomics

Post-doctoral Position ’V Plant Evolutionary Genomics and Evolutionary Ecology

Prof. Marc Johnson’Âs EvoEco Lab (www.evoeco.org) is seeking applications for a Post-Doctoral Researcher to study Plant Evolutionary Genomics and Evolutionary Ecology in the Department of Biology at the University of Toronto Mississauga (UTM). The successful candidate will have the ability to work on one of two projects. Project 1 builds on the Global Urban Evolution project (GLUE, see www.globalurbanevolution.com) to examine how urbanization influences evolutionary processes (gene flow, genetic drift and adaptation) using a large dataset of whole genome sequences of ca. 1000 Trifolium repens plants, sequenced from 100s of populations in 50 cities worldwide. Project 2 examines how hybridization and a loss of sex contribute to rapid phenotypic and species diversification in the plant genus Oenothera in South America. Project 2 may also involve field work in South America and lab work. Both projects require expertise in bioinformatics (PERL, Python or equivalent programming languages) and statistical methods (in R and comparable programmes) related to whole genome sequence data, including analyses of population structure, demographic modeling and gene flow. The successful candidate will have substantial intellectual freedom to tailor research questions to their own interests. Previous work on plants or urban systems is not required.

In addition to being a part of the EvoEco Lab, the post-doctoral researcher will have the opportunity to be a member of the Department of Biology (http://www.utm.utoronto.ca/biology), the Department of Ecology and Evolutionary Biology (http://www.eeb.utoronto.ca), and the Centre for Urban Environments (www.urbanenvironment.ca).

The UTM campus has excellent facilities for research (wet and dry lab infrastructure, growth chambers, greenhouses), and 225 acres of fields, forests, many trails and a wild salmon/trout river for recreation. Toronto and Mississauga are world-class cities that are interconnected and culturally diverse. They boast an abundance of restaurants, excellent transit systems, a diversity of cultural activities (theatres, sports, bars, clubs), and an abundance of parks and water.

Starting salary: Commensurate with experience + benefits Start date: Flexible, but preferably before Sept. 1, 2021 Required qualifications: Ph.D. by the start date, and skills related bioinformatics of whole genome sequence data and associated analyses. Duties: Include but are not limited to collection of data, analyses, writing scientific papers for publication, mentoring students, attending lab meetings, seminars and journal clubs Duration: 1- 3 years (conditional on favourable annual performance review) Application Deadline: Review of applications will commence January 15, 2021, and continue until a successful applicant is selected. Please send applications to marc.johnson@utoronto.ca Applications should include: i) a cover letter (describe which project you are interested in), ii) CV, iii) PDFs of top three publications, and iv) contact information for three references.

This job is posted in accordance with the CUPE 3902 Unit 5 Collective Agreement. The normal hours of work are 40 hours per week for a full-time postdoctoral fellow recognizing that the needs of the employee'Âs research and training and the needs of the supervisor'Âs research program may require flexibility in the performance of the employee'Âs duties and hours of work. The position may require evening and/or weekend work.

The EvoEco Lab and the University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. For the lab'Âs equity, diversity and inclusion statement please see here: https://evoecolab.files.wordpress.com/-2020/09/edi-statement_final.pdf Marc Johnson <marc.johnson@utoronto.ca>

UUtah HumanEvolutionaryGenetics

Postdoctoral Scholar Position

The Leffler Lab in the Department of Human Genetics at the University of Utah is recruiting a Postdoctoral Scholar broadly interested in human genetics, malaria, and/or structural variation. The Postdoctoral Scholar will lead a new project in the lab in one of our areas of focus, depending on his/her interest and expertise. Potential projects include (1) dual transcriptomics of malaria infections and (2) characterizing mechanisms of structural variant formation. The Postdoctoral Scholar will also have flexibility to develop independent lines of research during their appointment. The position is available as early as February 2021 and the start date is negotiable. A remote start with a later move to Salt Lake City is possible.

The Leffler Lab uses evolutionary and genomics approaches to study adaptation to infectious disease, especially malaria. We value inclusivity and support professional development of trainees' both inside and outside academia. Please see our lab website for more information (lefflerlab.org). We are located in the Eccles institute for Human Genetics at the University of Utah (http://www.genetics.utah.edu/) among a strong community of evolutionary, computational, genomics, and infectious disease researchers, with links to the Biology Department (https://www.biology.utah.edu/-) and other medical school departments including through the Immunology, Inflammation, and Infectious Disease Initiative (https://uofuhealth.utah.edu/-immunology-inflammation-infectious-diseases/). We are located in Salt Lake City, which is a dynamic place to live with remarkable access to outdoor activities in the nearby mountains and deserts.

Candidate qualifications: A Ph.D. in a biological or quantitative discipline is required. Working knowledge of evolutionary and population genetics, experience with genomics and bioinformatics analyses, programming experience, and a strong quantitative background are preferred. Previous experience analyzing large transcriptomic or genomics data sets would be an advantage. The candidate should have a track record of scientific publications and conference presentations commensurate with career stage.

Compensation: Full salary and benefits available for up to three years. The initial appointment will be for one year, renewable upon satisfactory performance.

How to apply: Please send a CV and a cover letter describing research interests and experience, future career goals, reason for interest in this position, and contact information for two references to Ellen Leffler at leffler@genetics.utah.edu.

leffler@genetics.utah.edu

UVienna ComparativeGenomicsCephalopods

Two postdoc positions to study multiscale genome evolution and cephalopod gene regulation (University of Vienna, Austria)

We are seeking two postdoctoral researchers to join our team and work on the ERC funded project "METASCALE: Modes of genome evolution during major metazoan transitions". The task of both positions will be to study co-evolutionary trends within animal genomes and their association with the emergence of new gene regulation. Our group employs methods of comparative and regulatory genomics to study the regulatory impact of transitions in animal genome architecture. More recently, we have identified a major genome reorganization in the "smart" coleoid cephalopod molluscs (squid, octopus, cuttlefish) that, together with other genomic changes, potentially comprises a unique path or mode of genome evolution among animals. We are thus interested in quantifying these modes of genome evolution across all available animal genomes and to test whether their shifts are associated with the emergence of novel regulation (e.g., in cephalopods). One of our main model species is the Hawaiian bobtail squid species Euprymna scolopes. The tasks of the two candidates will be complimentary and highly collaborative with one position focusing on comparative genomics analyses across all metazoans and the other position on regulatory genomics in the squid. A solid background in in bioinformatics and comparative genomics is highly desired for the first position, whereas the second position will benefit from experience in molecular and regulatory genomics methods such as HiC, ATAC-seq, RNA-seq or single cell transcriptomics.

The postdocs will join an international group and network of researchers at the University of Vienna studying a diverse range of species and questions in molecular evolution, development, morphology and genomics. Our group is also part of the large evolVienna network of more than 50 evolutionary biology labs in Vienna, across several universities and research institutes. Our Faculty will be relocating to a new campus at the Vienna Biocenter in summer 2021 (https://-biologiezentrum.univie.ac.at/en/). Vienna is a vibrant historic European capital with a high QOL. Information about postdoctoral salaries in Austria can be found on this webpage: https://www.fwf.ac.at/en/research-funding/personnel-costs/ Earliest start date will be after July 2021. Initial term of employment is for two years with the possibility of extension. Remote working, at least initially, is a possibility.

Requirements: - PhD degree or equivalent by the start date - Publishing record in peer-reviewed journals or evidence thereof - At least 2 letters of support

Applications including a letter of motivation should be submitted via the Job Center to the University of Vienna (https://personalwesen.univie.ac.at/en/jobs-recruiting/job-center/, job reference number 11615).

Application deadline: January 15th 2021. Application link:

https://univis.univie.ac.at/ebewerbung/flow/-?ausschreibungsTidÂ377.28

Further information on the group and the Department: https://neurodevbio.univie.ac.at/simakov-research/ If you have any questions, please write to oleg.simakov@univie.ac.at

oleg.simakov@univie.ac.at

WashingtonStateU EvolutionaryGenomics

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 have 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 conduct 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 The Fred Hutchinson Cancer Research Center, the 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/).

A rolling review of applications will begin on December 18, 2021 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics experience and a strong computational/ bioinformatics background is required. Desired qualities also include experience in population genomics, infectious disease evolution, and/or cancer genomics. Start date is negotiable between January and June, 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 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.

Andrew Storfer, PhD Professor School of Biological Sciences Washington State University Pullman, WA 99164-4236 (509) 335-7922 astorfer@wsu.edu www.storfer-lab.org "Storfer, Andrew" <astorfer@wsu.edu>

YaleU Macroevolution

Postdoc Position - Global Macroecology and Macroevolution

A two-year postdoc position is available in the Jetz Lab and the Yale Center for Biodiversity and Global Change (Yale BGC Center). We are seeking someone with strong quantitative background who is interested in addressing macroecological and biogeographic questions using macroevolutionary tools. The postdoc is expected to leverage vertebrates as focal study system, but work on plant or invertebrate systems is also welcome. Qualifications for the position include a PhD in ecology, macroevolution, biogeography, or biological informatics. The preferred candidate will have experience in the ecological and macroevolutionary analysis of large datasets, a dedication toward conscientious work in a team, attention to detail, and strong communication and writing skills. We are looking for someone who can traverse ecological and evolutionary perspectives and who has experience in phylogenetics, spatial analysis, and/or biodiversity informatics. The postdoc will benefit from working closely with a growing group of Center-based biodiversity scientists, modelers, and informaticians, and a network of collaborators including those engaged in the VertLife project. Support for project-related travel and workshops is available. Target start date for the position is Spring through Fall 2021.

We strongly encourage applications from women and minorities. Diversity, equity, and inclusion are core values in our group, and we believe that a diverse team will enable a broader perspective and enhance creativity.

The Yale BGC Center connects biodiversity scientists from across campus and hosts a range of speaker and workshop events. It supports research and training around the use of new technologies and data flows for model-based inference and prediction of biodiversity distributions and changes at large spatial and taxonomic scales. Flagship Center projects include Map of Life and activities supporting the Half-Earth Map and the development of the GEO BON Species Population Essential Biodiversity Variables. Other initiatives associated with the Center include the integration of macroevolutionary and biogeographic inference (e.g., VertLife, ButterflyNet), NASA-supported remote sensing-informed layers and tools for biodiversity modelling (EarthEnv), the Max Planck-Yale Center on Biodiversity Movement and Global Change, and the Wildlife Insights initiative for camera trapping data.

Yale University offers postdoctoral researchers competitive salaries and a generous package of benefits. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. New Haven is renowned for its classic Ivy League setting, 75 miles northeast of New York City.

To apply please send, in one pdf, a short motivation (i.e. cover) letter, CV and names and contact information for three referees to megan.blake@yale.edu, subject "BGC Postdoc - Macroecology". Review of applications will begin on 20 December 2020 and continue until the position is filled.

"Jetz, Walter" <walter.jetz@yale.edu>

WorkshopsCourses

KITP SantaBarbara PolygenicAdaptation Jun13-Jul15

Towards an Integrative View of Adaptation: Bridging Population and Quantitative Genetics

Coordinators: Alison Etheridge, Kavita Jain, Christian Schlötterer, and Naomi Wray

Location: KITP Santa Barbara, California

Dates: Jun 13, 2022 - Jul 15, 2022

Application deadline: March, 1, 2021

https://www.kitp.ucsb.edu/activities/adapt22 The study of adaptive evolution in molecular population genetics and quantitative genetics have remained rather isolated disciplines despite the shared research theme. While quantitative genetics describes adaptation of quantitative traits as a collective effect due to small shifts in the allele frequencies of a large number of underlying genetic loci (polygenic adaptation), molecular population genetics has focused on adaptation due to a small number of favorable loci in which the allele frequencies sweep to fixation. The connection between these two areas became possible when molecular markers were introduced. Since then Quantitative Trait Locus (QTL) mapping and, more recently, Genome-Wide Association Studies (GWAS) developed into powerful approaches to link phenotypes of interest with their genetic basis. Furthermore, stochastic models of evolution that borrow techniques from statistical physics provided a link between the bottom-up and top- down approaches in understanding adaptive dynamics. As a result, it is now becoming increasingly clear that both “sweeps” and “small shifts” are rather the endpoints of a scale than exclusive alternatives.

This program will bring together theoreticians and empiricists to develop the basis for a unified framework of adaptive genetic architectures. The new framework will integrate molecular population genetics and quantitative genetics, addressing three main questions:

1. What are the different adaptive scenarios that need to be distinguished and what are their defining characteristics?

2. What are the key factors that determine these scenarios?

3. How can we develop powerful statistical tests to detect polygenic adaptation from empirical data?

KITP programs provide a fantastic opportunity for scientific exchange and interdisciplinary collaboration.

A typical day starts with 2 lectures and includes ample opportunity for discussion. In the afternoon we will have discussion groups and workshops on specific subtopics as well as bottom up activities of the participants. Long-term participants will be provided office space at KITP. The scientific activities will be accompanied by joint social events such as BBQ, wine tasting or beach volleyball. Social and scientific interactions are facilitated with many long-term participants staying at the Munger Physics Residence.

Because the program encourages scientists to stay as long as possible, KITP has several family friendly measures in place (https://www.kitp.ucsb.edu/visitors/-before-your-visit/family-fund).

We are aiming to gather a stimulating group of participating scientists covering the full spectrum from theoreticians to experimentalists. Female scientists and representatives of minority groups are particularly encouraged to apply.

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at Christian Schlötterer <christian.schloetterer@vetmeduni.ac.at>

Online AdaptationGenomics May17-21

Dear all,

the registrations are now open for the Physalia course on Adaptation Genomics, which will take place ONLINE from the 17th to the 21st of May: https://www.physalia-courses.org/courses-workshops/-courseadaptationgenomics/ Instructors: Dr. Anna Tigano (University of New Hampshire, USA) and Dr Claire Merot and Yann Dorant (University Laval, Canada).

This course provides an introduction to the study of the genomic basis of adaptation using population genomics approaches applied to the analysis of both sequence and structural genetic variation. The instructors will guide the participants from the handling of raw genomic data and data exploration (e.g., summary statistics and population structure) up to more advanced methods, including genotype-environment associations based on both sequence and structural variants. Through hands-on exercises, the course will teach basic bioinformatics skills and how to manipulate, visualize and interpret genomic data and patterns.

Learning Outcomes

1) Handling genomic data from raw reads to genetic variants

2) Calculating basic population genetic statistics

3) Visualizing genetic population structure

4) Searching for signatures of selection in the genome

5) Accounting for putative structural variants

6) Understanding the potential and the limitations of different methods to study the genomic basis of adaptation

Programme: https://www.physalia-courses.org/-courses-workshops/courseadaptationgenomics/-curriculumadaptationgenomics/ Our other online courses: https://www.physalia-courses.org/courses-workshops/ All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org 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 AdvancedProgramminginR Mar8-12

Dear all,

the 3rd edition of the Physalia course on "Advanced programming in R for biologists" will be held online from the 8th to the 12th of March.

Instructor: Dr. January Weiner 3rd (Staff scientist, Berlin Institute of Health, Germany).

This is a very practical course that aims at giving the students abilities in R programming that go beyond basic R usage. This includes both learning important frameworks as well as tips and tricks and coding style.

Participants will learn:

1) how to import, clean, reshape and visualize their data in R using tidyverse

2) create complex/customized graphics in R

3) how to code in R (good coding practices and common fails)

4) create their own R packages

5) build reproducible reports with RMarkdown

6) create their Github page to share your code & materials with others.

For more information, please see: (https://-www.physalia-courses.org/courses-workshops)(https://www.physalia-courses.org/courses-workshops/-course47/)

Our other online courses: (https://www.physalia-courses.org/courses-workshops/)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org 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 DNASkills Jan11-Mar11

PDNA-7001-WA Virtual DNA Skills Training Course:

The Virtual DNA Skills Training Course is designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation. This non-credit course is offered as an online virtual course.

The cost of the online virtual training course is $600.00 CDN.

The next scheduled time for the Virtual DNA Skills Training Course is: January 11 to March 11, 2021.

For more information please contact us at 807-343-8877 or email paleodna@lakeheadu.ca or visit our website at www.ancientdna.com and click on 'Training Courses'.

Thank you.

Karen.

Karen Maa Administrative Assistant Lakehead University Centre for Analytical Services (LUCAS) 955 Oliver Road Thunder Bay, ON P7B 5E1

Karen Maa <kmaa@lakeheadu.ca>

Online EvolutionaryBiogeography Jan4-8

Dear evoldir members,

A few spots are still available on the Transmitting Science LIVE ONLINE course 'Model-Based Statistical Inference in Evolutionary Biogeography'.

Instructor: Dr. Nick Matzke (University of Auckland, New Zealand)

Dates & Times: January 4th-8th, 2021 8:00-12:00 (GMT+1, Madrid time)

Preliminary programme:

Basics: - Intro to R and phylogenies - How to read and use phylogenies - A short history of historical biogeography methods and assumptions - Likelihood-based statistical model choice - Phylogenetic biogeography - New probabilistic models for historical biogeography in BioGeoBEARS. - Using BioGeoBEARS and interpreting results.

Advanced: - Biogeographical stochastic mapping. - Including geographical and environmental distance in models. - Integrating biogeography with traits trait-dependent dispersal - Running analyses over multiPhylo objects (posterior distribution) and interpreting results. - State-dependent Speciation/Extinction models (SSE) basics in R - State-dependent Speciation/Extinction models (SSE) for large biogeography problems in Julia - Integrating GIS & paleogeography data (e.g. GPlates)

Help session for student projects.

For more information and registration: https://-www.transmittingscience.com/courses/evolution/model-based-statistical-inference-evolutionary-biogeography-2 Contact: courses@transmittingscience.com <haris.saslis@transmittingscience.com>

All the best,

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com haris.saslis@gmail.com

Online Galaxy Dec9

Options for using Galaxy: everywhere and right now.

Wednesday, December 9th, 11am Eastern US time (see your time: https://bit.ly/2VABo3X)

https://galaxyproject.org/events/2020-12-webinar-where/ This Galaxy webinar will introduce the many options for using Galaxy right now and anywhere in the world. We'll cover * Publicly accessible Galaxy servers on the web (there are over 100 of them) * Research and commercial cloud platforms, from Australia (Nectar) to the US (Jetstream, AnVIL), and everywhere in between (CloudLaunch) * On your laptop, using pre-packaged containers and virtual machines.

The webinar will be at 11am Eastern US time (see your time). Enis Afgan, Anton Nekrutenko, and Mike Schatz will present.

Interested? Please sign up now: https://bit.ly/2020-12-

webinar-register About Galaxy

Galaxy (https://galaxyproject.org/) is a web-based data integration and analysis platform for the life sciences (and more). It is open source and freely available and installed at organizations around the world.

– https://galaxyproject.org/ –

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

Online GenomeAssembly Jan11-14

The University of Connecticut's Computational Biology Core within the Institute for Systems Genomics is offering a workshop on the design and execution of a genome assembly.

The workshop will cover basic concepts and walk through several strategies on a high performance computing cluster. The goal is to familiarize attendees with the steps necessary to sequence, assemble, and evaluate a reference genome. All code required to complete the full analysis will be provided in a public github repository, and session recordings will be available to all participants after the workshop.

The workshop will take place over 4 days for three hours each day.

Dates: January 11-14 (4 days) Time: 9.00am - 12.00pm Location: Online Cost: $300

Workshop schedule: Day 1: Introduction to Linux/HPC Day 2: Introduction to k-mer plots, high throughput sequencing, quality control of sequence data, contaminant detection Day 3: Genome assembly strategies and short-read assembly Day 4: Long-read and hybrid assembly, post-processing, assembly benchmarking

Registration:

To register, please follow this link: https://docs.google.com/forms/d/e/-1FAIpQLSe9F6MOUrri_xbtJZ3LrbV2sEgZS_vIlG-4Qr6H9E1Zef2Ltw/viewform Workshop FAQ:

Who should attend?

Anyone who wants to learn the fundamentals of genome assembly.

What are the prerequisites?

Prior bioinformatic experience is not required. We have dedicated the first day of the workshop to the basics of Linux and high performance computing.

What do I need?

You will need your own laptop to use, have a recent version of R, RStudio installed, and some other applications. We will send you details of software and installation instructions with your registration acknowledgement email.

Can I bring my own data?

We will provide experimental datasets for use during the workshop, as this helps to keep the workshop moving. There will be time, however, to discuss your own datasets and how you might work with them outside of the workshop.

How much does it cost?

The registration fee is $300.

How do I pay?

The fee is due at the time of registration. UConn affiliates can use KFS accounts. The only other means of payment we currently accept is credit card. Due to some complications we cannot accept international wire transfers at this time.

Where is the workshop?

It will be held on Blackboard-Collaborate platform, and will run from 9:00am to 12:00pm on the dates indicated.

How do I apply?

All registration is "first-come, first-served." There is no application process. Sign up as soon as possible to ensure your place in the workshop.

Questions?

If you have any questions, please don't hesitate to contact us at cbcsupport@uconn.edu

"Reid, Noah" <noah.reid@uconn.edu>

Online GenomicPrediction Feb8-12

Dear all,

we still have a few seats available on the Physalia course "Genome-wide prediction of complex traits in humans, plants and animals":(https://www.physalia-courses.org/courses-workshops/course49b/)

It will be held online from the 8th to the 12th of February.

This course will introduce students, researchers and professionals to the steps needed to acquire expertise in the genomic prediction area applied to animals, plants and humans. We will start by introducing general concepts of Quantitative Genetics and mixed model theory, progressively describing all steps and putting there seamlessly together in a general workflow.

LEARNING OUTCOMES

- Interpreting and calculating the genomic breeding value and genomic risk score - Understanding the different steps involved in a typical genomic prediction analysis and how to implement computer tools to carry them on. - Implement cross validation design to estimate the ability of genomic data to predict complex traits, and its application in human genetics and breeding programs.

Here you can find the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org 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 ProteomicsUsingRBioconductor Mar15-17

Course: Proteomics Using R/Bioconductor

ONLINE, 15th-17th March 2021

Instructor: Dr. Laurent Gatto (de Duve Institute, UCLouvain, Belgium)

Course website: (https://www.physalia-courses.org/courses-workshops/course58/)

This course will introduce participants to the analysis and exploration of mass spectrometry (MS) based proteomics data using R and Bioconductor. The course will cover all levels of MS data, from raw data to identification and quantitation data, up to the statistical interpretation of a typical shotgun MS experiment and will focus on hands-on tutorials. At the end of this course, the participants will be able to manipulate MS data in R and use existing packages for their exploratory and statistical proteomics data analysis.

Program

Monday

During the first day, we will focus on raw MS data, including how mass spectrometry works, how raw MS data looks like, MS data formats, and how to extract, manipulate and visualise raw data.

Tuesday

The second day will focus in identification data, how to combine them with raw data, quantitation of MS data, and introduce data structure of quantitative proteomics data

Wednesday

The last day will focus on quantitative proteomics, including data structures, data processing, visualisation statistical analysis to identify differentially expression proteins between two groups.

For the full list of our courses and Workshops, please see: (https://www.physalia-courses.org/courses-workshops/)

All the best,

Carlo

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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.