EvolDir

July 1, 2020

Month in Review

Foreword

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

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

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

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Conferences

Marseilles 24thEvolutionaryBiol Sep21-24 2021

Dear Colleagues

because of the situation due to the Covid 19 The 24th EBM is postponed to 2021 September 21 - 24. We want to organize this event in the best conditions and this is impossible for September 2020

best regards Pierre web site aeeb.fr

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

Online ConGen2020 PopGenomics Sep7-18

ConGen 2020 Online: Population Genomics, Conservation Genetics & Data Analysis Workshop

Theme: New this year is slightly more focus on genome sequencing, assembly, and re-sequencing of whole genomes to prepare participants and instructors for the future which will involve far more whole-genome data production and analyses.

Instructors: Craig Primmer, Maren Wellenreuther, Eric Anderson, Chris Funk, Brian Hand, Paul Hohenlohe, Marty Kardos, Brenna Forester, Joanna Kelley, Gordon Luikart, Mike Miller, Rena Schweizer, Amanda Stahlke, Robin Waples, and more TBA.

When: September 7-18, 2020

Where: Online due to Covid-19

For details on ConGen-2020: see http://www.umt.edu/-ces/conferences/congen/ Course Objective: The goal of ConGen is to provide training in conceptual and practical aspects of data analysis to understand the evolutionary and ecological genomics of natural and managed populations.

Emphasis will be on next-generation sequence (NGS) data analysis (RADs, DNA capture, and whole-genome sequence analyses, and gene expression) and interpretation of output from recent novel statistical approaches and software programs. The course promotes interactions among early-career researchers (students/participants) and leaders in population genomics to help develop the “next generation” of conservation and evolutionary geneticists. We will identify and discuss developments needed to improve data analysis approaches.

This course will cover analysis methods including the coalescent, Bayesian, and likelihood-based approaches.

Special lecture sessions and hands-on exercises will be conducted on population structure, detecting selection, and genetic monitoring (of Ne, FST, etc.), landscape genomics, inbreeding detection (RoH), GWAS to identify adaptive loci, genomic vulnerability assessment and more. It will also include lectures and hands-on activities on gene expression mechanisms underlying rapid adaptation to environmental change.

Who should apply: Advanced Undergrads, M.S. & Ph.D. students, post-docs, faculty, agency researchers, and population biologists that have taken at least one university-level course in population genetics and a course in population ecology. Priority will be given to persons with their own NGS data to analyze and/or experience analyzing NGS data.

Registration & Cost: The cost to participate in ConGen 2020 is $790 US if you pay before July 1st or $850 US if you pay after July 1st. This includes lectures (live and recorded) by 12 expert instructors, question & answer sessions (live and recorded), question and answer sessions, copies of all lecture PowerPoint slides, hands-on exercise work sheets with dummy datasets, along with ConGen-2020 Swag (T-shirt, mug). Course materials will remain available for many months after the end of the course to all students in a box repository including all recorded lectures. Scholarships are available based on availability and financial need.

Participants will also receive advice installing programs through multiple online help session and also through tutorials and email. Students with PC can receive help installing a Linux virtual machine on their PC in the weeks BEFORE the course. Linux line commands will be used for several analyses during the course. A brief tutorial on Linux will be given the first day for those interested in learning Linux line commands important for population genomics data analysis.

The course will be Online this year using Zoom along with a static forum/blog for writing questions to and getting answers from instructors (during and after each lecture). Participants outside North American time zones (e.g., Europe, Australasia) can watch recorded lectures (if they cannot participate live) after lectures are given and still participate in Q & A sessions and blogs within a few days after each lecture. Because all lectures and hands-on sessions are recorded (in Zoom), participants can watch (or re-watch) them the next day and still ask questions and get instructor feedback (via the blog or live).

This course is sponsored by the American Genetic Association, the Journal of Heredity, NASA (the National Aeronautics and Space Administration), NSF (the Dimensions in Biodiversity program), along with PacBio, DoveTail Genomics, support from publications such as eDNA, Evolutionary Applications, Conservation Genetics and more TBA. It includes 12 expert instructors and hands-on data analysis using your data (with instructors) and dummy data sets provided by instructors. It has led to publications describing main topics and outcomes of the course in past years, with the goal of facilitating data analysis for population geneticists worldwide.

Leif Howard

"Howard, Leif" <leif.howard@umconnect.umt.edu>

Online EvolutionEcol Jun29-Jul3

Dear EvolDir,

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

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

Now that many departmental seminar talks and conferences have been cancelled or postponed, we believe there is a great opportunity to replace that otherwise missing stimulus, and to keep our international research community connected. To that end, we are inviting some of the most exciting scientists in the community to share their research.

When: 5-6PM BST / 9-10AM PDT, up to 3 seminars/week Mon, Wed, Fri

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 'ÂEvolution and Ecology Seminars'Â here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-ev4fe0io-M7B˜D6p74blV_ZRcDtmAcg Our talks this coming week are:

—

Mon 29 June

Dr. Rob Salguero-GÂÂmez- (Dept. of Zoology, University of Oxford, UK)

"Using insights from life history theory to forecast global population responses to climate change"

—

Wed 1 July

Prof. Christopher Wheat (Dept. of Zoology, Stockholm University, Sweden)

"The evolutionary history of an ancient alternative life history strategy "

—

Fri 3 July

Prof. Owen Petchey (Dept. of Evolutionary Biology & Environmental Studies, University of Zurich, Switzerland)

"Why ecologists should avoid putting things into groups "

—

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 EvolutionEcology Jun15-19

Dear EvolDir,

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How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg Our talks this coming week are:

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Mon 15 June

Prof. Andrew Read (Dept. of Biology & Entomology, Penn State University, USA)

"How to use antibiotics without driving the evolution of antibiotic resistance"

—

Wed 17 June

Prof. Mariana Wolfner (Dept. of Molecular Biology & Genetics, Cornell University, USA)

"Effects of a Drosophila male's seminal proteins on his mate and on rival males"

—

Fri 19 June

Prof. Anne Charmantier (CEFE-CNRS, Montpellier, France)

"Great Tits in the city: from phenotypes to (epi)genomes"

—

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—- Dr. Elizabeth Duxbury

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

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

Online EvolutionEcology Jun22-26

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Mon 22 June

Dr. Lucy Aplin (Cognitive & Cultural Ecology, Max Planck Institute of Animal Behaviour, Germany)

"Animal culture in a changing world: from diffusion of innovation to cultural evolution in birds"

—

Wed 24 June

Prof. Craig Packer (Lion Research Center, University of Minnesota, USA)

Title TBC

—

Fri 26 June

Dr. Jessica Metcalf (Dept. of Ecology & Evolutionary Biology, Princeton University, USA)

Title TBC

—

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—-

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

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

Online EvolutionEcology Jun8-12

Dear EvolDir,

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

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

Now that many departmental seminar talks and conferences have been cancelled or postponed, we believe there is a great opportunity to replace that otherwise missing stimulus, and to keep our international research community connected. To that end, we are inviting some of the most exciting scientists in the community to share their research.

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

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—

Mon 8 June

Prof. Thorsten Reusch (GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany)

"Clonal reproduction is not an evolutionary dead end"

—

Wed 10 June

Dr. Christopher Wheat (Dept. of Zoology, Stockholm University, Sweden)

Title TBC

—

Fri 12 June

Prof. Bill Sutherland (Dept. of Zoology, University of Cambridge, UK)

Title TBC

—

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—-

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

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

Online GreatLakesEvolutionaryGenomics Jul20-24

The Great Lakes Annual Meeting in Evolutionary Genomics will be held online the week of July 20. GLAM-evogen is an annual symposium that brings together faculty and trainees in the Great Lakes region from a range of backgrounds who work at the interface of genomics and evolutionary biology. The meeting is trainee-oriented and a great venue to meet others, present your work, and hear about undergraduate, graduate, and postdoctoral research projects. Our keynote speaker will be Dr. Liz Mandeville from the University of Guelph.

We are planning for live talks via zoom on -Mon 20 July: 10 am - 12 pm EDT -Wed 22 July: 10 am - 12 pm EDT -Fri 24 July: 2 - 4 pm EDT, followed by a zoom happy hour

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

Registration for the meeting is now open here: https://forms.gle/XH3FT9qvhvv4JZdSA. The abstract submission deadline is July 3. Registration will remain open, but all participants must register to get zoom and slack information. More information is online at: http://blogs.rochester.edu/EEB/?page_id=30552 . You can order T-shirts here: https://www.customink.com/g/hkt0-00c8-anf5 If you would like to stay updated and receive information about the meeting, you can join the GLAM-evogen group here: https://groups.google.com/forum/#!forum/glamevogen – *Nancy Chen, Ph.D.* Assistant Professor Department of Biology University of Rochester popgenchenlab.github.io/

Pronouns: she/her/hers

Nancy Chen <nancy.chen@rochester.edu>

Online QuantitativeEvolution Jan11-Feb19

Dear colleagues,

We are organizing a program titled *“Quantitative evolution, phylogeny and ecology: from models to data and back”* at the *IHP in Paris* from *Jan 11 to Feb 19, 2021*, leaving ample time for discussions and collaborations. The program will in particular include two week-long conferences: Jan 11-15, 2021: “Ecology and co-evolution: from models to data and back” Feb 1-5, 2021: “Phylogeny and inference: from models to data and back”

If you are interested, *please pre-register* at: https://indico.math.cnrs.fr/event/5760/registrations/432/ preferably by *June 15*. Registrations are and will remain free of charge.

We are aware of the uncertainties regarding travel in the next months, and we would like to stress that these pre-registrations are non-binding, but necessary for organizational reasons.

Please encourage your colleagues and group members to pre-register too if they are interested.

More information is available here https://indico.math.cnrs.fr/category/389/, and a pdf flyer is available too: https://indico.math.cnrs.fr/category/389/attachments/2568/3234/Poster_T1A_2021_WEB.pdf Sincerely, The organizers (Anne-Florence Bitbol, Claude Loverdo, Mikhail Tikhonov, Aleksandra Walczak)

Anne-Florence Bitbol <anne-florence.bitbol@epfl.ch>

Online Recomb Jun25-26

RECOMB-GENETICS 2020 will be taking place virtually Jun25th-26th. Keynote speakers are Richard Durbin and Alicia Martin.Schedule and registration link here: http://recomb2020.org/recomb-genetics #RECOMB #RECOMB20“

”Belbin, Gillian“ <gillian.belbin@icahn.mssm.edu>

TulaneU MEEGID XV Nov2-5 2021

Dear Colleagues,

The MEEGID XV congress will be held at Tulane University, New Orleans, 2-5 November 2021 (not 2020).

https://www.elsevier.com/events/conferences/meegid Please circulate.

Hoping to see you in New Orleans,

Best regards,

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.com/locate/meegid Maladies Infectieuses et Vecteurs Ecologie, Génétique, Evolution et Contrôle MIVEGEC (IRD 224-CNRS 5290-UM1-UM2) IRD Center BP 64501 34394 Montpellier Cedex 5 France E-mail : michel.tibayrenc@ird.fr Website : https://www.micheltibayrenc.com/

See announcement of the MEEGID XV congress at: https://www.elsevier.com/events/conferences/meegid michel.tibayrenc@ird.fr

GradStudentPositions

Denmark 2 InsectEvolBiol

Two PhD positions are open in my research group. Below is a summary of the projects.

Two PhD positions are available at Aalborg and Aarhus University in Denmark within production of high quality protein for food and feed based on insects. The project involve topics such as screening insect species and diet types to detect species with high potential for production of protein, develop a sustainable breeding program for this species, select for important production traits and assess regions of the genome explaining variation in traits of interest.

We seek candidates with a strong interest within some of the topics entomology, physiology, evolutionary biology, and quantitative genetics and genomics.

You may obtain further information from the PI on the project Professor Torsten Nygaard Kristensen by e-mail: tnk@bio.aau.dk or phone +45 61463375.

The positions are announced at the following homepages:

https://phd.tech.au.dk/for-applicants/apply-here/-august-2020/optimization-of-insect-production-for-animal-feed-through-breeding/ https://-www.stillinger.aau.dk/vis-stilling/?vacancy=1104682

Kind regards Torsten

Torsten Nygaard Kristensen Professor|Vice Head of Department | Department of Chemistry & Bioscience

Tlf.: (+45) 61463375 | Email: tnk@bio.aau.dk| Web: www.bio.aau.dk Aalborg University | Fredrik Bajers Vej 7H | 9220 Aalborg East

Torsten Nyg??rd Kristensen <tnk@bio.aau.dk>

FUBerlin NeuralCircuitEvolution

PhD student position on *The evolution of neural circuits for insect navigation * in Berlin, Germany

A PhD student (65% E13) position is available in the laboratory of Prof. Mathias Wernet at the division of Neurobiology of the Free University of Berlin, Germany, to contribute to our ongoing research on the development and function of neural circuits underlying insect navigation behaviors. This research program will be conducted in collaboration with Katja Nowick (Professor of Human Biology) within the frame of the DFG-funded collaborative research unit SPP 2205 (Schwerpunktprogramm “Evolutionary Optimization of Neural Processing”). The position is available immediately but should ideally be filled by autumn 2020 the latest. Deadline for application is July 20th, 2020.

Using a combination of molecular genetic tools, Drosophila transgenesis, immuno histochemistry, and transcriptomics we study evolutionary conservation of those neural circuits underlying insect navigation behaviors (see Sancer et al, Current Biology 2019; Sancer et al., Journal of Comparative Physiology A, 2020, or the Wernet Lab website (http://www.flygen.org/wernet . The Free University Berlin is located in the center of the German capital, an international and lively city, and offers an excellent scientific environment for the conducted research. In addition to the SPP 2205 consortium, the project will be performed in close cooperation with other research groups at the Free University of Berlin (AG Hiesinger, AG Sigrist, AG Menzel, etc).

Candidates should hold a Master's degree (M.Sc.), have a strong interest in molecular and cellular aspects of developmental biology, as well as evolution ('Evo-Devo'), and Neurobiology. Previous experience with the Drosophila is preferred, but not essential. Proficiency in English is absolutely required.

To apply (deadline: July 20th, 2020), please e-mail your CV and names of two referees to: Mathias F. Wernet Mathias.wernet@fu-berlin.de

Freie Universität Berlin Fachbereich Biologie, Chemie & Pharmazie Institut für Biologie - Neurobiologie Königin-Luise Strasse 1-3, 14195 Berlin.

Katja Nowick <katja.nowick@fu-berlin.de>

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iDiv Leipzig PlantFrugivoreInteractions

DOCTORAL RESEARCHER (M/F/D)ON FLEXPOOL PROJECT 3 "MACROECOLOGY AND MACROEVOLUTION OF PLANT - FRUGIVORE TRAIT MATCHING IN THE TROPICS"

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

65 % of a full-time position

Salary: Entgeltgruppe 13 TV-L

Leipzig University seeks to fill the following position at the German Centre for Integrative Biodiversity Research (iDiv), Flexpool, in Leipzig (Germany) at the earliest opportunity.

Background

iDiv, the German Centre for Integrative Biodiversity Research Halle-Jena-Leipzig, invites applications for five doctoral researcher positions in its 4th Flexpool call beginning in October 2020 (see overview in published Flexpool general announcement).

This PhD project integrates phylogenetic, distribution and functional trait data for plant (Arecaceae, Annonaceae and Fabaceae) and frugivore (birds, mammals) clades to assess how their mutualistic, frugivorous interactions have affected macroevolutionary (e.g., trait origins, diversification dynamics) and macroecological (e.g., spatial (mis-)matching of plant-frugivore traits) patterns. This project will identify places and plant/frugivore lineages prone to ongoing (co-)extinctions of their interaction partners. This project is supervised by Renske Onstein, Ingolf Kühn, Isabell Hensen and Irene Bender. Read more here:https://onsteinison.wordpress.com/ Tasks

Developing specific research questions and hypotheses within the scope of the project

Assembling/cleaning plant and animal frugivory-related traits, phylogenetic and distribution data from online databases, literature, monographs and herbarium visits (already partially complete)

Applying macroecological and macroevolutionary methods to test the specific hypotheses

Writing and publishing scientific papers in peer-reviewed journals

Presenting results at national and international conferences

Requirements

MSc or equivalent degree in a project-related field (e.g., biosystematics, (macro-)ecology, (macro-)evolution, environmental sciences)

Expertise and experience in phylogenetics or working with phylogenetic data

Interest and ability in handling spatial data and functional traits

Strong statistical skills (in R)

Excellent English communication skills (spoken and written)

Team-oriented and strong organisational skills

Please send your application, quoting reference number 113/2020, 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)

Dr Christa Genz

Deutscher Platz 5 e

04103 Leipzig

The deadline for submissions is 10 July 2020. Selected candidates will be invited to the online joint recruitment symposium on 31 August until 1 September 2020.

All applications should include:

Cover letter describing the applicant's 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's certificate or equivalent

Queries concerning the application process should be directed to Ms Christa Genz (christa.genz@idiv.de); for project-related questions, please contact Dr Renske Onstein (renske.onstein@idiv.de). Severely disabled persons are encouraged to apply and will be given preference in the case of equal suitability. Please note that applying via email is not entirely secure under data protection law. The sender assumes full responsibility.

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.

Renske Onstein <onsteinre@gmail.com>

ImperialC London EcolEvolConservation

Ecology, Evolution and Conservation Masters course at Imperial College London, UK

We would like to advertise the EEC Masters program at Imperial College. The MSc and MRes courses provide a broad education and training in the disciplines of ecology, evolution and conservation. We want to highlight that the academic year 2020/21 will begin on schedule (start October) and teaching will be through multi-mode delivery. We ask that applications be submitted by 1st August. Students on this course will be taught by internationally recognised researchers on some of the most recent advances in the EEC disciplines, as well as being integrated into their groups as part the student's research project(s). The course has the flexibility of combining on-campus learning and assessment, including laboratory/field work, with the benefits of remote learning and assessment.

Based at the leafy campus of Silwood Park, we have a plethora of research projects to offer on a large variety of organisms and biological systems that can be undertaken remotely and onsite. We also welcome project ideas from students that we can help to develop. All research projects will benefit from the large pool of expertise and multidisciplinary skills we have at Silwood and across the College. Students can take advantage of the connections and collaborations we have with external academic institutes and organisations, and all will come away with excellent quantitative skills.

The course has an excellent track record of students continuing on to PhD, as well as non-academic research posts in prestigious organisations and respected companies. Many of our students are successful in getting their work published in international peer review journals. Overall, our EEC graduates are highly competitive candidates for future career opportunities.

For more information on the course please visit: https://www.imperial.ac.uk/life-sciences/postgraduate/masters-courses/masters-in-ecology-evolution–conservation-msc-and-mres/ Guidelines on eligibility and applications visit: https://www.imperial.ac.uk/study/pg/life-sciences/ecology-evolution-conservation-research/ To contact the Directors with questions about the course please email Dr Julia Schroeder (MSc; julia.schroeder@imperial.ac.uk) or Dr Richard Gill (MRes; r.gill@imperial.ac.uk).

Any specific questions on applications please email Dr David Orme (d.orme@imperial.ac.uk)

For info. on other Masters courses available at Silwood park, Imperial College London, visit:

https://www.imperial.ac.uk/silwood-park/prospective-students/msc-and-mres-courses/ Coronavirus (COVID-19) updates and guidance regarding education visit:

https://www.imperial.ac.uk/about/covid-19/students/-learning-experience/ Hope you are all safe and well,

Drs Julia Schroeder and Rich Gill EEC Course Directors Silwood Park Imperial College London UK

"Gill, Richard J" <r.gill@imperial.ac.uk>

Isreal EvolutionCommunication

The evolutionary basis of honest communication

We are looking for an enthusiastic PhD student (that already has an MSc degree) for a multidisciplinary project on the evolution of honest communication in rock hyrax. The project involves capturing, marking, sampling, observing, recording, and carrying out acoustic manipulation experiments in the Ein Gedi Nature Reserve, near the Dead Sea, Israel. The ideal applicant has a strong background in behavioural ecology and vocal communication, field experience handling wildlife, and an ability to work both independently, and as part of a team. Financial support includes a scholarship from Bar Ilan University, tuition, and TAship. For more information, please contact Dr. Lee Koren (Lee.Koren@biu.ac.il). Please include a CV and a cover letter with field experience and interests. Start date: October 2020.

Lee Koren, PhD The Mina and EverardGoodman Faculty of LifeSciences Bar-Ilan University Ramat Gan, 5290002 Israel

Institute of Nanotechnologyand Advanced Materials(Building 206) Office B-940; Lab B-935 (9thfloor) Telephones: office +972-3-7384371 lab +972-3-7384372 Skype: leezik Lee.Koren@biu.ac.il https://leekoren.wixsite.com/korenlab http://dsi.biu.ac.il/team/prof-lee-koren/ Lee Koren Lab (Facebookpage) @LeeKoren2 (Twitter)

Lee Koren <Lee.Koren@biu.ac.il>

JagiellonianU EvolutionaryPhysiology

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

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

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

Conditions of employment: A warranted scholarship for 48 months of 5000 PLN / month, equivalent to mean gross income in Poland. Additional scholarships can be obtained within the Jagiellonian University PhD programs. Formal requirements

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

§admission in one of PhD programs at JU: the International PhD Biology (preferably) or regular Biologia, effective on 1.10.2020 (https://science.phd.uj.edu.pl/).

Merit requirements

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

§Previous experience in molecular or biochemical laboratory as well as working with terrestrial vertebrates (preferably rodents) are considered advantageous. Preliminary enquiries: email to the principal investigator - PaweÂ³ Koteja (pawel.koteja@uj.edu.pl) The formal application should be sent by email (pawel.koteja@uj.edu.pl) by 31.07.2020, as a single pdf file including: a) CV (academic achievements included, 2 page maximum) b) Cover letter in English, which must a) explain the applicant's interest in the topic, b) provide the names and email addresses of two people with first-hand knowledge of the applicants skills and past research experience, c) contain the following statement: "I hereby give consent for my personal data included in my offer to be processed for the purposes of recruitment, in accordance with the Personal Data Protection Act dated August, 29,1997 (uniform text: Journal of Laws of the Republic of Poland 2014 item 1182 with further amendments)".

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

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

The Evolutionary Physiology Research Team http://www.eko.uj.edu.pl/en_GB/zespol-fizjologii-ewolucyjnej/badania Institute of Environmental

Sciences Jagiellonian University 7 Gronostajowa Street, 30-387 Kraków, Poland e-mail: pawel.koteja@uj.edu.pl office phone: +48 12664 5209 skype: pkoteja ORCID: 0000-0003-0077-4957 ResearcherID: O-4039-2015 Scopus Author ID: 6603751464

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

JagiellonianU Poland InsectMicrobiomes

Ph.D. Student position: The diversity and evolution of hemipteran symbioses at Jagiellonian University in Kraków, Poland

The Symbiosis Evolution Research Group (www.symbio.eko.uj.edu.pl) at the Institute of Environmental Sciences of Jagiellonian University (www.eko.uj.edu.pl) is seeking a motivated Ph.D. Student to join the project focused on the evolutionary dynamics of heritable nutritional symbionts of hemipteran insects.

We aim to systematically describe the evolution of microbial symbioses of hemipteran insects from the suborder Auchenorrhyncha. For about 300 million years, these insects, including cicadas, spittlebugs, leafhoppers, treehoppers, and planthoppers, have specialized on nutrient-poor diet of plant sap thanks to nutritional contributions of specialized microbial symbionts that live in their tissues. These symbionts have been strictly heritable, transmitting from mothers to offspring for a long time, often for hundreds of millions of years, and losing up to ~98% of their genome during that time. But in many host clades, some of them were replaced or complemented by other microorganisms. We are describing the incidence and nature of these symbiont replacements, the origins of the replacing microbes, their genomic evolutionary patterns, their current biological roles, and the effects of the replacements on the ecology and evolution of the insects.

The Ph.D. Student will focus on bioinformatic reconstruction of the symbiont co-diversification and replacement patterns, and on phylogenomic analyses of the host and symbiont relationships. Depending on skills and interests, they will have an opportunity to participate in international fieldwork, work with collected insects, conduct laboratory experiments, conduct molecular work (automated DNA extraction, next-generation sequencing library preparation), comparative genomics, and advanced microscopy. The system provides great potential for a dedicated student to explore their own ideas and evolutionary questions related to insect symbioses, and acquire cutting-edge research skills. The Student will be encouraged to work closely with project collaborators, including Gordon Bennett (University of California - Merced), Insect Biome Atlas consortium members in Sweden and Madagascar, and Anna Michalik (Jagiellonian University).

The Student will join a dynamic, collaborative, multilingual group established recently at one of the top research institutes in the fields of Ecology and Evolution in Central Europe, in a medieval city known as the cultural capital of Poland, with good access to outdoor recreation opportunities and well-connected to the rest of Europe. The student will be supported by a generous 48-month tax-free stipend from the Ph.D. Program in Biology at Jagiellonian University and/or the Polish National Science Center grant, ensuring a good standard of living in Kraków. Ambitious Ph.D. Students will be encouraged and supported in applications for additional stipends and research grants. The official start date of the Ph.D. Program is October 1st, 2020, but there may be flexibility.

The successful candidate will have an M.Sc. degree in a relevant field by September 2020; a demonstrated interest in Evolution, Entomology, Microbiology, and/or Genomics; experience with, or a keen interest in learning, Bioinformatics, and Computational Biology; and strong English language, communication, and organizational skills. Previous experience with insect diversity, ecology, evolution and symbioses, molecular biology, microbiome surveys, phylogenomics and/or comparative genomics, and willingness to travel are advantageous.

The applicants should send a cover letter, a CV, and the details of two references to the principal investigator, Dr. Piotr Lukasik (p.lukasik@uj.edu.pl). The review of applications starts on 1st July 2020. The selected candidates will be invited to apply for a place in the Ph.D. Program in Biology at Jagiellonian University (https://wb.uj.edu.pl/studia/phd-biology). Also, one candidate will be selected as the doctoral stipend recipient. More details are provided in the extended version of the advert at the group website (symbio.eko.uj.edu.pl)

For further information and informal inquiries, please contact Dr. Piotr Lukasik.

Piotr ukasik Assistant Professor - Symbiosis Evolution Research Group Institute of Environmental Sciences Jagiellonian University ul. Gronostajowa 7 30-387 Kraków Poland

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

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

MaxPlanck Animbehav EvolCognitionBehav

3-year PhD position on the effect of seasonal reversible brain size changes on cognitive abilities of common shrews in a collaborative Human Frontiers-funded project on the causes and consequences of Dehnels Phenomenon.

In our long-term project on the evolution of reversible individual size changes in small high-metabolic mammals we are filling a position for a 3-year PhD starting as soon as possible. The common shrew is unique in that juveniles reach a first maximum size, then shrink towards winter, including a size reduction of up to 25 % of the brain, followed by a regrowth in the following spring along with sexual maturation. This is thought to be an energy saving strategy, resulting in lower food requirements in the winter (as these tiny shrews don't hibernate and constantly need to eat high quality food), which we have confirmed with a first metabolic study at ambient conditions. We have followed the size change for the first time in the individual, have described how brain regions change as well as shown that the brain size reduction results in decreased spatial navigation skills. We are starting to keep shrews in large outdoor enclosures and you would use a combined approach of repeated state-of-the-art MRI imaging and behavioral assays of the same individuals as they go through the cycle. The MRIs will be with Dominik von Elverfeldt in nearby Freiburg, where you will spend part of your time (https://www.uniklinik-freiburg.de/mr-en/-members/current/elverfeldt.html).

This is a HSFP-funded collaborative project with Liliana Davalos from Stony Brook University (looking at the molecular basis of this phenomenon) and John Nieland from Aalborg University (looking at the lipid metabolism) and their students.

The Max Planck Institute of Animal Behavior at its sites in Konstanz and Radolfzell offers an international, interdisciplinary and collaborative environment that opens up unique research opportunities. The goal of our basic research is to develop a quantitative and predictive understanding of the decisions and movements of animals in their natural environment.

What we are looking for:

If you are fascinated by evolution and questions such as how seasonal change affects animals, how the brain is shaped by evolutionary pressure, or how brain size is linked to behavior and cognitive abilities, this may be the right position for you. This project has already started and as the cycle of size change starts in June, we are interested to fill the position asap. You will be encouraged to provide input with regards to where you want to take the project within the given framework. Field work, although not very strenuous, is necessary, including setting and checking traps year-round at all hours. Some behavioural observations may also run for several hours and may have to be carried out during evenings and weekends. Ideally you are a biologist with also a background in or inclination for physics or bioimaging as the MRI (which we will be the first to do with shrews) will be a large and important part of the project. Good English skills are also a requirement. You must have a drivers' license and A FELASA certificate for handling of laboratory animals or equivalent would be great. Experience with handling small animals is expected. Even though for your project no animals need to be sacrificed, we expect you to help when shrews are sampled for the associated genomics project, i.e. you need to be willing to be present (but not euthanize yourself) and help with the sampling. A master degree is required.

What you will find:

The Dechmann Lab works on several projects with small high-metabolic mammals, all focusing on how animals have evolved to deal with changing resource landscapes. Our group has been working on these shrews for years, working out many (but never all) of the potential kinks of working with the sensitive shrews. As an institute we offer a responsible and varied work place in a growing interdisciplinary and international research environment. The payment is made in accordance with the collective agreement for the public service (TVöD-Bund). Our graduate school IMPRS for Organismal Biology provides added background where you can profit from a large spectrum of courses and support.

The Max Planck Society endeavors to employ more severely disabled people. Applications of severely disabled persons are expressly welcome. The Max Planck Society strives for gender and diversity equality. We welcome applications from all backgrounds.

Your application

Interested? We are greatly looking forward to receiving your CV, a motivation letter and a research statement by June 30 under this link: https://s-lotus.gwdg.de/-mpg/maor/perso/ornr_w008.nsf/application Have more questions? contact me: ddechmann@ab.mpg.de

MIZ Poland BeetlePhylogenomics

Graduate position: MIZ_Poland.BeetlePhylogenomics

Call for a PhD position

The research group led by Dr Dagmara Ây‘a at the Museum and Institute of Zoology, Polish Academy of Sciences (MIZ, PAS) is looking for candidates for a PhD position. The PhD project is part of the larger project entitled: “The Impact of the Paleocene-Eocene Thermal Maximum on diversification dynamics in Paederinae rove beetles” funded by the Polish National Science Centre. The main goal of this larger project is to investigate the evolutionary response of Paederinae predatory beetles to the most rapid and significant climatic warming event in Cenozoic. To do so, a set of innovative methods, such as machine learning for species identification, Next Generation Sequencing, and Bayesian statistical phylogenetics will be combined with modern approaches in insect systematics.

The PhD project is entitled: “Phylogenetic relationships and evolution of Paederinae rove beetles (Staphylinidae) based on genomic and morphological data” and will be primarily focused on the phylogeny of Paederinae with some flexibility in joining other parts of the larger project, depending on the student’s interests, abilities, and performance. The main aim of the PhD project will be to build the first large-scale phylogeny of Paederinae rove beetles based on Ultraconserved Elements (UCEs) and morphological data of extinct and extant species. This will be the first genus-level phylogeny using genomic data in the whole family Staphylinidae and will allow introducing the group to macroevolutionary research.

The project will also give the opportunity to attend several field trips (e.g. to South America) and international conferences (e.g. Evolution Meeting) as well as to visit museum collections.

Scope of work

- performing laboratory work, i.e. DNA extractions, library preparation, enrichment with UCE baits, sequencing
- processing and preparing raw sequences for the phylogenomic analysis
- participating in morphological data matrix preparation
- participating in data analysis and interpretation of the results
- writing publications with other members of the team
- presentation and dissemination of the obtained results in the form of conference talks and scientific papers
- participation in lectures and other activities required by the PhD School

Requirements

- MSc degree in biological sciences or a related area, awarded or to be awarded before October 2020
- experience with working on rove beetles or interest in learning the group to the extent that would allow interpretation of the results
- experience in following molecular lab protocols or willingness and ability to learn this in a reasonable time
- theoretical knowledge on phylogenetics and evolutionary biology
- experience in bioinformatics and/or phylogenetics is an advantage
- fluency in English (at least B2 level)
- enthusiasm for science
- communication and organizational skills
- creativity, high motivation and ability to work alone and in a team

Conditions of employment and study:

The PhD student will be based in the Museum and Institute of Zoology in Warsaw. The fellowship starts on 1.10.2020 (if the epidemic situation allows) and is expected to be completed with the thesis submission within 3 years.

A tax-free stipend is available for the PhD student in the amount of 5000 PLN (˜ 1100 EUR) per month. This is sufficient to cover the living expenses of a single person and assures a good standard of living in Poland.

The successful candidate will be required to enroll in the BioPlanet Doctoral School of the Polish Academy of Sciences https://szkoladoktorska-bioplanet.pl/en/home/. The School does not charge tuition fees and provides classes for PhD students. All classes are in English.

Research environment

The research at MIZ is focused on a broad range of themes in animal biology, including systematics, biogeography, evolutionary biology, ecology, and population genetics. Dagmara Ây‘a’s research group will be part of the Department of Systematics, Zoogeography and Ecology of Invertebrates led by Prof. K. Wioletta Tomaszewska focused on insect systematics, taxonomy, evolution, and phylogeny. MIZ laboratories contain modern equipment for genomic analyses, including the Illumina MiSeq System, as well as tools for studying morphology, like SEM and micro-CT. The Museum's zoological collection is among the largest and most valuable in Europe. The institute and PhD School offers an international working atmosphere with a multicultural PhD student community.

Application process

The deadline for submitting the application is 31.07.2020 11:59 pm GMT+2.

The application must be in English. Please submit the documents as one PDF file named with your surname to zyladagmara@gmail.com with the email subject "Application for a PhD position". Informal inquires should also be sent to zyladagmara@gmail.com

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MIZ Poland DolphinEvolutionaryEcology

Dear EvolDir subscribers,

A fully-funded PhD position is available in a project integrating functional genomics and 3D skull shape modelling of bottlenose dolphins globally. The project is led by Dr Andre E. Moura at the Museum and Institute of Zoology of the Polish Academy of Sciences, whose research group is focused on cetacean ecology and evolution. The research group is based at the Research Station of the Museum and Institute of Zoology (MIZ), Polish Academy of Sciences in GdaÃ"sk Gorki Wschodnie.

The successful candidate will be enrolled as a PhD student in the Bioplanet Doctoral School of the Polish Academy of Sciences, with starting date of October 1st 2020 (application to the Doctoral School is required, and attendance of the required oral entry exam). A tax-free stipend is available for the 4 years of the PhD and is not extendible. The stipend is sufficient to cover life expenses of a single person and ensures a good standard of life in Poland. The School does not charge tuition fees, and includes mandatory and optional classes for PhD students, which are run in English. Travelling from GdaÃ"sk to Warsaw will be required to attend the classes.

The project involves collaboration with international institutions, including the Smithsonian Museum (Washington, USA) and the National Museum for Nature and Science (Tokyo, Japan), and will likely require travelling to museums worldwide for data collection (funding is provided). This includes a 3 month stay in Japan for data collection and learning of 3D modelling techniques (will require funding application to relevant scheme). We are mindful that travelling might be disturbed under the current Covid19 situation, and any decisions regarding travelling for this project will take the situation into account as it develops.

How to Apply:

A list of the required skills can be found at the end of this email. To apply an email message with the subject "Application for PhD position in dolphin evolutionary ecology" should be sent to avmoura@miiz.waw.pl no later than 03/07/2020, and including the following documents:

1. Copy of the master's or bachelor's certificate if the master's degree is still ongoing. 2. Curriculum vitae including the publication list, with the following statement provided at the end and signed:

"I give my consent to the processing of personal data provided in my application documents by the Museum and Institute of Zoology PAS for the purpose of the recruitment process, pursuant to the Personal Data Protection Act of 10 May 2018 (Journal of Laws 2018, item 1000) and in agreement with Regulation (EU) 2016/679 of the European Parliament and of the Council of 27 April 2016 on the protection of natural persons with regard to the processing of personal data and on the free movement of such data, and repealing Directive 95/46/EC (General Data Protection Regulation; L 119 from 04.05.2016)".

Applications that do not include this statement won't be considered.

3. Motivation letter (maximum one page) 4. If available, a copy of one research paper to be evaluated in the recruitment process. If this is not available, a copy of undergraduate or Master thesis is acceptable. 5. Contact details of two persons who can be contacted for references.

The interviews of shortlisted candidates will take place in early July, and will be held by teleconference (Skype, Zoom, etc.). Interviews in person at the Research Station in GdaÃ"sk Gorki Wschodnie are possible, but only if it is logistically feasible and safe to do so. Informal inquiries can also be addressed to Andre Moura.

Requirements

Candidates can have a background in biology, zoology, bioinformatics, or related fields. The candidate must have a master's degree completed at the time of registration at the doctoral school. Authorship in peer-review publications as a first author is highly valued. The following essential criteria must be met:

1. Masters degree in biology or other relevant fields 2. Self-motivated character 3. Willingness to learn new methodologies 4. Highly organised and capable of independent work 5. Willingness to travel during the PhD studies 6. Ability to communicate with a multi-disciplinary team;

In addition, the following criteria will be favoured:

7. First authorship in peer-review publications 8. Experience with morphological analyses 9. Experience with genetic analyses 10. Knowledge of cetacean biology 11. Experience working in an international team.

Research environment

The research at the MIZ is focused on a broad range of themes in animal biology, including systematics, biogeography, evolutionary biology, ecology and population genetics. Andre Moura's research group is part of the Laboratory of the Molecular and Biometric Techniques led by Prof. Wieslaw Bogdanowicz, grouping researchers focused on population genetics, phylogeography and evolutionary genomics of a broad range of

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MPIEVA Leipzig BoneProteomics

Marie-Curie Early Stage Researcher position in Palaeoproteomics (ESR7, PUSHH)

The Department of Human Evolution at the Max Planck Institute for Evolutionary Anthropology, Leipzig (Germany), invites Early Stage Researchers to apply for a PhD position that is part of the European training Network "PUSHH: Palaeoproteomics to Unleash Studies on Human History", funded by the European Union's Horizon 2020 Research and Innovation Programme (grant agreement No 861389). More information on the network and its international partners can be found on the www.pushh-etn.eu . In the Department of Human Evolution, palaeoanthropological research is conducted within a multidisciplinary environment involving biological anthropologists, Palaeolithic archaeologists, archaeological scientists, and geochronologists. The ESR position builds on existing expertise within the department on the analysis of ancient proteomics to address questions of relevance in palaeoanthropology and archaeology. In particular, we are looking for highly motivated applicants with an interest in combining palaeoanthropology, archaeological sciences, and zooarchaeology.

Job description

As part of the PUSHH network, ESR7 will work on developing and applying a novel proteomic approach to identify the biological species of archaeological bone fragments. Palaeoanthropology utilizes peptide mass fingerprinting to screen sample sets encompassing thousands of bone chips from caves known to be occupied by anatomically modern humans, Neanderthals and Denisovans to identify hominin remains and further characterise them through deep palaeogenomic sequencing. Despite being cheap and robust, peptide mass fingerprinting has some clear limitations, because it commonly uses MALDI-TOF-MS instruments that are less sensitive and have lower resolution compared to what is now the state-of-the-art proteomics technology, i.e. Orbitrap (commercialised by partner organisation Thermo). Furthermore, peptide mass fingerprinting data interpretation is still manual and as such tedious and error-prone. ESR7 will apply the same approach based on data-independent acquisition (DIA) tandem MS and the ultra-fast peptide separation technology (~8 mins/run), developed by partner organisation EvoSEP, to screen bone proteomes at low cost with Orbitrap technology. The advantages over peptide mass fingerprinting will be represented by the acquisition of a much richer dataset per sample, higher sensitivity, higher automation, and the ability to use off-the-shelf spectral identification software. As a result, the ESR will acquire advanced laboratory, proteomics, and bioinformatics skills during the duration of the project. Part of this research will be accomplished by a secondment to the Centre for Protein Research, Olsen group, University of Copenhagen (Denmark).

The ESR will have a significant amount of freedom in designing the research project within the scope of the PUSHH network and the high-throughput screening of archaeological bone proteomes, supervised by Prof. Hublin and Dr. Welker. The position commences on the 1st of September for 36 months (full time).

Your key tasks will consist of: - Sample selection and ancient protein extraction; - Protein data analysis, including quantification of damage and assigning taxonomic species identity. - Acquire in-depth knowledge of DIA mass spectrometry data acquisition and associated bioinformatics. - Integration of palaeproteomic data with existing chronological, environmental, and zooarchaeological datasets for the analyzed archaeological assemblages.

You will be expected to complete a PhD thesis within the duration of the position. Due to the composition of the PUSHH network, there are significant opportunities for further training and knowledge-exchange with other network members. This includes mandatory network-wide activities that might take place outside of Europe. Your work will result in scientific articles and/or book chapters in collaboration with other PUSHH ESRs and supervisors, and, whenever possible, opportunities will be sought to communicate your research to a broad audience. The research is expected to be compliant with the highest scientific standards, as set out in the European Code of Conduct for Research Integrity.

Qualifications profile - By September 1st 2020, have a completed university degree (Ma/MSc) in archaeology, evolutionary biology, proteomics, or related disciplines. - Ability to work collaboratively and independently in relation to multi- disciplinary research teams. - Experience with bioinformatics and molecular/evolutionary biology is preferable. - Proficiency in English.

Eligibility To be eligible to apply for this role you must, on the 1st of September 2020, be in the first four years (full-time equivalent research experience) of your research career and have not been awarded a doctoral degree. In accordance with the applying mobility rule for

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NMNH Paris HumanMigrations

THESIS: BODY PIERCING AND PAST HUMAN MIGRATIONS PHD THESIS PROPOSAL NATIONAL MUSEUM OF NATURAL HISTORY, PARIS, FRANCE

Recommended background: Archaeology, or Anthropology, or Human Population Genetics

Lab: Eco-anthropologie UMR 7206, Musée de l'Homme, Paris, France Duration: 3 years (starting Fall 2020) Supervisors: Franz Manni and Evelyne Heyer Net salary: 1,400 Euro Contact Email : franz.manni@mnhn.fr

How to apply: Contact us before the 11th of June 2020, sending a short motivation letter, a CV and a list of available Master 2 exams scores. Candidates will be contacted back.The best candidate will have to prepare some paperwork by the June, 19, 2020 to be admitted to a formal Skype interview of 20 minutes (10 minutes to illustrate the project and 10 minutes for questions) to be set 1-3, July, 2020.

Description of the PhD project For a French version see the PDF below at page 85 http://formation.mnhn.fr/sites/depf.mnhn.fr/files/atoms/files/catalogue_sujets_concours_ed227_edition2020.pdf This PhD project is aimed at investigating the spread of ancestral body piercing practices in relation to past human migrations. This is to say that body piercing is here considered as a vertically transmissible cultural trait, maybe having a limited number of origins in time and space. Like other body modifications (skull deformations, teeth alterations, scarifications, tattoos, neck elongation, etc.), body piercing relies on a very specific and quite complex know-how. Although its symbolism is variable, diachronically and synchronously, the practice actually relies on the method used to create, heal and enlarge a "tunnel" in the flesh: when the know-how is lost, the practice becomes hardly possible. This is the research hypothesis of the thesis: The ancestors of the populations who practice(d) body piercing learned how to do it by contact with other populations. The history of body piercing is likely to mirror past human contacts and migrations. To be clear: This doctoral project concerns ONLY the study of traditional body piercing practiced by many peoples in the world, it DOES NOT directly concern "modern" body piercing emerged in California (the "Modern Primitives") in the mid-1970s. Nevertheless, this recent renaissance has shown that several years have been necessary to develop, ex nihilo, a viable body piercing technique, meaning that it is not easy to reinvent body piercing. This is why ancestral ("traditional") body piercing may have persisted only where the know-how related to it has been transmitted through direct learning, generation after generation. The oldest body piercing ornament is dated 46,000 years ago (Langley et al. 2016). Although other body modifications (ex: tattooing) can be as old, body piercing leaves more durable evidence: the ornaments. Easily recognizable by their shape (rounded, cylindrical, conical, or toroidal), their symmetry, weight and polishing, body piercing ornaments will be the major object of study of the thesis. Contemporary or old, they are available in many collections (public or private), this is why fieldwork will not be necessary. The project stems from an exhibition that took place at the Musée de l'Homme , Paris, France (March 2019/2020; curator F. Manni) and related work. The candidate will benefit the help of the research network at the origin of the exhibition (40 researchers, 12 countries: archaeologists, ethnologists, anthropologists, curators). Currently the Network is involved in the writing of a manual on body modifications to be published by an international academic publisher. The outcome of the thesis can be included in it.

Objectives of the thesis and worksteps Which ones are the populations practicing or having practiced body piercing? Where are they located? When was body piercing invented? How many times was it invented? How did it spread? None of these issues have been addressed so far. Although body piercing ornaments are not uncommon in archaeological excavations, they have not yet been the subject of systematic attention. At first, the PhD student will create a georeferenced database of the populations practicing (or having practiced) traditional body piercing. Then, she/he will address the issue of its spread. The aim is to test if body-piercing transmission relies on independent origins or, rather, on a vertical transmission in a limited number of populations, disseminating through their migrations and contacts. Likely, some of these migrations are known, described by population geneticists and historical linguists. The interpretation of the diachronic and synchronic cartography of piercing will be based also on them. Studied ornaments will be classified according to their i) shape, ii) materiality, iii) manufacturing techniques and iv) decorations,

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NorthDakotaStateU PlantEvolutionaryGenomics

A PhD position is available to study adaptive introgression in Poplar with Jill Hamilton at North Dakota State University, as part of a new NSF Plant Genome-funded collaboration with Jason Holliday (Virginia Tech), Stephen Keller (Vermont) and Matt Fitzpatrick (U of Maryland).

Understanding how interspecific hybridization leads to the generation of complex adaptive traits across environments is a central objective of species management, particularly considering rapidly changing climates. Natural Populus hybrid zones provide a 'living laboratory' to test the impact a long history of natural selection and weak barriers to reproduction have had on the origins of adaptations and the maintenance of species barriers. The graduate student will leverage replicate natural hybrid zone transects between Populus trichocarpa and P. balsamifera spanning the Rocky Mountains in conjunction with modern sequencing (whole-genome resequencing, long and short reads), large common garden experiments, and novel computational approaches to study the genomic and phenotypic consequences of hybridization across environments. Broadly this research will ask: (i) how is introgression arrayed across the genome and landscape? and (ii) what regions of the genome contribute to hybrid fitness and what are their environmental drivers? This project will enhance our understanding of the relationship between adaptive introgression and fitness across environments.

The PhD student will be prepared to combine field-based research monitoring phenotypic trait variation across replicated common garden experiments with whole genome resequencing, and environmental and spatial data. The ideal graduate student will have some experience in population genomics and/or quantitative genetics. There is plenty of room to pursue particular interests in adaptive introgression and the origin of species barriers depending on the interest and experience of the candidate. The student will be involved in a range of outreach activities associated with the project, including engaging with collaborator institutions and ArbNet (based at the Morton Arboretum, Chicago) to develop educational modules on climate adaptation using Poplar mini gardens planted across the United States. The ability to work independently and a some background in genetics is needed.

For more information on the Hamilton Lab please visit the lab website at: http://www.jillahamilton.com. More information on the Department of Biological Sciences at NDSU can be found at https://www.ndsu.edu/biology/. Fargo is the largest city in the northern Midwest and as 'Gateway to the West' is a vibrant, growing community that has access to numerous outdoor opportunities for all seasons.

For consideration, please send a cover letter summarizing your research interests and experience, a current CV, and contact information for three references to Jill Hamilton (jill.hamilton@ndsu.edu) with the email subject line "PhD application: [your full name]".

This position is funded via the NSF-Plant Genome Research program and includes full tuition waiver plus competitive stipend. The start date is flexible with a tentative start date of Spring 2021. Applications are being accepted now and the position will remain open until filled.

Jill Hamilton, Ph.D.

Assistant Professor Department of Biological Sciences North Dakota State University http://-jillahamilton.com/index.html jill.hamilton@ndsu.edu

"Hamilton, Jill" <jill.hamilton@ndsu.edu>

PoznanPL ParasiteEvolution

"Parasite evolution in response to climate warming"

The position is available from 1st October 2020 and limited to 3 years.

The proposed research is a collaboration between Polish and German research teams: PD Dr. Slawek Cerbin from Adam Mickiewicz University (Poland) and Prof. Justyna Wolinska from IGB and Free University Berlin, jointly financed by the Polish National Science Centre and German Research Foundation. The position is mainly based in Poland; however, a six-month research stay at the IGB-Berlin is planned. Funding for attending national/international conferences is available.

Project description:

It is commonly believed that global warming will result in a "sicker world", with infectious diseases increasing in prevalence and virulence. However, these predictions are based on short-term experiments that have not recognized evolution that could lead to thermal adaptation. This project aims at answering the question whether parasites' prevalence and virulence is altered under elevated temperatures and if long-term exposure to warming amplifies this effect. The successful candidate will use a combination of experimental evolution and field approaches to generate new predictions regarding the evolution of parasites in a warmer world. The candidate will use a model system consisting of the crustacean Daphnia and their microparasites.

Duties and responsibilities

* designing and conducting laboratory experiments * generating molecular and genomic data * conducting field work (including artificially heated lakes which serve as a globally unique model of "warmer world") * analysing experimental and field data using advanced statistical methods * writing scientific publications

Requirements

* MSc degree in biology (or related fields) * knowledge of evolutionary biology, population genetics or ecology * basic knowledge in statistical programming (e.g. R) * excellent communication and writing skills in English * hands-on experience in conducting experiments or field studies and/or experience in molecular or genomic research would be an advantage (but is not required)

— Conditions of Employment:

The prospective student receives a stipend (4500 PLN/month gross, good standard relative to the low living costs in Poland) from the National Science Centre grant for 3 years.

Enquiries or questions should be directed to dr. Slawek Cerbin (cerbins[at]amu.edu.pl).

How to apply:

Please send complete application documents as a single pdf-file by email to dr. S. Cerbin (cerbins[at]amu.edu.pl; in the subject field include "Paradapt PhD"): no later than 30th June 2020.

The application should include:

1) CV

Please include the following statement in your CV: "Pursuant to Article 6 (1) of the General Regulation on the Protection of Personal Data of 27 April 2016 (Journal of Laws EU L 119/1 of 4 May 2016) I agree on the processing of personal data such as: name, (names) and surname, parents' names, date of birth, place of residence (correspondence address), education, course of previous employment, included in my job offer for the needs of current recruitment."

2) A letter of motivation

3) A scan of MSc diploma

4) Contact details to two/three potential referees, including MSc supervisor

The beneficiary of the National Science Centre stipend will be chosen by a selection committee based on regulations about scientific scholarships for young researchers in research projects financed by the Polish National Science Centre. The recruited person will be required to enroll as a regular PhD-student in the PhD School of the Adam Mickiewicz University.

Prof. Justyna Wolinska

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) Mueggelseedamm 301 12587 Berlin, Germany

Group Leader at the IGB & Professor for Aquatic Evolutionary Ecology at the Free University of Berlin

Phone: +49 (0)30 64181 686; Fax: +49 (0)30 64181 682; email:wolinska@igb-berlin.de

http://www.igb-berlin.de/en/profile/justyna-wolinska-0 http://www.igb-berlin.de/en/wolinska Justyna Wolinska <wolinska@igb-berlin.de>

SGN Frankfurt InvertEvolutionaryGenomics

Job offer ref. # 12-20012

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

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

PhD Position (m/f/d)

Evolutionary genomics of invertebrates

(part time, 50 %)

Your tasks:

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

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

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

§Taxonomic description of new species from the Northern and Southern Hemisphere

Your profile:

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

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

§Interest in mobile DNA and its genomic influences

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

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

What is awaiting you?

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

§Access to unpublished genomes from exotic animal phyla.

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

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

Please send your application, mentioning the reference of this job offer (ref. #12-20012) before June 28th, 2020 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your certification to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

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

recruiting <recruiting@senckenberg.de>

Sweden BehaviouralGenetics

PhD position in Behavioural Genetics at the biology department at Linkoping University, Sweden.

Deadline August 21th 2020

Apply/Advert: https://liu.se/en/work-at-liu/vacancies?rmpage=3Djob&rmjob=14038&rmlang=3DUK Project Description Many aspects of animal behaviour differ consistently between individuals and this has given rise to the growing field of animal personality. However, this does not mean that the behaviour of a given individual is readily predictable, because while some individuals show low levels of variation around their behavioural mean, others show high levels of variation. Comparisons between individuals in stress research often rely on single measurements of phenotypic traits, which is potentially problematic since variation in trait predictability between individuals can render single measurements of labile traits such as behaviour unreliable as indicators of stress. Using a combination of large-scale genetical genomics analysis the candidate will determine the genetic architecture underlying variation in behavioural predictability (within-individual variation) across a range of anxiety related behaviors, as well as the mechanisms underlying their effect and correlate these predictability genes with effects of prenatal stress, to see if individuals with genes that cause low or high trait predictability are more or less sensitive to environmental disturbance.

The candidate will work with myself Dr Rie Henriksen and Professor Dominic Wright at Linkoping University. Email me for further details: rie.henriksen@liu.se

Rie Henriksen, Assistant professor

IFM Biology

Linkoping University

58183 Linkoping

SWEDEN

email: rie.henriksen@liu.se

Phone: +46 (0) 70 089 50 84

https://www.researchgate.net/profile/Rie_Henriksen https://liu.se/en/research/henriksen-group
rie.henriksen@liu.se

TrentU AvianEvolutionaryPhysiology

MSc and/or PhD positions in avian evolutionary physiology Position background: My research group is seeking 1-2 MSc/PhD students interested in lab and/or field studies of avian physiology. Areas of planned research include: the impact of temperature during development on adult physiology, climatic warming as a constraint on activity in wild birds, and factors that impact the fine-scale movements of individuals in the field (using automated radio-telemetry). Specific thesis topics are flexible, and you are encouraged to contribute your ideas.

Requirements: You should have an interest in animal physiology/evolutionary physiology. Experience and/or interest in use of R would be an asset (although not required). To apply for an MSc, you will require a B.Sc. Hons (or equivalent) in Biology or a related field. PhD applicants will require a completed MSc or equivalent, by the start date. Positions are open to Canadian citizens or permanent residents, but strong international candidates are encouraged to apply. We seek a diversity of ideas and perspectives in the lab, so we especially welcome applicants from under-represented groups.

Funding: The minimum stipend for an MSc student is $19,274 for each of 2 years; a PhD student is $21,274 for each of 4 years. Students holding external funding are particularly encouraged to apply.

How to apply: Please send an email with your CV, a brief statement of research interests and an unofficial transcript to: garyburness@trentu.ca. Enquires are also welcome.

Start date: Jan 2021. Applications will be considered until positions are filled.

Links to the Graduate program and Department of Biology are found at: https://www.trentu.ca/els/ https:/-

/www.trentu.ca/biology/ Gary Burness, PhD Professor Dept. of Biology Trent University, Peterborough, ON K9L 0G2 CANADA

garyburness@trentu.ca www.facebook.com/BurnessLab Twitter: @GaryBurness

Gary Burness <garyburness@trentu.ca>

UBern GenomicsBioticInteractions

PhD Project on Genomics of Plant Toxin Resistance

Background: Plant secondary metabolites play a key role in multitrophic interactions. We recently found that natural enemies of herbivores can adapt to secondary metabolites that are taken up from the plant by a specialist herbivore (https://www.pnas.org/content/-116/46/23174). The capacity to deal with plant toxins determines the predation success and biological control potential of these organisms. Yet, the genetic and biochemical mechanisms of this phenomenon are unclear, which hampers our capacity to exploit it for sustainable agriculture. The current PhD project aims at filling this gap of knowledge by uncovering the genetic basis of benzoxazinoid resistance in entomopathogenic nematodes. The project is embedded in a collaboration between the Biotic Interactions and Ecological Genomics Groups at the Institute of Plant Sciences at the University of Bern.

We look for an enthusiastic and ambitious PhD student with a strong interest in genomics and multitrophic interactions. Applicants should have a firm background in computational biology and an interest in combining bioinformatics with laboratory work. All our projects are highly integrative and require willingness to embrace multiple biological sub disciplines. Fluency in English is a prerequisite for this position. A MSc. degree or Diploma with competitive grades is required.

We offer an inspiring and dynamic research environment, including state-of-the art research facilities, extensive supervision and an exciting project of considerable fundamental and applied relevance. Specific project tasks can be tailored to the interests and training priorities of the student. The Institute of Plant Sciences is located at the shore of the river Aare, close to the vibrant city center of Bern. PhD students are paid according to University standard rates and have the possibility to join the graduate program in Molecular Life Sciences. More information about our current activities can be found here: https://www.ips.unibe.ch/research/interactions/

How to apply: Send a single pdf including i) a letter of motivation, ii) a detailed CV, iii) copies of University grades and iv) the names and addresses of two referees to matthias.erb@ips.unibe.ch. The position is available from August 2020 and open until filled. For more information, feel free to contact Matthias Erb directly.

Christian Parisod Institute of Plant Sciences 'V University of Bern Altenbergrain 21 'V 3013 Bern 'V Switzerland Phone: +41 (0)31631 4949 e-mail: christian.parisod@ips.unibe.ch http://www.ips.unibe.ch/-research/ecogen "christian.parisod@ips.unibe.ch" <christian.parisod@ips.unibe.ch>

UBristol MacquarieU MaternalEffects

PhD studentship: Maternal effects and host-microbiome-pathogen interactions in disease vectors Supervisors: Dr Sinead English (University of Bristol), Dr Fleur Ponton (Macquarie University)

The aim of this PhD project is to develop a formal framework to understand host-microbiome- pathogen interactions using important insect vectors of disease (mosquitoes, tsetse) as exemplars. Most organisms harbour a community of microbes that interact with pathogens, either by direct resource competition or indirectly through by affecting the host immune system. In insect vectors of disease, there is increasing interest in manipulating these microbes to decrease the vector population size or interfere with pathogen transmission. Formal mathematical models are important tools to show how perturbing one aspect of host-microbe-pathogen system (e.g. removing microbes) changes the overall dynamics.

The condition of the mother 'V her age, nutrition 'V can also shape the microbial community and immunity of her offspring. How these transgenerational effects change the predictions of host- microbe-pathogen interactions is yet to be explored. The student will build on recent modelling work (King & Bonsall 2017, BMC Evol Biol) to incorporate maternal effects into the host-microbiome-pathogen system, and how this differs across insect disease vectors. Maternal effects may be particularly important in vectors such as tsetse flies which produce one enormous larva at a time compared to mosquitoes which produce batches of many small eggs.

The PhD position will be jointly hosted at the University of Bristol, Bristol, UK and Macquarie University, Sydney, Australia. The PhD position is fully funded for 3.5 years and will cover research costs, tuition fees, stipend and flights between UK and Australia. The student will be supervised by Dr Sinead English (Bristol) [evelab.org] and Dr Fleur Ponton (Macquarie) [pontonlab.wordpress.com], as well as benefiting from guidance from Professor Mike Bonsall (Oxford) and Dr Antoine Barreaux (Bristol). The student will spend 2 years in Bristol and 1.5 years in Sydney during the project, developing models (Bristol/Oxford) and testing predictions from these models in empirical systems such as tsetse flies and mosquitoes (Bristol/Macquarie).

The project would suit a student with strong quantitative skills, particularly in mathematical biology, and a background in, or demonstrable enthusiasm for, evolutionary ecology and entomology. The student will have to be willing to live in two different countries (2 years in Bristol, UK, and 1.5 years in Sydney, Australia). Conditions of funding mean that the position is available only to UK/EU students and an MSc qualification is desirable. The studentship can start 1 January 2021 or 1 April 2021.

To apply, please email Dr Sinead English (see below) with a 1-page cover letter describing your suitability and eligibility for the position, a CV (max 2 pages) and contact details for two academic (or other relevant) referees by 15 July 2020. Video-conference interviews will take place in the week commencing 20 July.

Please direct any informal enquires to Dr English, sinead.english@bristol.ac.uk

Sinead English <sinead.english@bristol.ac.uk>

UCollege Dublin ChemosensoryGenomics

Title: Deciphering the evolution and fine-tuning of vertebrate chemosensory systems using comparative genomics

About the project

Animal adaptation to different environments involves the accumulation of changes in physiology, feeding ecology, social structures, environmental habitats and circadian rhythm. As such, the ability to infer and process environmental chemosensory information is a crucial step in adopting a novel niche, placing sensory perception at the forefront of evolutionary adaptation.

Sensory perception is governed by a variety of different 'sense-specific' membrane-bound 7-transmembrane G-protein coupled receptor gene families encoded throughout the genome, e.g. olfactory receptors, trace amine-associated receptors, vomeronasal receptors and taste receptors. Each gene family contains varying numbers of coding sequences expressed in numerous cell types on different sense organs. The fine-tuning of these different sensory modes reflect life-history traits (e.g. sociality), niche-specific evolutionary adaptations (e.g. diet) and available sensory-space. However the relationships between these remain poorly understood. Given the current trend of cheaper sequencing costs, there are now more vertebrate genomes available than ever before, allowing an unprecedented, in-depth exploration of sensory evolution at the genomics level in a taxonomically diverse sample set. This project will combine comparative genomics, bioinformatics and phylogenetics to explore chemosensory evolution, answering questions such as 'what is the background rate of evolution in chemosensory genes?', 'Do convergent life-history traits reflect sensory sequence convergence?', 'Does positive selection at key residues reflect lineage-specific spectral tuning?', 'When is loss of sensory function adaptive?'

Core objectives in this project that you will research include:

Objective 1: Establishing rates of evolution, loss of function and duplication across sensory genes and background rates of gene evolution

Objective 2: Develop novel methods to explore positive selection in multigene families.

Objective 3: Correlate loss, gain and lineage-specific sensory evolution with life-history traits and ecological niche adaptation to explore available sensory-spaces, e.g. diet, sociality and pheromones and odorants.

Objective 4: Reconstruct ancestral sensory gene repertoires across the species tree, comparing extant and ancestral gene evolution over vast time-frames.

This project is an Ad Astra-funded studentship, and will be largely completed in silico, using the latest computational methods. Informal enquiries are welcome. The studentships are open to EU and non-EU candidates and are for a maximum of four years, renewable each year, subject to satisfactory progress. UCD supports equal opportunities and does not discriminate against individuals on the basis of gender, age, race, colour, nationality, ethnic or national origin, religion, marital status, family status, sexual orientation, disability or membership of the traveller community.

Requirements

- Applicants must have, or expect to have, reached a minimum of an upper second-class (2.1) degree or equivalent in a relevant honours Bachelor's or Master's degree in a relevant biological/computational/mathematical field.

- Excellent written and oral communication skills and a high level of competence in the English language are essential.

- Experience working with quantitative and qualitative data

Desirable

- Due to the computational nature of this project, applicants are expected to be familiar with a Linux OS, and command line usage.

- A programming language, e.g. Python or Perl is desirable, though not necessary. It is expected that the applicant will learn and become proficient in at least one of these languages throughout the project.

- Experience using R.

- An MSc in a related field

Application Details Applicants should submit the following g.hughes@ucd.ie as a single .pdf document:

1. A cover letter outlining their interest in the project and any relevant experience 2. A detailed CV 3. The names and contact details of two academic referees

Interviews will take place via video call in early August, and the PhD will be expected to commence in September 2020.

Funding Notes The studentship award includes full tuition fee waiver, a PhD stipend of euro 18,000 per annum, and a research budget to cover research costs associated with the project.

Further info

For further information and to apply, please contact Dr. Graham Hughes Email: g.hughes@ucd.ie https://people.ucd.ie/g.hughes Graham Hughes <g.hughes@ucd.ie>

UGuelph PopGenMetagenom

Several graduate student positions are open at both the MSc and PhD levels in my research group. Below is a summary of projects with funding.

[1] Metagenomic analysis and theory

This project will apply and extend theory that studies metagenomic data using population genetic principles. The starting point is recent theory from my group that focuses on amplicon-based approaches and uses the coalescent to detect whether subsets of individuals within a species or taxonomic group go unamplified using genetic sequence data at hand. The project can then be extended to shotgun-based methods. A link to a foundational paper related to the project is https://journals.sagepub.com/doi/full/-10.1177/1176934319883612 [2] Modelling polyploid population genetics and evolution

This project would apply and extend recent multilocus population genetic models of polyploids to understand the evolution of recombination rates and the diploidization process in polyploids. It follows from interesting research that indicates recombination rates readily evolve in polyploids and that the diploidization process is not equal across genomes. Papers related to the multilocus theory are https://academic.oup.com/-jhered/article-abstract/110/7/866/5674929 and https:/-/www.nature.com/articles/hdy201744 [3] Ancestral graph theory of ecological communities

My group has started modelling ecological communities using ancestral graph approaches. I am looking for a student interested in extending this approach to modelling the evolution of core and flexible genomes in bacterial communities. In addition, the approach can be applied to inferring processes shaping eukaryotic communities. A paper related to this work is https://www.sciencedirect.com/science/article/-abs/pii/S0022519318306325 A student can join my lab either through the Department of Integrative Biology or Bioinformatics graduate programs at the University of Guelph, Canada. If you are interested in applying, please send me a short statement of interest, a brief CV and a relevant academic transcript (which can be unofficial). Also, if you have questions about the projects, feel free to contact me by email.

Links to the graduate program webpages are Integrative Biology: https://www.uoguelph.ca/ib/-grad_program_overview and Bioinformatics: https://-www.uoguelph.ca/bioinformatics/programs Cortland Griswold Associate Professor Department of Integrative Biology University of Guelph email: cgriswol@uoguelph.ca

"cgriswol@uoguelph.ca" <cgriswol@uoguelph.ca>

UHelsinki SalmonEvolution

Doctoral student position in salmon ecology and evolution

A Doctoral student position is available at the University of Helsinki, Finland, to work in Academy Research Fellow Tutku Aykanat's research group. The position is a part of a 5-year Academy of Finland funded project, and aims to understand the processes shaping Atlantic salmon demography in the wild.

Atlantic salmon is a great organism to study gene-phenotype-fitness relationship in the wild. The presence of substantial material from past research and monitoring efforts, and a simple 2-locus system broadly controls important life history variation (see refs below) allow for an integrated framework to track adaptive genetic variation in Atlantic salmon in the wild.

Using multigenerational, multi population datasets composed of genetic and phenotypic information, the PhD student will employ age structured population models and whole food web approaches to understand the evolutionary processes and ecological constrains shaping Atlantic salmon life history variation and demography.

Professor Anna Kuparinen from the University of Jyväskylä will co-supervise the PhD student. The student is expected to visit Kuparinen's group at the University of Jyväskylä up to 12 months to master dynamic food web modelling and apply it on Atlantic salmon.

The ideal candidate should demonstrate strong mathematical / statistical understanding, experience in a statistical computing software such as R, JAGS, or matlab, and interests in ecology and evolution, and familiarity with quantitative genetics.

The appointee should either already have the right to pursue a doctoral degree at the University of Helsinki by the start of the appointment, or apply for the right and obtain it within the probationary period of six months of their appointment. If the candidate does not already have the right to pursue a doctoral degree at the University of Helsinki, it must be applied for separately. (https://www.helsinki.fi/en/research/doctoral-education/the-application-process-in-a-nutshell#section-3079).

Funding is for 3 year 8 months for the four-year project. Funding for the remaining four months is uncertain due to covid-19 related complications, but good opportunities exists to fill this gap. The starting date is January 2020.

The salary will be based on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance with the overall starting salary amount being about 2240 EUR per month, before taxes.

Your application should include (in a one pdf-file) a motivation letter with a summary of your interests, your CV, and two letters of reference.

Please submit your application, together with the required attachments, using the online application form using the University of Helsinki electronic recruitment system by clicking on Apply for the position (https://www.helsinki.fi/en/open-positions/doctoral-student-aykanat). The deadline for applications is 2 August 2020.

Informal inquiries should be directed to Tutku Aykanat (tutku.aykanat(at)helsinki.fi).

Finland is a member of the EU, has high quality free schooling (also in English), generous family benefits and healthcare, and was recently ranked as the happiest country in the world. The University of Helsinki is a top 100 ranked university in most ranking lists, and is currently investing heavily in life sciences research (see hrefhttps://www.helsinki.fi/en/helsinki-institute-of-life-sciencehttps://www.helsinki.fi/en/helsinki-institute-of-life-science).

Relevant research: - Barson NJ*, Aykanat T*, Hindar K, Baranski M, Bolstad GH, et. al (2015) Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. Nature, 528, 405-408 (*: equal contribution). - Kuparinen A, Hutchings J (2017) Genetic architecture of age at maturity can generate divergent and disruptive harvest-induced evolution. Philosophical Transactions of the Royal Society B 372: 20160035. - Czorlich Y, Aykanat T, Erkinaro J, Orell P & Primmer CR (2018) Rapid sex-specific evolution of age at maturity is shaped by genetic architecture in Atlantic salmon. Nature Ecology and Evolution, 2, 1800-1807. - Kuparinen A, Perälä T, Martinez NDM, Valdovinos FS (2019) Environmentally- induced noise dampens and reddens with increasing trophic level in a complex food web. Oikos 128:608-620. - Aykanat T, Rasmussen M, Ozerov M, Niemelä E, Paulin L, ey. al. (2020) Life history genomic regions explain differences in Atlantic salmon

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

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UKiel SelfishChromosomes

*PhD position on **the evolutionary maintenance of selfish accessory chromosomes***

A PhD position is available for three years to study the *mechanism of the evolutionary maintenance of accessory chromosomes in a fungal plant pathogen *with the Max Planck research group "Environmental Genomics" headed by Prof. Dr. Eva H. Stukenbrock and supervised by Dr. Michael Habig. The Max Planck group is affiliated with the *Max Planck Institute for Evolutionary Biology* in Plön and the *Christian-Albrechts University of Kiel* in the North of Germany. The position will also be associated with the Kiel Evolution Center, the Kiel Plant Center and the International Max Planck Research School for Evolutionary Biology - providing a unique scientific environment. The position is compensated at 65% of TV-L 13 and candidates are expected to complete a PhD.

*Background***

Selfish genetic elements are widespread in all groups of organisms. These elements are likely to have shaped the evolution of diverse biological systems, including genome structure, sex determination, and meiosis. To date, surprisingly little is known about the exact processes that underlie the spread of these elements. This project aims at understanding the transmission mechanism and its evolutionary consequences of selfish accessory chromosomes in a fungal pathogen with a particular focus on the role of histone modifications.

Recently, we could show that the accessory chromosome of the commercially important wheat pathogen /Zymoseptoria tritici/ show a chromosome drive, i.e. are inherited to more progeny than expected by Mendelian segregation. In addition these chromosomes show a negative fitness effect and could therefore be considered selfish elements. The mechanism of this chromosome drive is however unknown - but recent data suggest that histone modifications might be involved.This project aims at understanding this previously unknown aspect of histone modifications and its exploitation by selfish chromosomes using the model organism /Z. tritici/.It will involve the establishment of in vitro crosses and the identification of the genetic and epigentic traits responsible for the chromosome drive.

Expectations and Requirements:

We seek a highly motivated candidate who wants to actively drive a research project. The candidate must have university degree (Master or equivalent) in biology or a related field. High competence in experimental design, and English writing is a must. Ideally, the candidate has comprehensive experience in molecular genetics, work with plant pathogens or performance of evolution experiments. The selected candidate will have the opportunity to collaborate in an interdisciplinary team of biologists (molecular biologists, evolutionary biologists and population geneticists) as well as to pursue unique research in the field of chromosome biology.

Kiel University aims at a higher proportion of women in research and education, and, therefore, specifically encourages qualified female scientists to apply. Female scientists will be preferentially considered in case of equivalent qualification, competence and achievements.

Kiel University specifically supports employment of severely handicapped people. Therefore, severely handicapped applicants will be preferentially considered in case of suitable qualification.

Kiel University specifically welcomes application from people with migration background.

Application

Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant's work), and copies of certificates. Deadline for applications is 15. July 2020. Applications should be sent to:

Dr. Michael Habig, Botanisches Institut, Christian-Albrechts-Universität zu Kiel, Olshausenstr. 40, 24118 Kiel

or _preferentially as a single-PDF-document_ by e-mail to: office@bot.uni-kiel.de

We explicitly do not require application photos and therefore these shall be omitted.

Further information can be obtained from Dr. Michael Habig (mhabig@bot.uni-kiel.de).

Please also check:

http://web.evolbio.mpg.de/envgen/ https://www.evolbio.mpg.de/imprs http://www.kec.uni-kiel.de/ https://www.plant-center.uni-kiel.de/en/about-kpc Michael Habig <mhabig@bot.uni-kiel.de>

UKonstanz EvolutionAvianEndocrinology

Hormonal correlates of social relationships in birds

—1 PhD position is available at the Department of Biology, University of Konstanz (Germany) in the lab of Michael Griesser to study the hormonal correlates of social relationships in Siberian jays. The fulltime position is funded for 3 years, starting preferably September 2020.

The project combines lab work (hormone assays) with field experiments and long-term data, and will use Siberian jays as system. This family living bird species does live in stable groups, but does not breed cooperatively. The fieldwork for the project will take place in Swedish Lapland in late winter and autumn, and involves fieldwork on cross-country ski and on foot, with temperatures ranging from -30C to +30C. The candidate will benefit from a strong interest in experimental field endocrinology and social evolution.

The Griesser lab is attached to Prof Iain Couzin's Chair of Biodiversity and Collective Behaviour and has links to the Centre for the Advanced Study of Collective Behaviour. The University of Konstanz one of the nine 'elite universities' in Germany, and is located a short ride outside the city of Konstanz, overlooking Lake Constance and the Alps. The University of Konstanz focuses on excellence in research, and the successful applicant will benefit from outstanding infrastructure, opportunities for training, and a highly collaborative, diverse, and international research environment. Our working language is English; applicants must therefore be fluent in this language; no knowledge of German is required.

—The University of Konstanz is committed to increasing the number of individuals with disabilities in their workforce and therefore we encourage applications from such qualified individuals. Furthermore, we seek to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply. We offer extensive support to help researchers balance professional and home life, including assistance with childcare and support of the elderly, and flexibility in how employees arrange working hours.

Required qualifications: 1) MSc in endocrinology, behavioural ecology, evolutionary biology or similar 2) Working knowledge of running hormone assays 3) Field experience of behavioural observations and experimental work 4) Bird handling experience (including mist netting) is beneficial 5) Highly motivated and sociable personality 6) Project management skills and ability to work independently 7) Driver's license 8) Basic knowledge of skiing (X-country or downhill) is beneficial

Reviews of application will start 15 July 2020, position remains open until filled.

If you wish to apply, send a motivation letter, CV, publication list, two contacts for references and short summary of your current research (as a single PDF) to michael.griesser@gmail.com

—- Michael Griesser Department of Biology University of Konstanz 78457 Konstanz, Germany

michael.griesser@gmail.com

ULausanne TheoreticalEvolEcol

Phd in Theoretical EvolutionaryEcology at the University of Lausanne

Introduction

UNIL is a leading international teaching and research institution, with over 5,000 employees and 15,500 students split between its Dorigny campus, CHUV and Epalinges. As an employer, UNIL encourages excellence, individual recognition and responsibility.

Presentation

The Group of Prof. Charles Mullon is proposing two Doctoral Student SNSF positions in Theoretical Evolutionary Ecology at the Department of Ecology and Evolution, University of Lausanne, Switzerland. The PhD Students will join a dynamic team working mainly on developing and analyzing mathematical models to understand the evolutionary origin and maintenance of polymorphism in complex traits and populations. For more information on the lab, visit

https://charlesmullon.wordpress.com

Job information

Expected start date in position: 01.01.2021 or to be agreed Contract length: 1 year, extendable to a total of 4 years Activity rate: 100% Workplace: Lausanne Dorigny Annual gross salary: CHF 47'040 (1st year)

Your responsibilities

The successful candidate will be based at the Department of Ecology and Evolution of the University of Lausanne, under the supervision of Prof. Charles Mullon.

The aims of the doctoral thesis will be to develop new theory in evolutionary genetics and evolutionary ecology to help understand the genetic and ecological bases of variation in quantitative traits, with specific interest in traits that influence non-random interactions between organisms and their environment, such as aggression, cooperation, resource utilization or mating behavior. Specific projects are flexible and may include investigating the emergence of polymorphism within spatially structured ecological communities, and the coevolution of polymorphic traits with their genetic architecture under non-random mating. These projects should explore the interplay between genes, the phenotypes they code for, and how these mediate ecological interactions within- and between-species.

Understanding of and confidence with mathematical modelling and evolutionary concepts are highly desirable.

Most of the time will be dedicated to the realization of the doctoral thesis but a contribution to teaching activities is possible. The University of Lausanne offers a world-class international research environment with state-of-the-art facilities.

Your qualifications

In order to complete our team, we are looking for someone with the following skills:

Essential :

Master's degree in a relevant area (e.g., biology, mathematics, physics, computer science)

Scientific research motivation and experience in evolutionary biology Good spoken and written English proficiency

Desirable :

Experience with mathematical modelling (e.g., dynamical systems, applied probability)

Confidence in theoretical evolutionary biology (e.g., population and quantitative genetics, invasion analysis, adaptive dynamics, evolutionary game theory)

Interest in evolutionary ecology and behavioural ecology Programming skills (e.g., in Python, Java, R or C)

Interpersonal skills :

Good cooperative skills with other researchers and team members Good communication skills, ability to keep an open-mind, ability to communicate your ideas to others

Be motivated and be able to motivate others

What the position offers you

We offer a nice working place in a multicultural, diverse and dynamic academic environment, with opportunities for professional training. Possibilities of continuous training, a lot of activities and other opportunities to discover.

The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. Although French is the common language in Lausanne region, the department research activities and seminars are conducted in English. The campus is located on the shore of the Geneva Lake, with the view on the Alps.

Contact for further information

For further information please contact Prof. Charles Mullon: charles.mullon@unil.ch

Your application

Deadline : 07.08.2020

Formal applications should include:

*a cover letter containing a short description of your research interests and research experience explaining why you reply to this job offer;

*your CV; *a copy of your master certificate; *Master's thesis summary (~one pargraph, max. one page); *the contact details of 2-3 referees.

Please, send your full application in Word or PDF.

To receive full consideration, application documents should be uploaded online through the University of Lausanne recruitment platform:

https://bit.ly/3hCd8Zf Charles Mullon <charles.mullon@unil.ch>

UMontpellier ModelsAssistedGeneFlow

Please find— below the short description of a PhD project funded by the French Canadian Research Funds, within a larger collaborative project between Montpellier and Vancouver. The PhD student will be based in Montpellier, enrolled at the University of Montpellier and co-supervised by Ophélie Ronce (Montpellier, France) and Sally Otto (Vancouver, Canada).

The PhD will be funded by the French Ministry of Higher

Education, Research & Innovation's Doctoral Contracts. Each year, three doctoral contracts are awarded to three French doctoral schools involved in three of the best projects selected by the FCRF Executive Committee. Beneficiaries of these doctoral contracts will receive a monthly sum of euro 1769 over a period of three years

If you know of interested candidates, please share— this announcement with your network. Thanks.

Strong taste and established experience with eco-evolutionary modeling is necessary for the success of the project. The candidate should also have a solid background in evolutionary biology, and/or ecology, population dynamics.

Candidates should send to Ophelie Ronce (ophelie.ronce@umontpellier.fr)

- a detailed CV showing clearly their training and experience in quantitative approaches and modeling (mathematics, coding, statistics), as well as in evolutionary biology and population biology.

- a letter explaining their interest in this specific phD project

- grades obtained during their master (M1 and M2) or equivalent degrees

- the reference of two persons, who may be contacted for more information about the candidate (preferably former supervisors on previous research projects)

Please send the application before June 15th. Final decision will be made in early July.

Do not hesitate to contact me for further information.

Thanks!

best regards

Ophelie Ronce

Research topic investigated during the PhD:

Contemporary climate change is currently altering biodiversity, and these impacts will intensify as temperatures continue to increase in the future, with projected massive mortality affecting keystone species - such as forest trees and corals. While increasing mismatch between local climate and local genetic variation may be resolved in time by a combination of natural selection and natural migration, there is concern about the slow spontaneous pace of these processes relative to the high speed of climate change. Assisted gene flow (AGF) describes the managed translocation of individuals within the current range of a species, to facilitate rapid adaptation to climate change. Only a few recent models have started to investigate how different AGF strategies may accelerate adaptation; even fewer have attempted to quantify its impact on persistence and functioning of populations. In particular, many species (trees, corals, alpine plants) that are targeted for assisted gene flow are long-lived and/or have complex life cycles with different stages having different ecology and sensitivity to climate change, which complicates the predictions about optimal AGF. This requires the development of models describing both the evolution and population dynamics of species for which assisted gene flow is considered as a beneficial management strategy. Our goal is to develop such models to guide assisted gene flow strategies and inform debates about the relevance of their use and their optimal implementation. The PhD student will contribute to this goal by developing new integro-projection models (IPM) to describe the demography of organisms with continuous growth, incorporating genetic variation in growth and other life history traits. The integration of evolution in IPMs is currently a subject of debates and developments, but also a much needed tool to predict eco-evolutionary dynamics in very long lived organisms, such as trees, for which discrete stages are relatively arbitrary. This model will be fitted to data from surveys of natural populations and common garden experiments (using extensive data sets on trees and perennial plants adaptation to climate). The model will be used to answer questions about the best source of seeds when replanting a population of long-lived organisms in a changing climate, optimal mixed sources strategies to deal with uncertainties of climate change, optimal number of migrants, the frequency of migration events and nature of the migrants (e.g. hybrids from crosses). In each of these scenarios, the emphasis will be in examining how the life cycle of organisms (lifespan, change in selection intensity or direction along life, intensity of natural gene flow) affects the performance of different AGF strategies.

Ophélie Ronce <ophelie.ronce@umontpellier.fr>

UMuenster 1 TransposonDynamics

The DFG funded Research Training Group "Evolutionary Processes in Adaptation and Disease" (EvoPAD) at the University of Münster, Germany, invites applications for a PhD Position in Biology (salary level TV-L E13, 65%)

The position is fixed term for 36 months, to be filled at the earliest possible date. Currently, the regular working time for full (100%) employment is 39 hours and 50 minutes per week. The DFG-funded Research Training Group "Evolutionary Processes in Adaptation and Disease" (EvoPAD, GRK 2220) unites biological, medical, and philosophical research at the University of Münster. The core idea is to use the theory of evolution to understand processes leading to adaptation and/or disease. The PhD students within the RTG make use of evolutionary thinking to address basic and medical questions.

The successful candidate will work on transposon dynamics in response to environmental changes supervised by Dr Francesco Catania and Prof Jürgen Gadau at the Institute for Evolution and Biodiversity. Transposable Elements (TEs) populate the genome of essentially all living beings. As the mobilization of TEs is potentially deleterious, cells have evolved molecular machineries that keep it in check. However, environmental stress can disturb these machineries, activating the propagation of TEs and/or impacting the excision of TE-derived sequences. What are the consequences of these stress-induced TE dynamics? This question is the focus of this project, which pays particular attention to the possibility that stress-induced TE dynamics are not entirely random. It leverages a computational approach - comparative genomics/transcriptomics - and uses the single-celled ciliate Paramecium and multicellular eukaryotes as model systems.

For a detailed project description, please visit the EvoPAD website: https://www.uni-muenster.de/-EvoPAD/application/index.html Requirements

- outstanding master's or equivalent degree in biology or a related field

- bioinformatics skills

- proven qualifications with particular relevance to EvoPAD projects

- capacity to formulate and solve research problems and effectively interpret research results

- willingness to interact with colleagues in an interdisciplinary setting

- motivation to manage a PhD project and participate in our multidisciplinary qualification program

- fluency in written and spoken English (knowledge of German is not required)

How to apply The application should include:

- CV containing details of former academic education and degrees, professional experience, publications, fellowships/awards, conference contributions, languages, and further relevant skills and abilities

- cover letter stating the candidate's expectation from EvoPAD, motivation to join the project and possible start dates

- master's thesis abstract

- certificates of bachelor and master's degrees

- two letters of recommendation (either included with the application documents or sent directly to evopad@uni-muenster.de by the referees)

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 recognised severe disabilities who have equivalent qualifications are given preference in hiring decisions, unless other project-related reasons apply.

Applications should be sent by email as one PDF file (max. 5 MB) to the EvoPAD Coordinator Dr Kristina Wensing (evopad@uni-muenster.de) no later than 31 July 2020. Review of applications will start 6 July 2020.

— Dr Kristina Wensing

Coordinator of the Münster Graduate School of Evolution < https://www.uni-muenster.de/Evolution/mgse/ > Coordinator of the DFG Research Training Group 2220 "Evolutionary Processes in Adaptation and Disease" < https://www.uni-muenster.de/EvoPAD/ > Westfälische Wilhelms-Universität Münster Hüfferstr. 1a, D-48149 Münster, Germany

Phone: +49 251 83-21252 E-Mail: mgse@uni-muenster.de or evopad@uni-muenster.de

"Kristina Wensing, MGSE" <mgse@uni-muenster.de>

UMunster PlantAdaptation

The Institute of Plant Biology and Biotechnology, University of Münster, Germany, invites applications for a

PhD Position: The Genetic Basis of Adaptive Plasticity

Wissenschaftliche/r Mitarbeiter/in

Salary level: TV-L E13 (65%)

in the Plant Defense Evolution group, headed by Dr Meret Huber (https://www.uni-muenster.de/Biologie.IBBP/aghuber/members/meret_huber.html).

The position is available for three years and will start in September 2020, or as soon as possible thereafter.

In the Plant Defense Evolution group, we study the molecular mechanism, ecological function and evolution of plant defenses using interdisciplinary approaches. In this collaborative project, we will investigate the biological importance and underlying genetic basis of adaptive plasticity by combining field and laboratory experiments as well as high-throughput sequencing approaches. This project is in collaboration with Prof Shuqing Xu (https://www.uni-muenster.de/Evolution/plantadapt/people/shuqingxu.html), who will also co-supervise the PhD candidate.

What we offer: The PhD candidate can expect a stimulating and international research environment. The position provides the opportunity to acquire a PhD and aims to facilitate successful career development. The candidate will be part of the Mu̇nster Graduate School of Evolution (MGSE, https://www.uni-muenster.de/Evolution/mgse/), which offers both a stimulating studying environment and opportunities to connect with excellent research in the fields of biology, medicine, geosciences, mathematics, and philosophy.

Requirements: We are looking for a highly motivated researcher of any nationality with the equivalent of a Master's of Science in biology, evolutionary genetics or computer sciences. The successful candidate is expected to analyze a large amount of next generation sequencing data (e.g. RNA-seq and whole genome resequencing) with a high degree of independence. Thus, a background in bioinformatics, biology and genetics is required. Applicants must demonstrate their skill in computer programming, statistics and large-scale data analysis. Experience analyzing next generation sequencing data is therefore an advantage. The new PhD student will work together with people from different 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 of 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. We also welcome applications from candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered provided they are able to carrying out the necessary project-related work.

Applications must be in English and include (1) a motivation letter outlining your research interests with reference to the stated requirements in a maximum of 2 pages, (2) a detailed CV including academic and extracurricular achievements, as well as all research experience, (3) abstracts of both the Bachelor's of Science and Master's of Science thesis, and (4) contact details of at least two referees. Applicants should send their documents in one single PDF file to Dr Meret Huber (huberm@uni-muenster.de). Screening will begin immediately and continue until the position is filled.

"Huber, Meret Sophia Claudia" <huberm@uni-muenster.de> "Huber, Meret Sophia Claudia" <huberm@uni-muenster.de>

UOttawa EvolBiolWildPop

Genetic variation in within-individual variance: is it important in the wild?

Most model of evolution consider that intra-individual variance, once corrected for environmental variation, is essentially random noise and is similar across individuals. However, recent studies in captivity showed that within-individual variance could in fact have a genetic basis. In addition, several studies on captive animal have shown the evolutionary importance of the genetic variance in individual variation. For examples, animal breeding try to select for milking cows with low daily variation in milk production to facilitate stock prediction and management. So if we start to understand the importance and the interest of the genetic basis of within-individual variation in breeding programs, the evolutionary importance of this genetic component remain relatively unknown in the wild. Consequently, to better understand evolution in the wild it is key to evaluate the existence and quantify the amount of genetic variance in the intra- individual variance of traits and how it correlates with other traits including fitness. Ideally to get a wider understanding of the phenomenon, such study would need to look at multiple type of traits and across multiple species. Since this has rarely been done, to get a better understanding this needs to be evaluated across multiple traits and species. The aim of this project is to used new quantitative genetic models, a statistical approach allowing to estimate the genetic variance in a trait in wild population, to quantify the genetic variation in within-individual variance in multiple traits across at least 5 species using long-term pedigreed natural populations including yellow-bellied marmots, alpine swifts, eastern chipmunks, bighorn sheep and red squirrels. The project will thus be based on over 150 years of field work (combined across all species). This project will offer opportunity to learn a variety of important methods in evolutionary biology and to participate in the field work on the marmot system. The student will be given a thorough training in field skills and in statistical modelling to tease apart the amount of trait variance explained by genetic and environmental effects.

Relevant publications - Prentice PM, Houslay TM, Martin JGA, Wilson AJ. 2020 Genetic variance for behavioural 'predictability' of stress response. Journal of Evolutionary Biology 33, 642-652. - Martin JGA et al. 2017. Genetic basis of between- and within- individual variance of docility. Journal of Evolutionary Biology, 30(4):796-805. - Westneat DF, Wright J, Dingemanse NJ. 2015 The biology hidden inside residual within-individual phenotypic variation. Biological Reviews 90, 729-743.

The project will be supervised by Pr. Julien Martin (uOttawa). The project will be done in collaborations with the project leaders of participating long-term studies. The student will be based at the Biology department of the University of Ottawa. He/she will have the opportunity to perform field work over the summer in Colorado on the yellow-bellied marmot long-term study and to visit project leaders in Canada (Ottawa, Montreal, Sherbrooke, Edmonton), United-States (Los-Angeles, Boulder) and United-Kingdom (Aberdeen).

Ottawa consistently ranks among the best Canadian cities. You'll love an easy-going lifestyle that appeals to urban adventurers and nature lovers alike. Enjoy a revitalized city that is bursting with energy. Gigs, festivals, theatre and art are all close by in a walkable downtown core. And, having the 2nd highest concentration of scientists and engineers in North America, you'll have lots of opportunities to build up your network and kick-start your career.

Financial support Financial support is available for 4 years. The student is expected to complete two teaching assistantship per year.

Candidate Profile For this PhD project our ideal candidate: - has a MSc in biology - is creative, highly motivated and can work alone or in teams - has strong interest in evolutionary biology and quantitative genetics - has strong interest for statistical analyses and past experience with R programming

How to apply Students that are interested should send a writing sample (thesis, paper or scientific article), a CV, a motivation letter, and the contact of two references to Pr. Martin (julien.martin@uottawa.ca). We will start interviewing candidates in early July and continue to consider applications until the position is filled.

Julien Martin

Professeur agrégé | Associate Professor Département de Biologie | Biology Department Université d'Ottawa | University of Ottawa 30 Marie Curie, Ottawa, ON, CANADA, K1N 6N5 Tel: (613) 562-5800 x2942 https://juliengamartin.github.io/ Julien Martin <Julien.Martin@uottawa.ca>

UPavia EvolutionaryBiology

University of Pavia Ph.D. program in Genetics, Molecular and Cellular Biology

The Institution: The University of Pavia (unipv.it), one of the oldest academic institutions in the world, today is an international multidisciplinary education and research institution that includes excellences in the areas of Biology, Medicine and Mathematics. The University is located in Pavia, a beautiful small city in Northern Italy, tailored for students.

The Program: The Ph.D. program in Genetics, Molecular and Cellular Biology focuses on offering an integrated approach to biological research. Objective of the program is training young researchers capable to tackle the challenges of modern biology, a discipline aiming at a deeper understanding of complex biological phenomena using interdisciplinary skillsets.

Ph.D. students are expected to combine laboratory research activity on one of the program research lines (http://phdsgb.unipv.eu/site/en/home/research-topics.html) with attendance to advanced courses held by faculty members and international speakers (10 courses during the three-year program). Seminars are also regularly organized. During the three-year program, students will have the opportunity to acquire knowledge on frontline topics and technologies, an essential background to perform high-level research in our rapidly evolving society. All activities, including the Ph.D. thesis, are in English.

Students of the program will have access to the research facilities of the University Departments involved in the program, including among others a high-performance computational cluster, a state-of-the-art cellular biology and microscopy facility (including a Cryo-EM microscope) and an ancient-DNA laboratory. The Scholarships: 13 scholarships are fully funded by the program. Three of these scholarships are reserved for international students graduated abroad and additionally include paid housing in a University college for the three-year duration of the program.

The Requirements: A Master???s Degree in related topics is required. The scholarships reserved for international students graduated abroad will be assigned in a two step-process: evaluation of CVs and skype interviews. For the open positions, the selection procedure will consist in the evaluation of the candidates??? CV, a written and an oral exam (exams will be held in September and will require the candidates??? presence in Pavia).

Dates: Applications will open in May 19th, 2020, and close June 24th, 2020. Selections will be held in July-September 2020, the program will start October 1st, 2020. Check the program website and University application portal for more information.

http://phdsgb.unipv.eu/site/en/home.html http://phd.unipv.it/call-36/ Davide Sassera <davide.sassera@unipv.it>

UPrimorska Bioinformatics

Dear EvolDir members,

There is an opening for a PhD position at the Faculty of Mathematics, Natural Sciences and Information Technologies < https://www.famnit.upr.si/en >, University of Primorska (Koper, Slovenia).

The PhD candidate's work will focus, using an interdisciplinary approach, on the understanding of ecosystem functioning, species evolutionary processes and how conservation actions should integrate this knowledge for long term planning. Specifically, in the course of his/her training, young researcher will investigate the evolutionary implications of hybridization, from the introgression of important phenotypic traits between species, to the creation of new species through hybrid speciation and adaptation to different environmental conditions. The young researcher will develop the bioinformatic tools to analyse, identify and categorise hybrids, their level of introgression, and the frequency of introgression in different populations/ecosystems. The work will also address the time of the hybridization event 'V recent vs. ancient 'V to understand the behaviour of introgressed loci in their new genomic background, their influence on survival, adaptation and expansion potential of the species. Young researcher will perform (meta-)analysis of the genetic introgression effects and genotypic diversity across individuals, populations and ecosystem levels of wild plant/animal and their domestic relatives or between lines of interest in order to: i) detect signatures of selection on introgressed genes, ii) investigate links between introgression and phenotypic variation and fitness.

This is a 4-year fully funded position (officially called young researcher position), which includes monthly net salary starting at 1050 Euro (this is an average salary in Slovenia), and additional funds for traveling and research.

The details about the open call can be found on the link https://www.upr.si/en/university/open-calls–tenders/research-open-calls/ < https://www.upr.si/en/university/open-calls–tenders/research-open-calls/ >by clicking on the name of the supervisor. Deadline for application is July 8th.

Best regards, Laura Iacolina < https://www.upr.si/en/university/open-calls–tenders/research-open-calls/ >

– PhD Laura Iacolina Mammalian Biology subject editor https://www.researchgate.net/profile/Laura_Iacolina/info https://lauraiacolina.wordpress.com/ Laura Iacolina <lauraiacolina@gmail.com>

UValencia SocialEvolution

PhD position available at Rafael Sanjuán lab, Institute for Integrative Systems Biology (University of Valencia, Spain). www.uv.es/rsanjuan < http://www.uv.es/-rsanjuan >

Keywords: virus social evolution, virus-virus interactions, experimental evolution, phage discovery, multidrug resistance, Klebsiella.

Start date: October 1, 2020.

For additional information, please contact rafael.sanjuan@uv.es

Rafael Sanjuán Associate Professor of Genetics Institute for Integrative Systems Biology (I2SysBio) University of Valencia, Spain Phone: +34 963 543 270 E-mail: rafael.sanjuan@uv.es URL: www.uv.es/rsanjuan Address: Instituto de Biología Integrativa de Sistemas (I2SysBio) C/ Catedrático Agustín Escardino 9, 46980 Paterna, Valencia Spain

Rafael Sanjuan <rafael.sanjuan@uv.es>

UZurich EvolutionHornwortPyrenoids

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

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

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

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

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

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

— / —

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

UZurich PlantPathogen HerbariumGenomics

PhD Position in Plant-Pathogen Herbarium Genomics University of Zurich, Switzerland

We are looking for a PhD student to explore phylogeographic patterns and (co-)evolutionary dynamics in plant pathosystems by means of herbarium genomics and population genetic analyses. This 4-year position starts in January 2021 and is funded by the University Research Priority Program (URPP) “Evolution in Action: From Genomes to Ecosystems” of the University of Zurich (UZH), Switzerland.

RESEARCH PROJECT

Plant pathogens have had a strong impact on human societies since historical times. Together with their hosts, plant pathogens also offer a great opportunity to study coevolution. In this project, you will generate and analyse next generation sequencing data for an economically important plant pathosystem with host and pathogen reference genomes available. Combining modern DNA with historical DNA isolated from herbarium specimens, you will compare patterns of past and present genetic diversity and infer evolutionary processes from these patterns. This project provides the unique opportunity of jointly analysing host and pathogen genomes to identify signatures of concerted evolution at individual genes and across the genome. The project also offers room for theory development. During your PhD, you will contribute to teaching at the Bachelor and Master level.

WHAT WE OFFER

- Cutting-edge clean-room laboratory specialised on historical/ancient DNA (aDNA) - In-house sequencing facility (Functional Genomics Center Zurich, www.fgcz.ch) - Co-supervision by experts in aDNA processing and population genomic analyses of NGS data (Prof. Dr. Dr. Verena Schünemann, Dr. Simon Aeschbacher) - Access to a network of herbarium curators across Switzerland - Training and networking opportunities, collaborative and integrative research environment, social events (www.evolution.uzh.ch) - Enrolment in Life Science Zurich Graduate School (www.lifescience- graduateschool.uzh.ch) - Working place at UZH Irchel Campus with outstanding research infrastructure, sports and catering facilities, recreational areas, and excellent links to public transport and Zurich Airport - Full-time employment with PhD salary according to the guidelines of UZH, an equal opportunity employer - The vibrant city of Zurich with a wide range of cultural and educational institutions, located at Lake Zurich and at the foot of the Swiss Alps

WHAT WE EXPECT

We are looking for a candidate with a background in ancient DNA research and a MSc degree in a relevant discipline. Candidates for this position must bring:

- Prior experience with ancient DNA processing for next-generation sequencing (NGS) technologies (tissue sampling, extraction, clean-room laboratory procedures, library preparation) - Willingness to travel internationally, visit numerous herbaria, and organise these trips independently - Good skills in spoken and written English - Good team working and communication skills

Basic bioinformatics skills (read processing, read alignment, variant calling) and experience in NGS data analyses (e.g. phylogenetic or demographic inference) are highly desirable, but not a must.

HOW TO APPLY

To apply, please send a single PDF containing a letter of motivation written in English, a CV, two letters of recommendation, and a transcript of your latest academic degree (if applicable) to Ursina Tobler (ursina.tobler@ieu.uzh.ch). We will start reviewing applications on 31 August 2020 und continue until the position is filled. If you have questions, please contact Verena Schünemann (verena.schuenemann@iem.uzh.ch) or Simon Aeschbacher (simon.aeschbacher@ieu.uzh.ch).

CONTACT ADDRESSES

Assistant Prof. Dr. Dr. Verena Schünemann Head Paleogenetics Group Institute of Evolutionary Medicine University of Zurich Phone +41 44 635 05 60 E-mail: verena.schuenemann@iem.uzh.ch

https://www.iem.uzh.ch/en/research/paleogenetics_group_schünemann Dr. Simon Aeschbacher Independent Group Leader Department of Evolutionary Biology and Environmental Studies University of Zurich Phone +41 44 635 49 72 E-mail: simon.aeschbacher@ieu.uzh.ch https://www.ieu.uzh.ch/en/staff/member/aeschbacher_simon Simon Aeschbacher <saeschbacher@mac.com> Simon Aeschbacher <saeschbacher@mac.com>

ZHAW Switzerland ComputationalCancerGenomics

2 PhD positions in Computational Cancer Genomics

ZHAW Wädenswil, Switzerland

Colorectal cancer (CRC) is one of the most frequently diagnosed cancers world-wide. Despite decades of research, 5-year survival for CRC patients is only 60%, and there exist few molecular biomarkers and treatment options. We are looking for PhD students who will conduct research in the framework of a collaborative SNSF Sinergia project "Trans-omic approach to colorectal cancer: an integrative computational and clinical perspective".

The successful candidates will work as part of Applied Computational Genomics Team lead by Maria Anisimova at the Institute of Applied Simulations, Zurich University of Applied Sciences (ZHAW Wädenswil) and will have a second affiliation to the University of Zurich. The group is also part of Swiss Institute of Bioinformatics, which provides additional training and networking opportunities.

The overall aim of the project is to improve colorectal cancer patient stratification, prognosis and treatment prediction using an integrated approach to trans-omic data.

In our group the PhD candidates will develop methodology to detect tandem repeat biomarkers based on fundamental principles of molecular evolution and our previous work (For example, see Schaper, Gascuel, Anisimova (2014) "Deep Conservation of Human Protein Tandem Repeats within the Eukaryotes" Mol Biol Evol, https://doi.org/10.1093/molbev/msu062)

The collaboration is between ZHAW, University of Bern, ETH Zurich and IBM.

The candidates will also contribute within the EU COST Action CA17118 and MSCA RISE network: https://refract-rise.eu Profile requirements:

MSc degree in bioinformatics, computational biology, computational science, statistics, or similarWorking knowledge of programming languages such as Python, C++ Some knowledge of phylogenetics and modeling molecular evolution is as advantageActive research attitudeExcellent presentation and communication skills

Duration: 4 years

Starting date: October 2020, but is flexible

To apply please send an email with the title "CRC-TRs" to maria.anisimova@zhaw.ch

Your application should be in one pdf file including your CV and letter of motivation.

"Anisimova Maria (anis)" <anis@zhaw.ch>

Jobs

ComplutenseU Madrid 3 EvolutionaryBiology

The Complutense University of Madrid has announced 43 permanent positions for candidates with Spanish I3 certification. Candidates need to possess the I3 certification and an accreditation for teaching at Spanish Universities (Contratado Doctor or higher) in order to be eligible. Details of the call are available here:

https://www.ucm.es/investigadores-i3-2020 The research group Evolutionary Biology and Conservation (www.ucm.es/bcveng) will support competitive candidates, as it has done successfully in previous editions of this and other programs directed to the attraction of talented researchers. Our Department (Biodiversity, Ecology and Evolution) is allowed to support three proposals, so that candidates will need to be prioritised before the call closes.

We are looking for candidates who can send us their proposals as soon as possible. Prospective candidates please send the following documents to jperez@ucm.es asap, and no later than June 17, 2020:

- Curriculum Vitae (preferably CVN format, see https://cvn.fecyt.es/). - ANECA Certificate of Accreditation (highest category awarded). - Spanish I3 Certification.

Best regards Javier Perez-Tris

JAVIER PEREZ TRIS <jperez@bio.ucm.es>

Copenhagen Oxford QuantGenetics

JOB ANNOUNCEMENT

Senior Quantitative Geneticist / Breeding Specialist

Locations: Copenhagen (Denmark) or Oxford (UK) Type: Full-time, permanent Deadline: 10 July 2020

Synomics aims to transform the efficiency of the agri-food industry by improving animal and crop production efficiency, and the economics and sustainability of the entire production value chain for multiple species. Our platform is a revolutionary advance in the analysis of high-throughput genotypic, phenotypic and environmental data to accurately measure and analyse protein production efficiency, health, accelerate genetic progress, and deliver more sustainable protein production from animals and plants. We're rapidly growing AI enabled genomics, breeding and precision agriculture company with global ambition and partnerships with some of the largest international livestock and plant breeding companies and research institutes. We are located in the city of Copenhagen, Denmark and near Oxford, UK.

We are expanding fast and have yet another job opportunity for a permanent full-time position as Senior Quantitative Geneticist / Animal Breeding Specialist to join our team at Synomics Ltd (UK) or Synomics ApS (Denmark) directly reporting to our CTO, Professor Haja Kadarmideen. The ideal candidate will have strong expertise and experience in quantitative genetics, statistical genetics, genomic prediction / genomic selection in animal breeding and large-scale genome-phenotype association studies (GWAS) using standard as well as new computational tools (e.g. AI/machine learning). Experience in breeding program designs and net merit indexes utilizing genomics (e.g. SNP, haplotypes etc) to make faster genetic gain would be an advantage.

The main responsibilities will involve identifying and interpreting novel associations within large, multi-dimensional mainly animal and poultry phenotypic, pedigree and genetic / genomic datasets but may also involve crop & aquaculture species. The ideal candidate will have a keen interest in creating insight and value from complex data from animal breeding organizations and agri-biotechnology companies, a good knowledge of animal science/biology and a passion for identifying and answering questions that help us solve real-world problems and build the best products. This is an exciting opportunity to help shape the direction of the business as a senior member of the rapidly growing team.

To know specific details of this position with respect to responsibilities, key requirements, key Attributes, relevant work permit requirements, what we offer etc, please go to: https://github.com/Synomics/jobvacancies and download the relevant job description matching with job title / reference ID. To apply, please submit cover letter, your CV, and publication list (if relevant) to jobs@synomics.ai

DEADLINE FOR ALL APPLICATIONS: 10 July 2020 (position is available for immediate start after interview)

Synomics is a new portfolio company of Wheatsheaf Group Ltd and it has a close collaboration with PrecisionLife Ltd. Wheatsheaf Group directly operates, invests in and helps to develop businesses in the food and agriculture sectors. PrecisionLife is an AI enabled precision medicine company, which is ISO27001 accredited, committed to equal opportunities and operates a carbon neutral business. To learn more, visit: http://www.synomics.ai/, https://www.wheatsheafgroup.com/ and https://precisionlife.com/ . Haja Kadarmideen <haja@synomics.ai>

GeorgiaTech ScienceCoordinator-ViralEcologyEvolution

Scientific Project Coordinator and Data Communications Specialist Viral Dynamics, Ecology, and Evolution Prof. Joshua Weitz School of Biological Sciences Georgia Institute of Technology Atlanta, GA, USA

screening of applications to begin June 22, 2020

A full-time position in scientific project coordination and data communication (2 years, with possibility of extension) is available in Prof. Joshua Weitz's group in the School of Biological Sciences at the Georgia Institute of Technology. This new position will help advance the group's research efforts to understand how viruses transform human health and the fate of our planet.

The coordinator will lead efforts to manage multiple extramurally funded collaborative projects, coordinate research activities with a network of national and international collaborators, communicate data, models, and software, develop platforms and initiatives to engage with the scientific and broader community, develop and implement strategic plans for fostering team science, and support early career development as part of an interdisciplinary research group.

Preferences for applicants include: (1) PhD/MS degree in biosciences, ecology, evolutionary biology, physics, applied mathematics, computing or related area; (2) Excellent communication skills, including experience writing, proofing, and editing science communication materials, web content, and other related documents; (3) Demonstrated organizational skills, including project management experience. Candidates with graduate degrees in related fields (PhD or MS) preferred, but not required; candidates with B.S. degree and relevant professional work experience in scientific project coordination will also be considered.

Position available as of August 2020, start date negotiable, includes competitive salary, benefits, and budget for professional development. To apply, please e-mail Joshua Weitz (jsweitz@gatech.edu) with a resume, a one page statement of how your professional interests are related to this position, and contact information for 3 references. Screening of applications will begin on June 22, 2020 and continue until position is filled.

More information on the group's research can be found at https://ecotheory.biosci.gatech.edu/. Georgia Tech is located in Atlanta, GA in the Midtown neighborhood - a vibrant, urban community: http://www.midtownatl.com/ . Georgia Tech is a unit of the University System of Georgia and an Affirmative Action/Equal Opportunity Employer.

Professor, School of Biological Sciences Courtesy Professor, School of Physics Director, Interdisciplinary Graduate Program in Quantitative Biosciences Georgia Institute of Technology 310 Ferst Dr. Atlanta, GA 30332

email: jsweitz@gatech.edu phone: 404-385-6169 office: Cherry Emerson 219 group: http://ecotheory.biology.gatech.edu/ web: http://www.biology.gatech.edu/people/joshua-weitz twitter: @joshuasweitz & @QBioS_GT QBioS PhD: http://qbios.gatech.edu viral ecology book: http://press.princeton.edu/titles/10642.html

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KULeuven EcolEvolGenomics

Assistant/Associate Professor in Ecological and Evolutionary genomics at KU Leuven, Belgium

The Division 'Ecology, Evolution and Biodiversity Conservation' at the Department of Biology at the KU Leuven (Belgium) is seeking candidates for a faculty position in Ecological and Evolutionary genomics starting 1 October 2021.

We encourage applications by outstanding candidates with a research program at the intersection of ecology and evolution which addresses fundamental research topics using a genomics toolbox with aquatic organisms. The successful candidate will be expected to build her/his own independent research group and further integrate and strengthen collaborations across research groups within the Division. The new faculty member will also have responsibility for part of the teaching in ecology, evolution and genomics.

After a pre-selection step by the Division, the successful candidate will be expected to continue the selection procedure at the university level for one of the two 'BOFZAP' categories of research professorships: junior BOFZAP for a researcher with high research potential proven by internationally recognized scientific publications, or Senior BOFZAP for a highly internationally recognized researcher in the field. A key selection criterion for BOFZAP positions is excellence in research reflected in both the scientific achievements and the research plan for the next five years. We aim for candidates with a research profile at the level of successful ERC applicants. Candidates should master up-to-date molecular and bioinformatic methods. Candidates are expected to teach students at all academic levels, including supervision of PhD students and postdocs. Candidates will be appointed in an academic staff position (ZAP) with a rank depending on the candidate's qualifications. BOFZA P researchers receive a BOF start-up grant. In addition the department of Biology provides a PhD fellowship of 4 years.

Information about the Division 'Ecology, Evolution and Biodiversity Conservation' can be found at https://bio.kuleuven.be/eeb. KU Leuven is a research-intensive, internationally oriented university that was elected Europe's most innovative university by Reuters and consistently ranks and features in Europe's top-15 universities within the Times Higher Education ranking < https://www.timeshighereducation.com/world-university-rankings/ku-leuven#ranking-dataset/589595 >. Leuven is a historic, dynamic and lively city located in the heart of Belgium, within 20 minutes from Brussels, the capital of the European Union, and less than two hours from Paris, London and Amsterdam.

For the pre-selection step by the Division please submit a motivation letter (max. 1 page), short CV (max. 2 pages), a scientific achievements track-record (max. 2 pages) including a list of five most important publications, and a first outline of a research plan for the coming 5 years (max. 2 pages). Please refer to potential collaborations within the Division in your research plan.

Questions can be directed to the Head of the Division, Professor Robby Stoks (robby.stoks@kuleuven.be). The application must be sent as a single PDF by email to Conny.coeckelberghs@kuleuven.be with as subject 'Eco-Evo Genomics faculty position'. The closing date for applications is June 25th 2020.

robby.stoks@kuleuven.be

KU Leuven ModellingComplexAdaptiveBiolSystems

"Modelling Complex Adaptive Biological Systems" https://www.kuleuven.be/personeel/jobsite/jobs/55653422 Complex systems science has been able to successfully describe and characterize a swathe of phenomena in biology, from the wiring of neurons in the brain to the structure of gene regulatory networks encoding phenotypic traits, or from the emergence of self-organized collective behaviour in animal societies to explaining complex ecosystem dynamics.

Recent work, however, has shown that these complex biological systems can only fully be understood by treating them as complex adaptive systems and as the outcomes of an evolutionary process that has shaped them through selection in complex environments.

This paradigm shift led to the development of a number of subfields in the study of complex systems, such as evolutionary systems biology, which aims to explain evolved features of gene regulatory networks, including their modularity and robustness, and which also considers the origin of complex genotype-phenotype mappings, eco-evolutionary dynamics, which injects evolution into ecological system dynamics and models the complex feedbacks between ecological and evolutionary processes and adaptive dynamics and evolutionary game theory, which model evolutionary dynamics in explicit ecological and social settings. In all these fields, it has been found that explicitly considering the evolutionary process can greatly help our understanding of the functioning of biological systems. Applications are numerous and range from explaining how evolution shapes the way in which microbial populations develop tolerance or resistance to antibiotics to explaining how populations or ecosystems adapt to changing or fluctuating environments, for example, in bioreactors or under the influence of global environmental change.

We are hereby advertising a full-time academic vacancy in the area of the theoretical modelling of complex biological systems at the KU Leuven. We are looking for internationally oriented candidates with strong expertise in the modelling of both ecological and evolutionary dynamics at various spatial and temporal scales and with educational competence within the field of computational ecology and evolution and/or evolutionary systems biology.

Suitable candidates could come from diverse fields, including computational ecology and evolution, complex systems science or evolutionary systems biology. We expect the candidate to develop a research program aimed at distilling common properties of complex adaptive biological systems and approach this from a highly interdisciplinary angle, involving the collaboration between evolutionary (micro)biologists, ecologists, theoretical biologists and systems biologists. Examples of questions that could be addressed are how and how fast biological systems adapt in response to changes in their environment or how robustness to environmental perturbations is created at the level of the cell, individual, population, community or ecosystem.

Ellen Decaestecker <ellen.decaestecker@kuleuven.be>

MaxPlanckInst Leipzig Archaeogenetics

Max-Planck-Institut für evolutionäre Anthropologie

Max Planck Institute for Evolutionary Anthropology
Department of Evolutionary Genetics

The "newly established" Department of Archaeogenetics at the Max Planck Institute for Evolutionary Anthropology in Leipzig (Germany) utilizes recent advances in molecular approaches on biomolecules, such as genome wide DNA sequencing, to uncover an entirely new spectrum of information that can be retrieved from sample repositories such as anthropological and archaeological collections.

In the context of the ERC Synergy Grant HistoGenes the department is seeking to fill the position of a Research Group Leader in Population Genetics (E15 100 %) with a start date as soon as possible.

Job Description We seek to fill a position at the level of a research group leader with a focus on large-scale human population genetics integrating comprehensive data sets from ancient human remains with modern reference data in an archaeological and historical context. The research group will reside within the ERC Synergy Grant HistoGenes1. This project aims to study the population shifts related to cultures such as Pannonians, Romans, Goths, Huns, Longobards, Gepids, Avars, Bulgars, Slavs and Franks in the Carpathian Basin in 400-900 CE. HistoGenes will analyse ˜6,000 ancient human samples from this region with cutting edge scientific methods and contextualize the interpretation of these data in their archaeological and historical setting. This will, for the first time, unite historians, archaeologists, geneticist, anthropologists, and specialists in bioinformatics, isotopic analyses and other scientific methods not only to advance our knowledge about this key period in European history, but also establish new standards for the historical interpretation of genetic data. The established group will operate in a close multidisciplinary network with non-geneticists, and communication within such a team is an important part of the project in order to fully contextualize and interpret the genetic data.

For the advertised position strong bioinformatics skills and literacy in related statistical methods are a requirement, in particular rare variant analysis, haplotypebased methods and SNP based approaches are wanted. The ideal candidate will have a PhD in a relevant discipline (bioinformatics, computer science, mathematics, population genetics, etc.) as well as extensive postdoctoral experience in those fields. The candidate has ideally worked in the field of ancient DNA before. Furthermore, strong competency in supervising and mentoring students is desirable. This is a full-time three-year contract position at a pay scale of TVoD E15, in accordance with the German pay grade system for public employees. The position can be extended to six years in total.

1 https://www.shh.mpg.de/1514048/histo-genes-erc-synergy-grant Your application

The Max Planck Society is committed to employing individuals with disabilities and relevant candidates are encouraged to apply. The Max Planck Society also seeks to increase the number of women in areas where they are under-represented and therefore explicitly encourages women to apply. Your application should include a curriculum vitae (stating previous academic performance indicators, publication history, and prior research and supervision experience) and a cover letter outlining in detail your qualifications, suitability for the position, and interest in working with our team.

Please submit your application in English via our online application platform (https://www.eva.mpg.de/career/-positions-available.html) and add three references (letter of recommendation). The deadline for submission of these letters is the same as the one for the applications.

Applications will be accepted until July 31.2020, but the position could be filled before.

For more details on the research program please contact: Prof. Johannes Krause, E-mail: krause@eva.mpg.de Dr. Alexander Herbig, E-mail: herbig@shh.mpg.de (For more details on the application process please contact: Stefanie Schmischke, E-mail: stefanie_schmischke@eva.mpg.de)

Information regarding the Max Planck Institute for Evolutionary Anthropology can be found at: https://www.eva.mpg.de and https://www.eva.mpg.de/-archaeogenetics/index.html Stefanie Schmischke <stefanie_schmischke@eva.mpg.de>

NorthCarolinaStateU GeneticsGenomicsDirector

https://www.nature.com/naturecareers/job/genetics-and-genomics-initiative-ggi-director-north-carolina-state-university-ncsu-726822 "North Carolina State University is seeking applicants for the Directorship of our Genetics and Genomics Initiative (GGI). With strong support at the university and college levels, this new initiative has brought together a collaborative research community with expertise that spans the breadth of genetics and genomics. Our 150+ affiliated GGI faculty are members of seven of the university's twelve colleges. They conduct experimental and theoretical genetics and genomics research that spans multiple dimensions, from chemical to organismal scales. Their research organisms include a diversity of microbes, plants and animals. Specific projects range from those aimed at expanding basic knowledge to others that address health, agriculture, and environmental issues."

(There's more at the link.)

–henry schaffer

Henry Schaffer <hes@ncsu.edu>

OklahomaStateU ResAssist FossilReconstruction

This advertisement is to fill a position working with a team of vertebrate paleontologists and evolutionary/comparative anatomists at Oklahoma State University in Tulsa. We are looking for a technician (Bachelor's or Masters Degree) to assist with 3D imaging and reconstruction of fossils and modern comparative vertebrates. This position will support 4 faculty members with diverse imaging projects focused on deep-time macroevolution, alpha taxonomy, phylogenetic comparative methods, ecomorphology, and functional anatomy/biomechanics.

Experience with 3D imaging (SlicerMorph, Avizo/Amira, Dragonfly, VGStudio, etc.) required.

Req ID:

req7816

Position Title:

Research Assistant

Position Type:

Staff Full-Time

Position Number:

533708

OSU Campus:

Center for Health Sciences - Tulsa

Department:

Anatomy and Cell Biology

Location Address:

1111 W 17th St Tulsa, Oklahoma, 74107 United States

Hiring Supervisor:

Hiring Range: (Contingent upon available funding):

15.38 - 17.31, Hourly

Work Schedule:

Typically 5 days/week, 8 hours/day

Faculty Appt Period:

Job Summary:

The Research Assistant will work in the Anatomy and Cell Biology department of OSU Center for Health Sciences. The Research Assistant will maintain the active volunteer department by overseeing and assisting with various projects being conducted. The Research Assistant will conduct and facilitate scientific research and outreach in support of the Translational Anatomical and Biomedical Imaging Laboratory within the department.

Environmental Hazards: May assist with microCT scanning with fully-X-ray shielded machined (0.000001 Seivert radiation exposure)

Physical Requirements: Ability to lift and carry 8-10 pounds, stoop, reach, stand, walk, finger, grasp, feel, talk, hear, see, and perform repetitive motions with or without reasonable accommodations.

(If you are viewing this job posting outsideof the actual OSU job application website, please go to jobs.okstate.eduto apply and submit a resume.)

Special Instructions to Applicants

Oklahoma State University, as an equal opportunity employer, complies with all applicable federal and state laws regarding non-discrimination and affirmative action. Oklahoma State University is committed to a policy of equal opportunity for all individuals and does not discriminate based on race, religion, sex, color, national origin, marital status, sexual orientation, gender identity/expression, disability, or veteran status with regard to employment, educational programs and activities, and/or admissions. For more information, visit http://eeo.okstate.edu . Education & Experience

Position Qualifications:

Required: - Bachelor's degree in Biology, Zoology, and/or Radiology with a focus in anatomy - Prior experience in 3D imaging lab reconstructing anatomical structures is desirable; experience concurrent with or as part of the degree is acceptable

Preferred: - Master's degree - Skills in finite element analysis, computational fluid dynamic analysis, geometric morphometrics, and/or soft-tissue contrast enhancement

Haley D. O'Brien, PhD

Assistant Professor Department of Anatomy and Cell Biology Oklahoma State UniversityCenter for Health Sciences 1111 W 17th Street Tulsa, Oklahoma USA 74107-1898

"O'Brien, Haley" <haley.obrien@okstate.edu>

SGN Frankfurt LabManager Biodiveristy

Job Announcement ref. #12-20013

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. The LOEWE Centre for Translational Biodiversity Genomics (LOEWE TBG, https://tbg.senckenberg.de) focusses on the genomic basis of biological diversity and makes it accessible for basic and applied research. We study the genomic variety across the Tree of Life to comprehend the origin and functional adaptations of diversity from genes to ecosystems (Comparative Genomics). The data addresses societal knowledge demands in applied fields, such as the genomic basis of biologically active substances (Natural Products Genomics), and the sustainable use and management of biological resources (Genomic Biomonitoring; Functional Environmental Genomics). TBG has been initiated as a joint-venture by the Senckenberg Nature Research Society, the Goethe University Frankfurt, the Justus Liebig University Gießen and the Fraunhofer

Institute for Molecular Biology and Applied Ecology IME and is initially funded by LOEWE programme of the State of Hesse, Germany.

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

Lab Manager, Functional Environmental Genomics Group (full time)

The position is part of the Functional Environmental Genomics research group. The group investigates the causes and consequences of ongoing biodiversity loss. We are asking how environmental change and human impact influence the composition and functioning of ecological communities. We answer these questions by adapting and developing approaches in molecular ecology, genomics, and eDNA research. The group has two main directions: soil invertebrate communities, and eDNA-based biodiversity time series. Currently we focus on genome sequencing of tiny soil organisms in Illumina and PacBio systems, and we experiment with shotgun metagenomics of invertebrates. We expect to work with ancient eDNA and metatrascriptomics in the closer future.

Your tasks

- Set up and manage the Functional Environmental Genomics laboratory - Adapt, establish and develop methods in genomics, metagenomics, metatranscriptomics, eDNASupport the research within the Functional Environmental Genomics group - Instruct and supervise labwork of students and scientists of group - Collaborate with colleagues from TBG on diverse aspects of biodiversity genomics

You are curious and keen to experiment with new techniques. You have excellent communication skills and strive to share knowledge and experience with colleagues and scientists. You have good management skills and can handle high workload. You strive for precise and reliable work.

Your profile: - experience with diverse molecular techniques, preferentially both DNA and RNA - Excellent spoken and written English It is a plus: - Experience with high molecular weight DNA - wetlab manipulations for genomics and transcriptomics - instruction of young and fellow scientists - automated liquid handling - high throughput sample processing - metabarcoding, metagenomics, metatranscriptomics - forensics, aDNA, eDNA - qPCR - other 'omics-type techniques might be interesting - spoken and written German

What is awaiting you? - An interesting task in a dynamic team of researchers in an international research group and joining the new LOEWE excellence centre with its 20 new research groups - The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics - Flexible working hours - leave of absence due to family reasons - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt - leave of 30 days/year

Place of employment: Frankfurt am Main Working hours: Full time (40 hours/week) Type of contract: initially limited until 31. December 2021 Salary: according to the German collective agreement TV-H (pay grade E 11)

Salary and benefits are according to a full time public service position in Germany (TV-H E11). The contract should start on 15.07.2020 and will initially be limited to the end of phase one of LOEWE-TBG in December 2021. Subject to further funding and extension of the project, an extension of the employment is envisaged.

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

How to apply

Please send your application, mentioning the reference of this job offer (ref. #12-20013) until 20.06.2020 by e-mail (attachment in a single pdf document) and include a cover letter detailing your interests and experience, a detailed CV, a list of publications and copies of your certificates, transcripts and grades to:

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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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Shenzhen 40 AgrGenomics

40 Faculty positions AGIS, CAAS, Shenzhen

The Agricultural Genomics Institute at Shenzhen (AGIS) is one of the 33 national institutes under the Chinese Academy of Agricultural Sciences (CAAS). Started at Shenzhen in 2014, it focuses on genomics and big data biology as well as their applications in agriculture, food, and environment. AGIS hosts a total of

300 faculties and staffs, and has secured competitive grants with an accumulative value of 200 million RMB up to the end of 2018. Moreover, the institute has published more than 100 scientific articles in Cell, Nature, Science, Nature Genetics, Nature Methods, and other high-impact journals. AGIS aims to become an international leader of agricultural genomics and an incubator of next-generation technologies and innovative start-ups. We welcome highly competitive and skilled scientists, technological developers, and innovative entrepreneurs to join us in developing and applying innovative ideas in the fields of agriculture, environment, and food industry. We believe genomics can make our world better.

POSITIONs

Leading Talents

Youth Talents

Benefits and Supporting Funds

1. Grants:

PI can receive research grants of more than 4 million RMB including 3-7.5 million research start-up funds, 1-3 million equipment funds and 1-5 million overseas talent funds;

Provided 60 m2of office and laboratory space;

Assisted in applying for research grants and in the recruitment of postdoctoral fellows and graduate students.

2. Benefits:

AGIS provides talents with competitive salaries, for details, please consult us.

3. Living allowance

The selected talents can receive a subsidy of 5.7 -12 million RMB including:

“Young Talents Plan” of the Chinese Academy of Agricultural Sciences: 1 million RMB for home-purchasing settling-in allowance;

“Pearl River Talent Plan” of Guangdong Province: 1.5-5 million RMB;

“High-level talents at home and abroad in Shenzhen”: 3.2-6 million RMB.

Research Field

Bioinformatics, algorithm development, biocomputing

Biochemistry and molecular biology

Genomics

Crop genetics and breeding

Animal genetics and breeding

Horticulture

Plant protection

Ecology and environmental science

Genomics for food safety

CONTACT

Add No.7 Pengfei Road, Dapeng New District, Shenzhen 518120, China

http://www.agis.org.cn Fax: +86-755-8925 2003; Tel: 0755-89252003

For more details, please contact us at

Dr. Li-Jing Bai,bailijing@caas.cn,zonghechu@caas.cn

Yongfeng Zhou <yongfez1@uci.edu>

UBasel Evolution

The Department of Environmental Sciences at the Faculty of Science of the University of Basel invites applications for a Tenure-Track Assistant Professorship in Ecology.

Your position The new Professor and her/his research group will be expected to develop and strengthen research and teaching in ecology within the Department of Environmental Sciences (http://duw.unibas.ch). Research may include community and/or ecosystem research at different spatial and temporal scales, with a focus, for example, in food-web dynamics, interaction networks, global change ecology, biodiversity research, population ecology and/or conservation biology. Particularly valued is research involving field work combined with quantitative tools and modelling.

The new professor is expected to develop a strong research program and to attract external funding, to teach both at the undergraduate and graduate levels, and to help expand and further develop the curriculum within the BSc and MSc programs in biology and geosciences.

Your profile Applicants should hold a PhD in ecology or a related field, and have a proven track record of research activities, a strong publication record and a history of externally funded research. We particularly welcome applications by candidates with knowledge and experience in a range of ecological techniques and with a demonstrated ability to combine ecological science with other environmental sciences in an interdisciplinary context. Applications from female researchers are encouraged.

We offer you The Department of Environmental Sciences at the University of Basel investigates the complex interactions between biosphere, geosphere and anthroposphere, and provides excellent research and teaching conditions in a stimulating and vibrant environment. It maintains a wide range of collaborations with other departments of the University of Basel, as well as national and international networks with other high-profile research institutes. The University of Basel is an equal opportunity and family-friendly employer.

Application / Contact Applications (including a letter of motivation, CV, list of publications, statements on research and teaching interests, and three names for referees) should be sent by e-mail as one single pdf document to Prof. Dr. Martin Spiess, Dean of the Faculty of Science, University of Basel, Klingelbergstrasse 50, 4056 Basel, Switzerland / Email: dekanat-philnat@unibas.ch.

For further information on the position, contact Prof. Dr. Moritz Lehmann, Head of the Department of Environmental Sciences, University of Basel (moritz.lehmann@unibas.ch)

The application deadline is 31 August 2020.

www.unibas.ch Prof. Dr. Walter Salzburger

Zoologisches Institut, Universität Basel Vesalgasse 1, 4051 Basel, Switzerland

phone: +41 (0) 61.207.0303; fax: .0301 eMail: walter.salzburger@unibas.ch web: http://www.salzburgerlab.org fb: http://www.facebook.com/waltersalzburgerlab Walter Salzburger <walter.salzburger@unibas.ch>

UCalifornia Davis Manager PopulationGenomics Programs

Job Title: Scientific Program Manager

Location: University of California, Davis in Davis, CA USA

Job Summary:

Under general direction of the Principal Investigator, develop, implement and provide ongoing scientific expertise, direction and management of multiple, large and complex, international scientific research programs impacting the overall success of a multi-campus, interdepartmental, global health malaria research project in selected field sites in Africa (specifically the Union of the Comoros and the Republic of Sao Tome and Principe). Assist and support the PI in planning and coordinating the scientific research aspects of the program and will work directly with individual post-doctoral researchers in ensuring the timely completion of individual components of the research agenda. Identify program objectives and strategies, manage very significant human, financial, and physical resources, and will function with a high degree of autonomy. Manage program timelines and deliverables, develop written reports, scientific papers, and presentations, and represent the program for diverse audiences. Collaborate, and work in partnership with, the Engagement Program Manager and Field Station Manager(s) at the African field sites. Strong background in population genomics required.

Position Information:

Salary Range: $5,683.33-$11,408.33/Month

Appointment Type: Career

Percentage of Time: 100%

Shift Hours: Monday-Friday, 8am-5pm

Location: Davis

Union Representation: No

Benefits Eligible: Yes

Apply By Date: 7/13/2020

Responsibilities:

SUPERVISORY DUTIES (60%)

- Provide scientific expertise needed to direct research projects and lab personnel.

- Work in regular collaboration and communication with Engagement Program Manager to ensure that entomology and engagement field teams are working together to achieve project goals and are adhering to project timeline.

- Hire, train and supervise staff; conduct performance appraisals; document and implement corrective actions and discipline; resolve disputes and complaints;

- Assign, supervise and monitor staff responsible for operating and maintaining the laboratory and insectary.

- Assist in the hiring and training of lab personnel.

PROJECT MANAGEMENT (30%)

- Assist in the preparation of manuscripts for publication in peer- reviewed scientific journals.

- Develop, review, and deliver presentations for diverse audiences including international stakeholders, undergraduate/graduate students, scientific researchers, international students, international communities, and public interest groups.

- Regularly communicate with scientific collaborators (national and international).

- Actively seek new funding sources to support scientific research and participate in the development of funding proposals and applications.

- Prepare regular project reports for project team and keep entire team informed about new and ongoing research programs and activities.

- Participate in the quarterly/annual review of program timeline, budget, and strategy.

- Assist in the development and review of scientific educational programs, materials, and tools for the engagement program (e.g. videos, educational booklets, and brochures) to ensure accuracy of scientific information.

- Represents the project in national and international meetings, conferences, workshops and discussions.

- Travel to field sites in Africa.

LABORATORY ADMINISTRATION (10%)

- Responsible for day to day management and operations of scientific research at the Vector Genetics Laboratory (VGL) at UCD.

- Collect, analyze and create scientific program reports and papers related to entomological field work in Africa.

- In collaboration with PI, develop written responses to published scientific work, prepare manuscripts, review manuscripts, and analyze and develop visual presentations of data.

- Analyze and review current laboratory protocols and procedures and suggest/develop improvement strategies.

PHYSICAL DEMANDS

- Remain in a stationary position, often standing or sitting for prolonged periods at a computer terminal.

- Occasionally works in outdoor weather conditions.

- This position requires travel to Africa on multiple 12+ hour long flights in economy level seating.

- Willing and able to travel regularly (domestic and international) with an understanding that there will be regular travel to field sites in Africa for up to 4-6 weeks at a time, multiple times during the year.

Work Environment:

- Moderate noise level in work environment.

- Work flexible schedule including occasional holidays and weekends on short notice to meet operational needs.

- Work in areas where hazardous materials are present.

- UC Davis is a smoke and tobacco free campus effective January 1, 2014. Smoking, the use of smokeless tobacco products, and the use of unregulated nicotine products (e-cigarettes) will be strictly

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UCalifornia Davis Tech FlowerEvolution

We –Jenny Gremer, Annie Schmitt, Sharon Strauss, and Julin Maloof– at UC Davis are looking to hire a technician to work on a collaborative project studying the evolution of the seasonal germination niche in a group of native wildflowers (Streptanthus). This is an ideal position for a recent graduate looking for research experience before graduate school.

Responsibilities include carrying out experiments in the field, lab, and controlled environment chambers, collecting field data and plant tissues, propagating plants and maintaining experimental populations. Field work will include plant surveys and collections of plant specimens and seeds. The technician will also oversee student assistants, manage databases, and perform basic statistical analyses, as well as coordinate supplies, equipment, and safety protocols.

Requirements: College-level course-work or equivalent experience/training in plant-related biological sciences or field biology. The applicant must possess excellent written and oral communication and strong organizational skills. Must be able to organize and coordinate lab, greenhouse, controlled chamber, and field research. Experience accurately recording, organizing, coordinating and curating data for analysis and reporting required, as well as skills to problem solve and trouble shoot, and ability to work independently and as a member of a research team. Research experience with plants, especially germination experiments, phenology, and field surveys preferred, as is experience using R software for data management and statistical analyses, experience working with herbarium specimens, and molecular biology lab experience working with DNA and/or RNAseq.

This is a full-time position. Starting date can be immediately or as soon as possible, with a proposed duration of one year with possibility of extension.

Application: Please go to the following link to access the UC Davis Human Resources application system and apply by June 6, 2020:

https://careerspub.universityofcalifornia.edu/psp/ucdavis/EMPLOYEE/HRMS/c/HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=HRS_APP_JBPST&JobOpeningId=7869&PostingSeq=1&SiteId=7&languageCd=ENG&FOCUS=Applicant Please contact Annie Schmitt (jschmitt@ucdavis.edu) and/or Jenny Gremer (jrgremer@ucdavis.edu) for inquiries or additional information.

Sharon Y. Strauss Professor, Evolution and Ecology 2320 Storer Hall, One Shields Ave., Davis, CA 95616

Sharon Strauss <systrauss@ucdavis.edu>

UCollegeLondon ResearchFellow StatisticalPhylogenetics

Research Fellow in Statistical Phylogenetics ref: 1867541

UCL Department / Division: Faculty of Life Sciences, Division of Biosciences Specific unit / Sub department: Research Department of Genetics, Evolution & Environment Grade: 7 Hours: Full Time Salary: 35,965 - 43,470 per annum (including London allowance)

Duties and Responsibilities

Working in Professor Ziheng Yang's group at University College London, the post holder will work on a project developing statistical methods and computer software to estimate species divergence times integrating information in genomic sequence data and in the fossil record and morphological characters. The project involves close collaborations with Dr Mario dos Reis of Queen Mary University London and Professor Philip Donoghue of the University of Bristol.

The successful candidate will participate in the development of Bayesian inference methods and implementation of computer software for analysing genomic sequence and morphological character data integrating information from genomic sequences, the fossil record, and morphological characters. They may be expected to design and implement computational algorithms, conduct simulation, compile and analyse genomic datasets, and writing up the results for publication in international peer-reviewed journals. For a sample of our recent work in this area, please see dos Reis, et al. (2016. Nat. Rev. Genet. 17:71-80), Warnock et al. (2017. Proc. R. Soc. Lond. B 284:20170227), Morris, et al. (2018. PNAS 115:E2274-E2283), and Alvarez-Carretero, et al. (2019 Syst. Biol. 68:967-986).

The post is funded by the BBSRC for 24 months in the first instance.

Key Requirements

We seek a research scientist with expertise in computer programming (such as C, R, and Python), Bayesian inference (MCMC), and molecular phylogenetics.

A PhD (or working towards a PhD) in one of the following areas is essential: computational statistics, computer science, molecular evolution and phylogenetics, and evolutionary and population genetics. Individuals with a biology PhD are invited to apply if they can demonstrate strong statistical/computational skills. Ability to work in a multi-disciplinary collaborative environment is essential, as is fluency with UNIX/Linux. A proven track record of effective research will be required.

Please note: Appointment at Grade 7 is dependent upon having been awarded a PhD; if this is not the case, initial appointment will be at research assistant Grade 6B (salary 31,479-33,194 per annum) with payment at Grade 7 being backdated to the date of final submission of the PhD thesis (including corrections).

Further Details

Full details on the role and the person specification can be accessed at the bottom of this page. Please ensure you read these carefully before applying for the post. Your application should include: a brief personal statement (within two pages), explaining how your qualifications and experience make you a good candidate for this job, a CV and names and email addresses of two referees.

For informal queries on the role please contact Professor Ziheng Yang FRS at z.yang@ucl.ac.uk.

For any queries regarding the application process, please contact Biosciences Staffing on biosciences.staffing@ucl.ac.uk and quote the reference 1867541

To apply for the vacancy please follow the link below: https://atsv7.wcn.co.uk/search_engine/jobs.cgi?amNvZGU9MTg2NzU0MSZ2dF90ZW1wbGF0ZT05NjUmb3du
1867541&vt_template=965&owner=5041178&ownertype=fair&brand_id=0&job_ref_code=1867541&posting_code=224

Closing Date: 2 July 2020

Ziheng Yang <z.yang@ucl.ac.uk>

UGreifswald NervousSystemEvolution

Research Assistant/PhD student - evolution of arthropod nervous systems

Job advertisement 20/Wi20

At the University of Greifswald's Zoological Institute and Museum in the Faculty of Mathematics and Natural Sciences, there is a job vacancy that is expected to be available as soon as possible, subject to budgetary regulations, for a part-time (65 %)

Research Assistant.

The fixed term contract is for a period of three years. Payment shall be made in accordance with pay group 13 TV-L Wissenschaft.

The position is made available as part of the DFG-funded project 'Evolutionary specialisation of neuronal core circuits in arthropod olfactory systems: structure and function of convergence/divergence in crustaceans versus insects' as part of the priority programme SPP 2205 'Evolutionary Optimisation of Neuronal Processing'. In a team that includes colleagues from the Max Planck Institute for Chemical Ecology in Jena and the University of Cologne, this project will analyse the evolution of neuronal core circuits in the central olfactory pathway of arthropods. The applicant will use techniques such as immunohistochemistry, classical histology and imaging techniques such as confocal laser-scan microscopy as well as connectomic approaches. As part of the multi-disciplinary project, this data will ultimately be integrated into a mathematical model of information processing in the olfactory system.

Job Description: - Neuroanatomical studies on the arthropod olfactory system at cellular and synaptic levels. - Hypothesis-driven literature and data research on the above- named topic. - Publication of articles written in English in internationally renowned journals. Tasks will be assigned that are also conducive to the preparation of a doctorate.

Job Specification: We are looking for a highly motivated candidate with above-average qualifications, enthusiasm for and experience in research, and willingness to play an active role in an interdisciplinary project. The candidate requires: - a university degree (M.Sc. or equivalent) in biology, zoology, neurobiology or a related experimental bioscience - Excellent knowledge of morphology, neurobiology and neuroanatomy, preferably of arthropods - Very good knowledge of histological and microscopic techniques, in particular 3D reconstruction, immunohistochemistry, fluorescence microscopy and confocal-laser scan microscopy - Experience in electron microscopy - very good knowledge of the data processing with 3D reconstruction software. - very good command of both written and spoken English for preparing scientific publications and presenting research results at international congresses - motivation to play an active role in an interdisciplinary research environment

The position is open to all persons, irrespective of gender.

The University would like to increase the proportion of women in areas in which they are underrepresented and thus applications from women are particularly welcome and will be treated with priority if they have the same qualifications and as long as there are no clear reasons which make a fellow applicant more suitable.

Severely disabled applicants with the same qualifications will be considered with preference.

In accordance with ç 68(3) PersVG M-V, the Staff Council will only be involved in staff matters of the academic or artistic staff on request.

Please only submit copies of your application documents as they cannot be returned. Unfortunately, the application costs (e.g. travel expenses for interviews) will not be reimbursed by the state of Mecklenburg-Vorpommern.

Applications with all usual documents must be sent with reference to the job advertisement number 20/Wi20 by 30/06/2020, preferably via email (one PDF file), to:

Universität Greifswald Zoologisches Institut und Museum Herrn Prof. Dr. Steffen Harzsch Professur für Cytologie und Evolutionsbiologie Soldmannstrasse 23 17489 Greifswald

Steffen.Harzsch@uni-greifswald.de

sharzsch <sharzsch@uni-greifswald.de>

ULyon BioinformaticsGenomics

A Full Professor position is susceptible to open early 2021 in the Laboratoire de Biométrie et de Biologie Ãvolutive (LBBE, UMR 5558 CNRS, Université Lyon 1). The profile being currently contemplated is given below (the definitive profile will be notified upon the opening of the call, early 2021). Any person interested is invited to contact nicolas.lartillot@univ-lyon1.frat their earliest convenience.

Models, algorithms and machine learning in bioinformatics and in genomics.

Biology is currently undergoing a major technological and conceptual revolution. This shift in paradigm is stimulated by the production of massive amounts of data, which open new perspectives on complex processes at the molecular, cellular, population or macro-evolutionary scales. In turn, these ongoing developments call for an increased integration between data analysis, stochastic modeling, statistical and machine learning, algorithmics and computer science.

In this context, a Full Professor position is susceptible to open early 2021 in the Laboratoire de Biométrie et de Biologie Ãvolutive (LBBE, Université de Lyon, France), for a teaching and a research activity in the fields of mathematics, statistics and/or algorithmics, such as applied to bioinformatics and genomics. A minimum of 5 years of service as a lecturer, and with the corresponding experience in teaching and supervising of MSc and PhD students, is typically expected. Owing to the specific challenges raised by the inherently multi-disciplinary nature of bioinformatics, a special emphasis in the recruitment will be put on the ability of the candidate to develop and promote an ambitious strategic and pedagogical perspective concerning the place of mathematics, statistics, computer and data sciences in the teaching programs and the current research in bioinformatics.

Teaching. Teaching will be primarily targeted to the bioinformatics master, with additional teaching effort also devoted to the local undergraduate and graduate programs of biosciences, ecology and health. In this context, the person recruited will have much freedom in the design of innovative courses in mathematics, statistics, stochastic modeling and/or algorithmics applied to bioinformatics and genomics. She/he will also have the opportunity to participate in the development of new multi-disciplinary programs, in partnership with the math and computer sciences departments of the university. Of note, some of the courses (in particular undergraduate programs) will have to be given in french (within two years after recruitment).

Research. The person recruited will be affiliated to the LBBE, where she/he will have the opportunity to develop a research project with a strong theoretical and methodological component, in relation with stochastic modeling and data analysis in bioinformatics, evolutionary, molecular or cellular biology. Her/his research activity may pertain to a broad range of themes, including: methods, algorithms and stochastic models applied to multi-omics; machine learning, AI and deep learning applied to the analysis of molecular and functional data; models and methods in population genetics, evolutionary or statistical genomics. Finally, the methodological research developed by the person recruited in the context of the present call may also happen to meet some of the current needs in ecology, evolution and health sciences, and as such, offer an opportunity for a broad range of possible collaborations within the host laboratory.

LARTILLOT NICOLAS <nicolas.lartillot@univ-lyon1.fr>

UMiami TropicalEvolution

Aresty Endowed Chair in Tropical Biology (Associate Professor 'V Professor)

The University of Miami' Âs Department of Biology < https://biology.as.miami.edu/ > invites outstanding tropical ecologists to apply for the Aresty Endowed Chair in Tropical Ecology. The ideal candidate will contribute to the Department's research strengths investigating the ecology and evolution of tropical systems. In addition to being outstanding, internationally recognized scientists, applicants must be excellent teachers with strong commitments to undergraduate education. Tropical fieldwork must be an integral component of an applicant' Âs research program. This prestigious chair includes a discretionary annual budget to support research. Applications will be considered at the Associate and Full Professor ranks.

Interested applicants must apply online: https://-umiami.wd1.myworkdayjobs.com/UMFaculty . Inquiries should be directed to the Search Chairs at: arestyfacultysearch@miami.edu.

We welcome applications from candidates who would enhance and complement our existing departmental programs in Biodiversity & Global Change, Development & Disease, Neuroscience & Behavior, and Microbiome Biology & Species Interactions. To be eligible for this tenure-track appointment, candidates must hold a Ph.D., and have a strong record of research accomplishments and research funding. The successful candidate will be expected to maintain a vigorous, externally funded research program, to teach at both the undergraduate and graduate level, to regularly teach an off-campus undergraduate field course in the tropics, and be committed to mentoring that supports diversity and inclusion. Applicants should submit a cover letter describing the interactions they foresee with existing research programs in the Department of Biology or other units at the University of Miami and a curriculum vitae online using the above link. More information about the Department and University can be found at https:/-/www.biology.as.miami.edu. To receive full attention, application materials must be received by August 15th, 2020.

The University of Miami is an Equal Opportunity Employer - Females/Minorities/Protected Veterans/Individuals with Disabilities are encouraged to apply. Applicants and employees are protected from discrimination based on certain categories protected by Federal law.

Christopher Searcy <casearcy@bio.miami.edu>

UtrechtU Biodiversity

Although the tenure track position is for an ecologist, we are looking for someone who has a keen perspective of evolutionary biology and is expected to strengthen teaching within the ecology and evolutionary biology paths.

TheEcology and Biodiversitygroup within the Department of Biology at Utrecht University is seeking a creative and forward-thinking Ecologist tocomplement and strengthen its team. You will be challenged to develop strong research links with the other members of the research group in addition to developing yourown research line within the group. Specifically, we are looking for a researcher who can bridge the gap between above and below ground ecological processes thatregulate biodiversity and functioning in our rapidly changing world. In addition, you are excited about contributing to the application of research results to the dailypractice of ecological resource management and/or nature conservation. Taking an evolutionary perspective in your research is seen as an advantage. You will beencouraged to actively seek funding for new research projects through personal, national, European and other international grant opportunities and supervise the researchof Postdoctoral Researchers, PhD candidates, Master'Âs students, and Bachelor's students. Furthermore, you have the ambition to actively participate in teaching activitiesof the group at Bachelor's and Master's levels, especially with respect to strengthening teaching within the ecology and evolution study paths.

You will start as an Assistant Professor and enter a five-year tenure track. At the beginning of the track, you will be asked to formulate a career development plan thatoutlines the goals of the track for research, teaching and personal development. Upon a positive evaluation, you will be awarded a permanent position.

Qualifications, to excel in this role, you are

- a terrestrial Ecologist with affinity for evolutionary perspectives;

- someone with the ability to link above and below ground processes and interactions that regulate biodiversity;

- willing to collaborate with stakeholders to apply research results in ecological resource management and/or nature conservation;

- the type of Researcher who is open to intense collaboration with fellow staff members, especially within theUtrecht University Biodiversity and Climate VariabilityExperimentexternallink(UU BioCliVE);

- an enthusiastic and creative educator who is able to strengthen the UU'Âs curriculum in ecology and evolution. We ask that you acquire a Basic Teaching Qualification if you do not already have one.

What do we offer:

- a full-time tenure track position for 5 years which will be subject to a mid-term evaluation after approximately 2.5 years and an end-term evaluation. If evaluations arepositive after 5 years, the position becomes permanent;

- a full-time gross salary - depending on previous qualifications and experience - ranging between pounds 3,746 and pounds 5,127 (scale 11 at the level of Assistant Professor(universitair docent; UD) according to the Collective Labour Agreement Dutch Universities (cao)) per month;

- benefits including 8% holiday bonus and 8.3% end-of-year bonus;

- a pension scheme, partially paid parental leave, andflexible employment conditionsexternallinkbased on the Collective LabourAgreement Dutch Universities.

- the research group is dedicated to provide you with necessary support on all aspects during the tenure track period, including appropriate training and mentorship.

In addition to the employment conditions laid down in the cao for Dutch Universities, Utrecht University has a number of its own arrangements. For example, there areagreements on professional development, leave arrangements and sports. We also give you the opportunity to expand your terms of employment yourself via theEmployment Conditions Selection Model. This way we like to encourage you to continue to grow. More information about working at the Faculty of Science can be found at:https://www.uu.nl/en/organisation/working-at-the-faculty-of-science TheEcology and Biodiversity research group(https://www.uu.nl/en/research/ecology-and-biodiversity)has the mission to understand and predict biodiversity and ecosystem functioningin a changing world. We investigate the mechanisms that regulate biodiversity and allow for the maintenance of ecosystem functioning in our changing world. We seek toobtain a process-based, mechanistic understanding of community assembly, species interactions and functional responses in order to predict the future impact of climateand land-use changes on biodiversity and ecosystem functions such as carbon sequestration, water safety and disease suppression. We pay special attention to themovement of

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UWyoming PlantEvolution

The University of Wyoming seeks to hire an outstanding Plant Evolutionary Biologist to serve as Director of the Rocky Mountain Herbarium (http://rmh.uwyo.edu). The search is open rank, and the faculty appointment will be in the Department of Botany (http://www.uwyo.edu/botany).

The Rocky Mountain Herbarium contains over 1.3 million specimens and is the largest collection of Rocky Mountain vascular plants. The herbarium has been a leader in the development of plant specimen imaging and informatics, and is poised to support new research and educational opportunities.

The Director will contribute to scholarship in the department and in interdisciplinary programs by leading a vigorous research program in plant evolutionary biology. The Director will lead the herbarium into a new era of research, education, and outreach, including providing a vision for new directions for collections-based research, building collaborations with other biodiversity initiatives at UW and with natural resource agencies, and seeking funds to support the herbarium. The Director of the RMH reports to the Vice President of Research and Economic Development, and will supervise a herbarium curator, who is responsible for managing the operations of the herbarium.

Minimum Qualifications

1. A Ph.D. in a relevant discipline 2. Record of academic accomplishment in plant evolutionary biology and management of biological collections

Desired Qualifications

1. Successful record of extramurally funded research in plant evolutionary biology 2. Expertise in herbaria and collections management 3. Exceptional vision for directing an herbarium 4. Excellent record of teaching in classroom or non-classroom settings 5. Experience in administration and fundraising for academic programs or collections 6. Experience in successful interdisciplinary collaboration and outreach 7. Prior appointment at the level of Assistant Professor or above, or equivalent within a museum or botanical garden

Required Materials Complete online application and including the following components that document the applicant's qualifications:

Cover letter

Curriculum vitae

Contact information for three references

Statement that describes the candidate's research program

Statement that describes the applicant's vision for directing the herbarium

Statement of teaching experience and philosophy

Statement that describes the applicant's commitment and ability to work with and include diverse participants in science education and scholarship

Review of applications will begin August 28th 2020 and will continue until a suitable applicant is found.

Cynthia Weinig <cweinig@uwyo.edu>

Vienna ResTech DrosophilaExptEvolution

Full-time Research Technician (40 hours/week) on polygenic adaptation in Drosophila using experimental evolution at the Institute of Population Genetics, Vetmeduni, Vienna

Two full-time Research technician (40 hours/week) positions are available in the group of Neda Barghi at the Institute of Population Genetics, Vetmeduni, Vienna. The main focus of the project is to study the genomic and phenotypic changes of Drosophila experimental populations as they adapt to a new environment. We will combine genomic, phenotypic and gene expression data.

The technicians will be responsible for maintenance of Drosophila stocks, and performing the selection experiments and high-throughput phenotyping assays. S/He will assist in developing a new protocol for maintenance of Drosophila in large populations.

We are looking for a reliable, highly organized and motivated candidate with good communication skills. S/He should have Bachelor's degree in Biology, Genetics, Molecular Biology, or a related field, and be willing to acquire new skills and contribute to the development of new protocols in Drosophila selection experiments. Excellent written and spoken English skills is a must. Experience with the Drosophila system, molecular biology and NGS library preparation is highly valued.

The positions will start September 1st, 2020 and are limited for 1-year with the possibility of extension up to 3 years depending on successful evaluation.

The gross salary is 1,994.6€/month.

In case of interest, please send your CV, including the required/desired skills for this position, to Neda Barghi (neda.barghi@vetmeduni.ac.at). You can visit the lab webpage here: https://www.vetmeduni.ac.at/en/-population-genetics/research/research-groups/barghi-lab/ Deadline for applications is June 30, 2020, but all applications will be considered immediately after receipt of the application documents.

Neda Barghi <barghi.neda@gmail.com>

Other

ArhtropodGenome Survey

It is National Insect Week in the UK. We would like to hear suggestions for high priority arthropod reference genomes that you would like to see sequenced as part of the Darwin Tree of Life project. The focus of the Darwin Tree of Life Project is to build high quality reference genomes for all 60k described species found in the UK, and we are currently working on the first 2000 species. You can read a bit more about the project at darwintreeoflife.org

Because over 1/3 of described UK species are arthropods, we would be grateful to hear from the wider scientific community as to which UK arthropod species would be most useful earliest in the project. Even if you are working on something that doesn't live in the UK, please consider nominating a closely related species to your organism if one ia found in the UK.

The survey is here: < http://www.tinyurl.com/-arthropodsurvey >

Please share with your entomology, ecology, and evolutionary colleagues.

Thank you! @darwintreelife

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 2B

mara@sanger.ac.uk

BlogWriters JournalHeredity

We are looking for eager undergrads, grad students, post-docs, faculty, scientists, and anyone interested in sci comm to highlight new papers in the Journal of Heredity, highlight recent work in other journals that is in keeping with the main aims and missions of the American Genetics Association and the Journal of Heredity, write about field work, or any other topic that fits the remit of the AGA. Blog posts are typically around 500 words, but can be longer (or shorter) depending in the topic. Interested writers should contact the AGA social media editor Stacy Krueger-Hadfield at sakh@uab.edu or Anjanette Baker at theaga@theaga.org.

Interested writers will be provided with recent J Hered papers from which to chose and the AGA social media editor will work with writers to edit their pieces. This is a great opportunity for gaining experience in Science Communication!

"Krueger-Hadfield, Stacy A" <sakh@uab.edu>

Frontiers Genetics

Frontiers in Genetics Research Topic on Scalable Bioinformatics: Methods, Software Tools, and Hardware Architectures

Guest Editors: Dr. Nikolaos Alachiotis (University of Twente) Dr. Tze Meng Low (Carnegie Mellon University) Dr. Pavlos Pavlidis (Foundation for Research and Technology - Hellas)

The field of Bioinformatics is dominated by resource-demanding kernels. This has attracted the attention of the computer engineering community to such a great extent that the well-known Smith-Waterman pairwise sequence alignment algorithm frequently serves as one of the test applications to demonstrate new engineering concepts in accelerator platforms. Yet, most performance-driven innovations for Bioinformatics problems frequently remain at the basic-research level.

This Research Topic aspires to connect computational problems in the fields of Bioinformatics and Computational Biology with software and hardware solutions from the fields of Computer Science and Computer Engineering. It is now open to receive submissions of both Original Research and Review articles that address existing challenges and present solutions.

Computational life sciences areas of interest include (but are not limited to):

- Sequence alignment - Phylogenetics - Population Genetics - Omics tools and databases - Microbes and microbiomes - Computational Epidemiology - Computational Neuroscience

Computer science and engineering areas of interest include (but are not limited to):

- Parallel and distributed algorithms - Data-aware and out-of-core techniques - Parallel computer architectures (multicore, manycore, GPU, FPGA, SoC)

Submission Deadline: October 16, 2020

URL: https://www.frontiersin.org/research-topics/13815/scalable-bioinformatics-methods-software-tools-and-hardware-architectures n.alachiotis@utwente.nl

Genes

Submit a paper in a special issue "Genome Diversity of Adaptation and Speciation"

Dear Colleagues,

A special issue is now open for submission in Genes (ISSN 2073-4425). This special issue belongs to the section "Population and Evolutionary Genetics and Genomics". https://www.mdpi.com/journal/genes/special_issues/Genome_Adaptation_Speciation Uncovering the underlying mechanisms of adaptation and speciation is perhaps the most significant quest of evolutionary science ever since the introduction of the concept in the "Origin of Species." Darwin recognized that for evolution to take place, individuals in populations had to be different from each other, and that these differences become the substrate of the divergence into different species. However, the science of his time was extremely limited in the type of diversity that could be documented. As we entered the genomics era, the situation has changed drastically: every time genome data is released for a new species, or a new sequencing technology or analytic tool is introduced, the scope of opportunities expands for exploring inter- and intra-specific variation. These new opportunities allow us to document and study the process of adaptation and speciation in a whole new way.

The process of speciation is a key aspect of understanding biodiversity. Explaining how species evolve is an essential step to reconstructing past and current biodiversity and predict its future. The availability of the genome data provides a unique window into speciation mechanisms with virtually infinite amounts of information. At the same time, recent computational developments are supplying an unprecedented power to simulations, analytic and reconstruction algorithms. Given these new opportunities, past evolutionary events that left important clues about the history of species can now be documented, interpreted, and explained. At the same time, these developments are raising new and challenging questions that require improved understanding of the underlying molecular mechanisms, evolutionary concepts, and factors to be addressed.

Whether at the level of the Tree of Life or within specific clades, the quest that evolutionary biologists now face is how to interpret the information embedded within genomes to explain biodiversity. This quest can be tackled with many different approaches that are rooted in the optimization and development of computational and analytical tools to interpret data. With a new arsenal of genomic data, bioinformatic and analytical tools, we are given an opportunity to answer pressing questions (i) on the predictions of evolutionary theory in the face of the environmental change, (ii) how mechanisms of adaptation and long-term survival are linked to the concepts of species diversity, genetic load, and extinction, and (iii) how evolutionary models can be refined to better represent the complexities of genome changes. All these questions have strong implications for conservation biology, ecosystem balance, and the genomics changes associated with the birth and death of species. We invite you to contribute to this Special Issue, which will showcase original contributions to the advancement in the genomic diversity of adaptation and speciation.

Please consider submitting to our issue.

I will be happy to answer any question regarding the issue

Sincerely yours

Taras Oleksyk

Taras K Oleksyk, Ph.D. University of Puerto Ricoat Mayaguez Mayaguez, PR 00680

taras.oleksyk@upr.edu

Genes SpecialIssue Inbreeding

Dear all,

The journal Genes (ISSN 2073-4425; IF 3.331) is preparing a Special Issue on "Inbreeding" Guest Edited by Dr. Jack J. Windig and Dr. Mirte Bosse (Wageningen UR Animal breeding and Genomics, Wageningen, The Netherlands).

In this Special Issue, we aim to bring together insights from all areas impacted by inbreeding, that is, in wild populations as well as in captive breeding settings such as livestock, pets and zoo animals. We welcome theoretical, quantitative genetic, and genomic analyses, as well as contributions evaluating the methods to mitigate the effects of small population sizes.

For further reading, please follow the link to the Special Issue Website at: https://www.mdpi.com/journal/genes/special_issues/inbreeding The submission deadline is 1 December 2020. You may send your manuscript now or up until the deadline. Submitted papers should not be under consideration for publication elsewhere. We also encourage authors to send a short abstract or tentative title to the editorial office in advance (mailto:guillem.navarro@mdpi.com).

Genes is an online, peer-reviewed, open access journal, with more than 2000 published manuscripts, indexed in major scholarly databases (SCIE, PubMed, and Scopus).— As an online open access journal, papers published in Genes receive rapid publication, immediate accessibility, and high publicity.

To support open access, Article Processing Charges (APC) of 1800 CHF currently apply to all accepted papers. For this Special Issue we are happy to offer discounts on the publication fee for all accepted manuscripts. You may be entitled to an additional discount if you have previously received a discount code or if your institute is participating in the MDPI Institutional Open Access Program (IOAP), for more information see: http://www.mdpi.com/about/ioap . For further details on the submission process, please see the instructions for authors at the journal website (http://www.mdpi.com/journal/genes/instructions).

Jack J. Windig Wageningen UR—Livestock Research Animal Breeding and Genomics PO Box 338, 6700 AH Wageningen Visiting address: Radix - Droevedaalsesteeg 1, 6708 PB Wageningen Details location: http://www.wageningenur.nl/en/show/-Radix-building-number-107.htm phone: +31 317 480543 e-mail: Jack.Windig@wur.nl internet: http://www.wageningenur.nl/en/livestockresearch —

“Windig, Jack” <jack.windig@wur.nl>

Online EvolCompGen Seminars

Dear colleagues,

The Evolution and Comparative Genomics COSI of the ISCB is organizing a webinar series (as part of the ISCBacademy). The first seminar will take place next week, Friday June 12, at 11:00AM EDT: Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies presented by Erfan Sayyari (from the team of Siavash Mirarab at UCSD). Participation is free for any member of ISCB, but registration is required. Please follow the link below. https://www.iscb.org/-iscbacademy-upcoming#sayyari The format of webinars is that abstract/papers are presented by their first author to promote presentations by young researchers, and questions and answers are exchanged throughout the presentation to value discussion and attendee input.

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

Hope many of us can you.

All the best,

Aida Ouangraoua, on behalf of the organizing committee.

“Aida.Ouangraoua@USherbrooke.ca”
<Aida.Ouangraoua@USherbrooke.ca>

PCR covid tests

dear and reputable members of the evoldir,

sorry to bug you again about this, but the covid-PCRing situation in most developing countries is truly desperate. Some countries had to stop testing all together.

They have a dire need to bypass the use of kits by using stock chemicals and enzymes.

They also need to mass-test people who work with risk groups (expected cov19+ frequency=0.0), using sample pooling to stop wasting resources with individual tests.

The pooling limits being touted so far range from 5x to ~30x. https://www.medrxiv.org/content/10.1101/-2020.03.26.20039438v1 ror https://www.thelancet.com/-journals/laninf/article/PIIS1473-3099(20)30362-5/fulltext

So please be kind, dear ancient- and forensic-DNA (and any others) wet-bench experts in evoldir, get together to generate a list of your best tricks for PCRing samples with very little target sequence. And don’t forget your stock solutions!

It should be shared with the WHO directly rather than circulated here.

It is not important if your tricks are for trace DNA, since the pooled RT step can be optimized separately (tricks for trace-RNA RT from forensists and neontologists?)..

Also tricks for samples with lots of garbage non-target

RNA and DNA are important.

And any tricks for field flash-prepping a sputum sample w/o need for subsequent cold storage? (directly dumping spit into a tube with phenol mix maybe). Like here:

https://www.bioscience.co.uk/cpl/safe-covid-19-sample-transport https://www.straitstimes.com/singapore/-transport/coronavirus-new-kit-to-allow-for-transport-of-covid-19-test-samples-at-room Again this should be shared with the WHO directly (but maybe also here?).

best

m

PS. and it would be great if anybody added comments about optimizing things for LAMP-detection in pooled samples with very little sample DNA.

https://www.conicet.gov.ar/it-was-approved-the-use-of-a-new-rapid-and-inexpensive-molecular-diagnostic-test-of-covid-19/ marcos.antezana@gmail.com

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RoyalSocPhilTransBJournal Special Issues

Collaboration in the COVID era

We all know that times are strange right now, and the lives of scientists very different from normal. For those who are missing conference travel, and the opportunity to discuss your work and build collaborations with other research groups, we would like to suggest a replacement project: why not edit a theme issue ofPhilosophical Transactions B? Each issue is carefully planned out, so is more like a book than a standard collection of related papers. The broad scope means that you are not restricted in terms of subject area, and you can be inventive with different article types. As Guest Editor, you will have the opportunity to build your network and gain editorial experience, with a high-profile Editorial Board and experienced staff to help you at every step of the way.

Read about the experience of former Guest Editorsand-download our flyer. Then, if interested, feel free to contact the Commissioning Editor,Helen Eaton, with your ideas.

Felicity Davie Royal Society Publishing

T 44 20 7451 2647

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

This email is sent on behalf of The Royal Society, 6-9 Carlton House Terrace, London SW1Y 5AG, United Kingdom.

“Davie, Felicity” <Felicity.Davie@royalsociety.org>

“Davie, Felicity” <Felicity.Davie@royalsociety.org>

Software BayesianEstimatorOfSelfing BES0 1 3

Hi,

I’m announcing the release of software called BES (Bayesian Estimator of Selfing) to estimate selfing rates from unlinked genetic data:

——— https://github.com/bredelings/-BayesianEstimatorSelfing New in version 0.1.3:

* allow using FastPhase and Phase 2 files for genetic data

* estimate the selfing rate more robustly when there are additional sources of inbreeding.

BES yields posterior estimates for the selfing rate, mutation rates, and the number of generations of selfing for each individual, as described in the following paper:

Redelings, Benjamin D., Seiji Kumagai, Andrey Tatarenkov, Liuyang Wang, Ann K. Sakai, Stephen G. Weller, Theresa M. Culley, John C. Avise, and Marcy K. Uyenoyama. “A Bayesian approach to inferring rates of selfing and locus-specific mutation.” /Genetics/ 201, no. 3 (2015): 1171-1188. https://www.genetics.org/-content/201/3/1171 -BenRI

benjamin.redelings@gmail.com

Species misidentification

Subject: Survey: Species misidentification in ecological research

Dear Recipient,

We are a research team studying species misidentification as a collaboration between Universities of Helsinki and Jyväskylä. We investigate errors in species identification in ecological studies. Thesurveyis aimed at researchers in any ecology-related field of science. The participation is voluntary and anonymous, and the answers will be used to discuss researchers' opinions about the issue in a peer-reviewed publication. Answering the questions will take 10-15 minutes, and it gives you the possibility to share your opinions and experience about species misidentification. If applicable, please forward the survey to your colleagues.

You can take the survey here (in English): https://link.webropolsurveys.com/S/2AFFC71A54DA2A30 Please do it by July01, 2020. If you encounter any difficulties or have any questions about this survey, please do not hesitate to contact us:sanja.hakala@gmail.com

We truly appreciate your participation in thesurvey.

Thank you in advance!

Species misidentification project team

"Wang, Shengyu" <shengyu.wang@helsinki.fi>

VoucheringPractics survey

Dear colleagues

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

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

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

Kindest regards

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

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

PostDocs

Barcelona 2 InsectAdaptation

Research Project The postdoctoral researcher will work on a project that aims at understanding the genetic basis of urban adaptation in Anopheles mosquitoes (BFU2017-82937-P, MINECO/AEI/FEDER, EU). Identifying the genomic basis of environmental adaptation is a growing field of research. Advances in whole genome sequencing and other high-throughput technologies allow us to identify and characterize the genes and traits more relevant for environmental adaptation. Most of our knowledge so far comes from the analysis of one type of genetic variant: single nucleotide polymorphisms (SNPs). Other types of variants such as transposable element insertions, that are complex mutations likely to play a role in adaptation, are largely ignored. Our laboratory is at the forefront of the research aimed at elucidating the contribution of transposable to adaptation. We are experts in population genomics, transposable element dynamics, and in the detection of signatures of natural selection. In this project, we will apply our proven expertise in these research fields to elucidate the role of transposable elements in adaptation in Anopheles. Adaptation to urban environments in Anopheles mosquitoes is highly relevant because it has direct consequences for the ability of these mosquitoes to transmit malaria. We are using the latest technological advances in long-read sequencing techniques to generate new reference genomes that allow us to de novo annotate transposable elements in these genomes. We will then use state-of-the-art methodologies to look for signatures of selection both in SNPs and in transposable element insertions to get a comprehensive picture of urban adaptation in Anopheles.

Duties The postdoctoral researcher will be responsible for the analysis of patterns of demography and selection in natural populations of Anopheles mosquitoes in the context of urban adaptation. Among others, the tasks involved in the postdoctoral research project will be identifying signatures of selective sweeps, identifying evidence of population differentiation, and looking for associations between genetic and environmental variables in the genome sequences of several natural Anopheles populations.

Candidate requisites A PhD in Evolutionary Biology or a related field, good organizational skills, and good writing skills are required. Previous professional experience will be considered.

What do we offer?

We offer a full-time position. Salary will depend on the experience of the candidate. The candidate will join a research team of three postdoctoral researchers and three PhD students. The lab also offers extensive networking opportunities as we are co?\leading the European Drosophila population Genomics Consortium (droseu.net) that brings together 61 research labs across 27 countries, and the Spanish excellence network in Adaptation Genomics (adaptnet.es).

Application process Please send your CV (including the contacts of potential references) and a brief letter of motivation to: josefa.gonzalez@ibe.upf-csic.es. Please include “Urban adaptation position” in the subject of your e-mail.

Application deadline: 15th June 2020.

Josefa González | CSIC Tenured Scientist Institute of

Evolutionary Biology (CSIC-UPF) Passeig Marítim de la Barceloneta 37-49/ 08003 Barcelona/ Spain. www.gonzalezlab.eu +34 932309500 ext 6058

@GonzalezLab_BCN

Co-organizer of the European Drosophila Population GenomicsConsortium(DrosEU) Science Outreach La Ciència Al Teu Mon euroscitizen.eu

melanogaster.eu

Most recent preprints/publications:T-lex3| TEs & Insecticides|DrosEU

Research Project The postdoctoral researcher will work on a project funded by the European Research Council that aims at identifying the genetic basis, the molecular mechanisms, and the functional traits relevant for environmental adaptation (H2020-ERC-2014-CoG-647900). Understanding how organisms adapt to their environments is a long-standing problem in Biology with far-reaching implications: adaptation affects the ability of species to survive in changing environments, host-pathogen interactions, and resistance to pesticides and drugs. Despite recent progress, adaptation is to date a poorly understood process largely due to limitations of current approaches that focus (i)on a priori candidate genes; (ii) on signals of selection at the DNA levelwithout functional validation of the identified candidates; and (iii) on small sets of adaptive mutations that do not represent the variability present in natural populations. As a result, major questions such as what is the relative importance of differenttypes of mutations in adaptation?, and what is the importance of epigenetic changes in adaptive evolution?, remain largely unanswered. To gain a deep understanding of adaptation, we need to systematically identify adaptive mutations across space and time, pinpoint their molecularmechanisms and

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BiologyCentre CzechAcademy PlantPhylogenomics

Postdoc:Biology.Centre.CZ.Plant.phylogenomics

Postdoctoral Position in Phylogenomics: Disentangling the Phylogeny and Evolution of Chemical Diversity in Willows

Workplace: Institute of Entomology, Biology Centre, Czech Academy of Sciences Employment relationship: Employment contract Job type: Post-doctoral Researcher Duration: 1.1. 2021 'V 30.11 2023, Fixed-term Job status: Full-time

Job description: We are looking for an enthusiastic postdoctoral researcher (max. seven years after obtaining a PhD degree) experienced in bioinformatics and phylogenomics to join our projects exploring plant-herbivore interactions and evolution of host-plant defences in willows. Using a series of complementary approaches, we aim at showing how chemical diversity in plants arises through biotic and abiotic pressures. Our studies combine field components, manipulative green-house experiments, with metabolomics and phylogenomics. The successful candidate will use WGS and RAD-seq data to reconstruct phylogenies of willow species from Europe and North America to dissect their evolution in response to the pressure of insect herbivory and abiotic factors. We expect the candidate to have an excellent background in bioinformatics and programming that will be required for developing a pipeline for handling the genomics data from both diploid and polyploid willow species. We also offer an opportunity to join our projects on the evolution of other plant genera, such as Ficus, Macaranga, and Syzygium.

Requirements: - a PhD degree - advanced skills in bioinformatics (polyploid and diploid genome assembly, RAD-locus contig assembly), phylogenomics, and programming (R, python, bash) - a deep interest in the ecology of insects or plants - fluency in spoken and written English - an ability to work independently - international experience (at least two years spent outside the Czech Republic within the last three years)

Benefits: - 5 weeks of holiday - Friendly international working environment - Subsidized lunch - Benefits from Social Fund - Support of leisure time activities - Health insurance - Budget for conferences and workshops

Other comments: The successful applicant will join the Laboratory of Evolutionary Ecology led by Dr. Martin Volf at the Institute of Entomology, Biology Center of the Czech Academy of Sciences in Ceske Budejovice (Czech Republic). The project offers an opportunity to conduct the laboratory work in the Czech Republic and abroad, within a collaborative network of our colleagues from Europe and overseas. The Department of Ecology, where our laboratory is based, is a diverse, international team (11 nationalities) studying ecology, evolution and biogeography, and a world-class centre for interaction network research with regular publications in leading journals. The Laboratory of Evolutionary Ecology is a new perspective team successful in fundraising and with a good publication record. The deadline for applications is August 5th 2020. Duration of the job contract is fixed (Jan 2021 'V Nov 2023). Applicants from all countries are eligible. To apply, please send a CV including your publication record, contact details for three references, a copy of your PhD diploma, and a cover letter stating qualifications, previous work and motivation to Dr. Martin Volf (volf@entu.cas.cz) where you can also send any queries.

Additional information: Laboratory of Evolutionary Ecology: https://www.entu.cas.cz/en/departments/-department-of-ecology-and-conservation-biology/-laboratory-of-evolutionary-ecology/ Institute of Entomology: https://www.entu.cas.cz/en/homepage/ Volf Martin <volf@entu.cas.cz>

ClemsonU PlantEvolutionaryEcology

Clemson Department of Biological Sciences Clemson, South Carolina Koski Lab

Position Details:

The Koski Lab in the Department of Biological Sciences at Clemson University seeks a postdoctoral researcher to study local adaptation in floral thermoregulatory mechanisms on an altitudinal gradient. The project involves a combination of lab-based ecological genetic studies (10mo/year at Clemson) and fieldwork in the San Juan Mountains in Colorado (2mo/year). The postdoc will examine mechanisms of differential floral thermoregulation and the impacts of floral temperature on pollen and ovule viability and plant-pollinator interactions. The postdoc will be encouraged to contribute to ongoing projects in the lab and develop new directions in the realm of plant evolutionary ecology and pollination biology. The postdoc will additional contribute to mentoring undergraduates in the lab in both research and educational outreach efforts. Support is for up to three years pending satisfactory performance after year 1. The Koski Lab and Clemson University are committed to building a culturally diverse community, and encourage applications from members of underrepresented groups in STEM.

Clemson University in upstate South Carolina on the shores of Lake Hartwell and surrounded by the Clemson Experimental Forest. It is close in proximity to the Blue Ridge mountains, as well as larger urban areas. The university hosts excellent facilities to conduct the advertised research. We have access to Clemson's Greenhouse Complex, Herbarium, Multi-User Analytical Lab and Metabolomics Core, Palmetto Computing Cluster, Light Imaging Facility, Genomics and Bioinformatics Facility, and Electron Microscopy Facility.

Qualifications:

Applicants should have a PhD in ecology, evolution, genetics, botany, or a related field; peer-reviewed publications; experience with botanical fieldwork and plant care; experience in research mentoring; and demonstrated skills in experimental design, data management, and data analysis. Basic molecular skills and proficiency with R are preferable.

Strong candidates will demonstrate the ability to work as part of a team of diverse individuals, and strong written and oral communication skills.

Application Instructions:

Applicants must submit the following: (1) cover letter, (2) a curriculum vitae, (3) a description of relevant research experience and motivation/interest in the current position (1 page maximum), and (4) contact information (including telephone numbers and e-mail addresses) for two to three professional references. Please apply at http://apply.interfolio.com/76288 Review of applications will begin June 22 2020 and continue until the position is filled.

For more information contact Matt Koski: mkoski@clemson.edu

Matthew Koski Assistant Professor Clemson University Biological Sciences https://koskimatt.wixsite.com/-matthewhkoski mkoski@clemson.edu

ColdSpringHarborLab ComputationalGenomics

ColdSpringHarborLab.PostDoc.ComputationalGenomics

Job ref. 02654-R

A postdoctoral position in COMPUTATIONAL GENOMICS is available in Dr. Adam Siepel's research group at Cold Spring Harbor Laboratory. The Siepel Group specializes in the development of probabilistic models, algorithms for inference, prediction methods, and application of these methods in large-scale genomic data analysis. Of particular interest is research relevant to existing, NIH-supported projects in:

1. COMPARATIVE GENOMICS including inference of natural selection on regulatory and other noncoding sequences, and estimation of rates of turnover of regulatory elements; and

2. TRANSCRIPTIONAL REGULATION in mammals, including the estimation of rates and patterns of transcriptional elongation from PRO-seq data and prediction of transcription factor binding sites from ATAC-seq data.

RELEVANT RECENT PAPERS INCLUDE THE FOLLOWING: 1. Danko CG, Choate LA, Marks BA, Rice EJ, Zhong W, Chu T, Martins AL, Dukler N, Coonrod SA, Wojno EDT, Lis JT, Kraus WL, Siepel A. Dynamic evolution of regulatory element ensembles in primate CD4+ T-cells. Nat. Ecol. Evol. 2(3): 537-548, 2018.

2. Huang YF, Gulko B, Siepel A. Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. Nat. Genet. 49(4): 618-624, 2017.

3. Kuhlwilm M, Gronau I, Hubisz MJ, Â, Siepel A, and Castellano S. Ancient gene flow from early modern humans into eastern neanderthals. Nature. 530(7591): 429-433, 2016.

4. Core LJ, Martins AL, Danko CG, Waters CT, Siepel A, Lis JT. Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. Nat. Genet. 46(12): 1311-1320, 2014.

Candidates from non-traditional and/or underrepresented backgrounds, broadly defined, are strongly encouraged to apply. More information about the position and to apply: https://cshl.peopleadmin.com/postings/17057 Informal inquiries are welcome. Interested applicants should email Dr. Siepel directly at asiepel at cshl dot edu.

Adam Siepel, Prof. Simons Center for Quant. Biol. Cold Spring Harbor Laboratory, Long Island, New York

Irene Gill Simons Center for Quantitative Biology Cold Spring Harbor Laboratory Office: 516-367-6834 | Fax: 516-367-5501 Email: gill@cshl.edu | http://www.cshl.edu/scqb "Gill, Irene" <gill@cshl.edu>

CornellU FishAdaptationGenomics

The laboratory of Nina Overgaard Therkildsen at Cornell University is looking for two highly motivated postdocs. The first postdoc will work on an NSF-funded project aimed at elucidating the genomic underpinnings of adaptive divergence despite extensive gene flow in the Atlantic silverside (Menidia menidia). The Atlantic silverside is a small estuarine fish that exhibits a remarkable degree of local adaptation in growth rates and a suite of other traits tightly associated with a climatic gradient across latitudes. Decades of prior lab and field studies have made the Atlantic silverside one of the marine species for which we have the best understanding of evolutionary tradeoffs among traits and drivers of selection causing adaptive divergence. Recently, our lab began examining the underlying genomic basis, and we have found striking patterns of differentiation involving multiple large inversions. Varying levels of gene flow across the species range create a natural experiment for testing general predictions about the genomic mechanisms that enable adaptive divergence in the face of gene flow, and key goals of the project include integrating patterns of variation in the wild with findings from trait mapping to 1) examine how genomic architectures underlying local adaptation vary across connectivity regimes and 2) elucidating the potential role of chromosomal rearrangements and other tight linkage among adaptive alleles in facilitating adaptation. The postdoc will have access to low-coverage whole genome sequencing for >1,000 individuals, a chromosome-level genome assembly, QTL maps, RNA-seq data, and will have flexibility to pursue different directions based on their interests.

The second postdoc will work on a NYDEC-funded project aimed at uncovering genome-wide patterns of variation in American shad across its distribution range and developing cost-effective genomic screening tools to aid conservation efforts and fisheries management. The American shad (Alosa sapidissima) is an anadromous fish native to the east coast of North America. It has for centuries been one of the region's most important fisheries species - so much that it in the US has been called "the fish that fed the nation's founders". More recently, however, the species has faced population extirpations across its range and despite extensive restoration efforts, abundances are at historic lows in many areas. Conservation planning efforts would substantially benefit from a better understanding of the population structure and degree of local adaptation in American shad and an ability to assign ocean-going adults back to their river of origin.

Earlier microsatellite work detected only weak genetic differentiation across the species range, but shad are distributed across very heterogeneous environments and divergent selection may have driven highly elevated levels of differentiation in localized genomic regions associated with local adaptation, a pattern now seen in many other fish species. The goal of this project is to conduct genome-wide scans to identify genomic regions that show maximal differences in allele frequencies across both small and large spatial scales, and based on these develop powerful genetic assignment tools for inferring where shad caught as bycatch in ocean fisheries originate from. The project will be carried out in close collaboration with the New York Department of Environmental Conservation and being based on linked-read whole genome sequencing of >500 individuals (haplotagging), it will provide an exciting opportunity to leverage novel haplotype-resolved genomic techniques to address practical management needs in a high-profile species while at the same time exploring more basic questions about the forces that drive genome-wide patterns of variation in high gene flow systems. Exhibiting a remarkable variation in reproductive strategy and other phenotypic traits across its range, and recently having successfully colonized the entire west coast of North America after being introduced to California in the late 1800s, the American shad has tremendous, but yet unexplored, promise as a model to study how species adapt to new conditions - an issue of urgent importance in our rapidly changing world. The postdoc will be encouraged to pursue and integrate both the applied and more fundamental lines of inquiry based on their interests.

Qualifications: Candidates should have completed or be within 1-3 months of completing a PhD in evolutionary genomics, molecular ecology, bioinformatics or a related field. We are looking for creative and talented scientists who are team players with good publication records and excellent organizational and communication skills. The successful candidates must have a strong computational/bioinformatics background and previous experience with analyzing large population genomics data sets. Experience working in the Unix environment is

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DukeU PopulationGenetics

The Goldberg lab at Duke University is hiring a postdoc in population genetics. Flexible start date.

Projects include a range of projects in theoretical and empirical population genetics, disease ecology, and human-environment interactions. Much of our work is in humans and other primates, though study system is flexible. Current projects include mathematical models of malaria transmission, machine learning methods to detect selection in admixed populations, primate immunogenetics, and genome-structure evolution in primates.

The Goldberg lab combines theory and computational data analysis; interest in biological applications of programming, statistics, and/or mathematics is required.

We are a computational lab with occasional wet lab or field collaborators. We are associated with the departments of Evolutionary Anthropology, Biology, and Mathematics at Duke University. With the knowledge that multiple groups continue to face barriers to inclusion and equity in the sciences, including BIPOC and LGBTQ+ people, we strive to be a supportive environment for everyone.

More information: http://www.goldberglab.org/ To apply: email Amy Goldberg with a CV and brief statement of research interests. Candidates should be specific about their interests in our work.

"amy.goldberg@duke.edu" <amy.goldberg@duke.edu>

ETH Switzerland Biodiversity

Eawag, the Swiss Federal Institute of Aquatic Science and Technology and WSL, the Swiss Federal Institute for Forest, Snow and Landscape Research, are the two environmental research institutes of the ETH domain. Within the new Blue-Green Biodiversity Initiative of Eawag and WSL, the Seehausen lab at Eawag and the Zimmermann lab at WSL have a vacancy for a Post-Doc in ecology/evolutionary biology (100 %) to work on

Biodiversity assembly in aquatic and terrestrial ecosystems - the roles of speciation versus immigration

Regional biodiversity assembles through immigration, sorting and speciation. Understanding their relative importance in different ecosystems and taxonomic groups is of fundamental interest for science and nature conservation. Dramatic losses of endemic species radiations have been documented in deep lakes and oceanic islands all over the world, but are likely also widespread in mountains. Physically rugged landscapes such as those of the European Alps give rise to endemic species radiations through the interaction of dispersal limitation with steep ecological gradients and insular habitat structure. Terrestrial and aquatic, plant and animal radiations in the Alps have been studied in isolation. In this project we want to analyse them in a common framework in order to identify factors that explain variation between taxa and ecosystems in the prevalence and distribution of species radiations within a common region. For this we have compiled large data sets for multiple large clades representative of biodiversity in and around the Alps: amphipods, fish, flowering plants, butterflies.

You will build phylogenetic trees based on sequence data, map current and reconstruct ancestral species ranges for classifying species as resulting from immigration, anagenesis or cladogenesis, and from geographical modes of speciation. You will extract climate and habitat preferences from occurrence data to determine if speciation events were associated with niche conservatism or niche divergence. You will map the relative importance of these alternative processes back to the physical landscapes and to phylogenetic trees to assess to what extent the same or different principles drive community assembly in distinct ecosystems within a shared landscape and climate history. You will synthesize the information into manuscripts for leading disciplinary or interdisciplinary journals.

The postdoctoral fellow will work with extensive existing datasets of the Seehausen and Zimmermann groups, as well as datasets of collaborators Florian Altermatt, Jakob Brodersen, Blake Matthews (all Eawag), Loic Pellissier, Catherine Graham (both WSL), and Lukas Rüber (Natural History Museum Bern). The project is funded by the Blue-Green Biodiversity initiative of Eawag and WSL. Please find more information on our homepage at https://www.eawag.ch/en/news-agenda/-news-portal/news-detail/blue-green-biodiversity-a-new-research-initiative-of-eawag-and-wsl/ Competitive applicants have experience in phylogenetic comparative analysis of ecological, trait and distribution data, excellent command of R and ability to work with large data. Applicants will be highly motivated, enthusiastic and independent scientists with excellent communication and writing skills and a track record of publishing in ecology, evolution or biogeography, good work ethics and creative thinking. You must have a PhD degree in Ecology, Evolutionary Biology, Biogeography or a related field. The successful applicant will be based in the group of Prof Ole Seehausen (https://www.eawag.ch/en/department/fishec/) at Eawag, Kastanienbaum, but will spend significant amounts of time at WSL in Birmensdorf in the group of Prof Niklaus Zimmermann (https://www.wsl.ch/de/-mitarbeitende/zimmerma.html). Funding is available for 12 months, but it is possible that it can be extended beyond that. The position should start as soon as possible, but no later than September 2020.

Switzerland is home to many research groups in ecology, evolution, biodiversity and conservation and enjoys an unparalleled quality of life. Eawag's Center for Ecology, Evolution & Biogeochemistry is located in the heart of Switzerland on the shores of Lake Lucerne. It has a strong nucleus of research groups that are committed to integrating evolutionary biology, ecology, and ecosystem science. Traveling to WSL Birmensdorf, to Zürich and to Bern is each just under an hour by public transport.

For further information about the position please contact Prof. Dr. Ole Seehausen Ole.Seehausen@eawag.ch. Applications from women and from minority groups are especially welcome.

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GeorgetownU PopulationGenomics

* Postdoctoral Position in Population Genomics of Range Expansion and Adaptation*

A postdoctoral position is available in the Armbruster lab (http://faculty.georgetown.edu/paa9/) at Georgetown University to study the population genomics of range expansion and climatic adaptation in the invasive mosquito, /Aedes albopictus/.The focus of the project is to: 1) use whole-genome sequence data to determine the evolutionary history of the world-wide range expansion of /Aedes albopictus,/ 2) develop genomic tools to rapidly identify the origin of new invasive populations, and 3) identify the genetic basis of life-history adaptation across the species range.The project will leverage historical data and samples to identify allochronic evolutionary changes at both the molecular and phenotypic level. This is a collaborative project with Gisella Caccone's lab at Yale that will involve extensive interaction between the research teams at Georgetown and Yale.The position will also include an opportunity to develop additional research projects. The initial appointment will be for one year, with extension for an additional 1.5 years based on excellent performance. Starting salary will be approximately $49,000 per year with benefits. The start date is flexible, but sometime in October thru December of 2020 would be ideal.

QUALIFICATIONS:

Candidates should have completed their PhD in evolutionary biology or a related discipline with a demonstrated record of research productivity and publication.The project will involve substantial insect husbandry, molecular biology and bioinformatics analyses.Candidates with expertise in two of these three areas will be given preference, and a desire to work in all three areas is essential.

APPLICATION:

Review of applications will begin July 1^st , 2020 and continue until the position has been filled. Applicants should submit the following material to Peter Armbruster (paa9@georgetown.edu <mailto:paa9@georgetown.edu>) with "postdoc application" in the subject line: 1) A CV including names and contact information of three references, and 2) A one-page research statement describing previous accomplishments and long-term goals. Informal inquiries prior to submission of a full application are encouraged.

The Biology Department at Georgetown (https://biology.georgetown.edu/) is housed in the recently constructed Regents Hall, a state-of-the-art facility.The Biology Department is a vibrant academic community with a diverse set of research groups studying a range of topics in evolutionary ecology. Additionally, Washington D.C. provides exciting opportunities to interact with scientists at other institutions (i.e., NIH, Smithsonian Institution, George Washington University and University of Maryland, etc.).Washington D.C. is also is an outstanding place to live with world-class cultural attractions and numerous (sometimes underappreciated) opportunities for outdoor activities.Georgetown University values diversity and is committed to equal opportunity for all persons regardless of age, color, disability, ethnicity, marital status, national origin, race, religion, sex, sexual orientation, veteran status, or any other status protected by law.

Peter Armbruster, Ph.D. Davis Family Professor Dept. of Biology, Regents 508 Georgetown University 37th and O sts. NW Washington, DC 20057-1229

Office Phone: 202-687-2567 Lab Phone: 202-687-1741 Fax: 202-687-2567

http://www9.georgetown.edu/faculty/paa9/ Peter Armbruster <paa9@georgetown.edu>

ImperialCollegeLondon PopulationGenomics

We are seeking a Research Associate or Fellow to work on antimicrobial resistance and evolutionary epidemiology of the major mould pathogen A. fumigatus. The post will be based in the MRC Centre for Global Infectious Disease Analysis (GIDA) within the School of Public Health at Imperial College London.

The position is funded by a Wellcome Trust funded 4-year Collaborative Award, led by Prof Matthew Fisher, and will investigate the escalating incidence of drug-resistant Aspergillus fumigatus coinfections in patients with pulmonary conditions such as cystic fibrosis, influenza and COVID-19.

The understanding we will achieve by this research will be critical for making informed decisions on current clinical and agricultural practice, as well as highlighting the most beneficial novel antifungal agents amongst those in current development (see Fisher et al. Worldwide emergence of resistance to antifungal drugs challenges human health and food security Science 2018).

The overarching aim of the project is to understand and quantify the risk that presents to public health within two countries, the UK and the Netherlands, where large and well characterised at-risk patient populations are showing an increasing incidence of aspergillosis that is resistant to the widely-used class of azole antifungal drugs. Our research will address the following research questions: 1. - What are the frequencies of environmentally-acquired and in- host evolved azole-resistant infections and what are the genetic backgrounds upon which they occur? 2. - Does azole-resistance combine with specific genetic backgrounds to heighten A. fumigatus fitness and virulence? 3. - Are there genetic barriers to the spread of the emerging spectrum of azole-resistant mutations? 4. - How does the emergence of azole-resistance impact the efficacy of new incoming antifungal drugs?

The post is offered initially for 12 months but can be extended for a total of 4-years. The successful applicant will have a key role on experimental design within the project, shaping the analytical framework, coordinating collaborations, supervising students and publishing analyses.

We are also recruiting a 3-year Research Assistant position also on this project - both jobs are advertised on jobs.ac.uk and the Imperial College Website

Closing date is 5th July for the PDRA and 19th July for the RA. Contact matthew.fisher@imperial.ac.uk for further details

Prof. Matthew Fisher MRC Centre for Global Infectious Disease Analysis/CIFAR Fellow Imperial College School of Public Health St Mary's Campus Norfolk Place London W2 1PG United Kingdom Phone: +44 207 5943787 http://www.imperial.ac.uk/people/matthew.fisher http://www.fisherlab.co.uk @fisher_mat Skype: matthew.c.fisher

"Fisher, Matthew" <matthew.fisher@imperial.ac.uk>

IST Austria EvolutionaryNeurobiology

Postdoc at IST, Austria

We are looking for an experienced postdoc to lead a project on the interface of neurobiology and evolutionary genomics. The project aims to understand the molecular basis of several aspects of Drosophila sensorimotor transformation using an organic synthesis of proteomics and genomics across Diptera. We are looking for a candidate with experience in modern proteomic and/or genomic experimental techniques willing to take a leading role in the design and execution of the project. The research has secured funding as a collaboration between the labs of Maximilian Jösch (https://joesch-lab.pages.ist.ac.at/) and Fyodor Kondrashov (https://ist.ac.at/en/research/kondrashov-group/) at the IST Austria and is part of the priority program from the DFG - "Evolutionary optimization of neuronal processing." We provide a competitive salary, an open, creative and supportive research environment. Further details about the project and conditions will be discussed with interested candidates at the interview stage. Interested candidates should write to Maximilian and Fyodor at maxjosch@ist.ac.at and fyodor.kondrashov@ist.ac.at with a short description of your interest and a CV.

Fyodor Kondrashov <fkondrashov@gmail.com>

JagiellonianU Poland InsectSymbioses

Postdoctoral opportunity: the diversity of insect microbiomes at Jagiellonian University in Krakow, Poland

The Symbiosis Evolution Research Group (symbio.eko.uj.edu.pl) at the Institute of Environmental Sciences of Jagiellonian University (eko.uj.edu.pl) in Kraków, Poland is looking to hire a Postdoctoral Researcher. This is a full-time position, funded by the Polish National Agency for Academic Exchange (NAWA) project "Insect Microbiomics", and the Polish National Science Center (NCN) project "Insect microbiome dynamics in time and space". The position is available from 1st October 2020, for 33 months.

The Postdoc will join a dynamic, multi-lingual, collaborative team aiming to describe the broad patterns of the microbial diversity across insects, and the dynamics of the insect microbiomes in time and space. The work will be conducted in close collaboration with a massive insect biodiversity project, Insect Biome Atlas (www.insectbiomeatlas.com) that does extensive insect community sampling and characterization in Sweden and Madagascar. The Postdoc will work on the implementation and testing of protocols for high-throughput, automated next-generation sequencing (NGS) library preparation in the context of insect microbiome studies, as well as develop bioinformatic pipelines for the analysis of the resulting data. Later, they will lead the microbiome characterization in extensive collections of insects from Sweden, Madagascar, and/or Greenland.

The Postdoc will be based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe, in a medieval city known as the cultural capital of Poland, with good access to outdoor recreation opportunities and well-connected to the rest of Europe. They will be encouraged to spend time in the laboratories of collaborators from the Insect Biome Atlas project in Sweden and engage in other international collaborations. We offer a competitive salary relative to the cost of living, flexible schedules, extensive opportunities to acquire cutting-edge research skills, and to network, as well as to develop and expand the project according to interests.

The candidates must have a Ph.D. in Biological Sciences or a related field, or anticipate the completion of doctoral studies by 30th September 2020. They should be able to demonstrate experience with molecular biology techniques and bioinformatic analyses of NGS data and be fluent in English. An ideal candidate will be able to demonstrate interest and scientific achievements related to the planned project, in particular regarding the diversity and biology of host-microbe interactions and the analysis of microbial communities using NGS. Laboratory experience in the preparation of NGS libraries, familiarity with the Linux / Unix shell and scripting languages such as Python / Perl / R, and interest in participating in international collaborations and research travel preferred.

The candidates are initially asked to submit a cover letter, a CV, and contact details of two references, to Dr. Piotr Lukasik (p.lukasik@uj.edu.pl). The review of applications starts on 1st July 2020.

For further information and informal inquiries, please contact Dr. Piotr Lukasik.

Piotr ukasik Assistant Professor - Symbiosis Evolution research group Institute of Environmental Sciences Jagiellonian University ul. Gronostajowa 7 30-387 Kraków Poland

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

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

KentStateU EvolutionaryGenomics

Postdoctoral Fellow in Evolutionary Genomics

The Lamichhaney Lab at Kent State University, Ohio invites applications for a postdoctoral fellow in the field of evolutionary genomics. Our lab broadly studies the molecular basis of organismal persistence to novel environments and is particularly interested in understanding the relative roles genetic adaptation and phenotypic plasticity underlying trait evolution. We integrate a variety of interdisciplinary approaches, including comparative 'omics' (genomics, transcriptomics, epigenomics, metagenomics and metabolomics) and field-based transplantation experiments to examine the processes of adaptive evolution. Research interests of the candidate is expected to align with ongoing projects in the lab which include; (a) comparative genomics of high-altitude adaptation in birds and mammals, (b) hologenomics of host-microbiome interactions along altitudinal gradients and (c) population genomics of parasitic fly invasion in Galapagos islands. In addition, the postdoctoral fellow will also have opportunities to pursue his/her own research interests relevant to the broad research theme of our lab. More information about the ongoing projects in the lab can be found at (https://theomicslab.wordpress.com/).

Our lab is part of vibrant community of Ecology and Evolutionary Biology at the Department of Biological Sciences (https://www.kent.edu/biology) as well as The Environmental Science and Design Research Initiative (ESDRI) (https://www.kent.edu/esdri) at Kent State University.

The successful candidate is expected to have a PhD in the field of genomics, bioinformatics, computational biology or other relevant fields. Previous working experience with bioinformatic analysis of large-scale sequencing datasets will likely be an advantage.

Expected start date - As soon as possible

To apply, please send an email to Sangeet Lamichhaney (slamichh@kent.edu), with following documents,

§A one-page summary of candidate's previous research experience and future interests

§CV, with full list of publications (including pre-prints)

§Contact information of three referees

Please email slamichh@kent.edu for any additional information or informal inquiries about this job announcement

Sangeet Lamichhaney

Assistant Professor Department of Biological Sciences Kent State University slamichh@kent.edu

sangeetvet@gmail.com

LouisianaStateU OrnithologyCurators

Louisiana State University is seeking postdoctoral research candidates to conduct research in coordination with one or more of the ornithology curators. The candidate will be responsible for helping with the laboratory supervision of graduate and undergraduate research assistants and management of the Museum molecular genetics core facility. Candidate will also help with minor curatorial tasks when and if needed. Ongoing projects in the lab include systematics and population genetics studies of birds.

Job Description: 70% Research: Conduct active lab research on a semi-independent basis. To prepare and publish scientific manuscripts under the direction of Dr. Nicholas A. Mason and collaborators. To attend, contribute, and where necessary lead relevant meetings. To take the responsibility for planning and developing research methods and techniques within the framework of the research program. Bring new expertise to the research program. To undertake any other duties relevant to the program of research, including field work. To collaborate with research colleagues and support staff internally as appropriate to the research and to actively develop appropriate external contacts and networks relevant to the project and to future funding opportunities. This postdoctoral position is expected to be part of the Museum's vibrant academic community, attending seminars, participating in journal clubs, etc. 20% Service, training, and mentorship: Responsible for helping with the laboratory supervision and training of graduate, undergraduate, and high school research assistants, and management of the Museum's shared molecular genetics facility. Ongoing projects in the lab include studies of systematics, comparative and population genomics, trait evolution, and ecotoxicology of birds. Assist in establish and enforcing lab rules and regulations, and orient new staff/students at beginning of each semester. Attend regular meetings with the research team and investigators as required. Work with external collaborators as agreed with the lead investigators. 10% Curatorial: Assist bird curators as needed in the upkeep and growth of the ornithology collection at LSUMNS. Curatorial responsibilities may include but are not limited to digitization and upkeep of digital records, reorganizing physical specimens and curatorial equipment, collecting and preparing new specimens, training new undergraduate and graduate students in specimen preparation.

Minimal qualifications: Ph.D. in Ecology, Evolution or related discipline; Experience in molecular methods, evolutionary biology, and computational biology; strong publication record; ability to manage an active laboratory; experience in collecting, preparing, and curating avian specimens.

Additional details: The Postdoctoral Researcher appointment will be a one-year appointment with the option to extend for a second year. The maximum appointment will not exceed two years. Applicants should provide a CV, three letters of recommendation, and a research statement .

LSU is committed to diversity and is an equal opportunity / equal access employer. Application deadline is 1:01am EST.

To learn more about this position or to apply please visit the LSU Career site: https://lsu.wd1.myworkdayjobs.com/LSU/job/0120A-MJ-Foster-Hall/Postdoctoral-Researcher_R00046270 Deadline: June 15,2020 at 1:01 am EST.

Andrea Sagnard Talent Acquisition Assistant Human Resource Management Louisiana State University 110 Thomas Boyd, Baton Rouge, LA 70803 O: 225-578-8830 | M: 225-578-8200 | F: 225-578-6571 Due to the current situation regarding COVID-19 and out of concern for the health and safety of our faculty and staff, LSU has implemented a remote work directive. I do not have access to my office phone, and will be responding via email only.

asagna1@lsu.edu|lsu.edu|lsu.edu/hrm

Andrea Sagnard <asagna1@lsu.edu>

MaxPlanckInst Jena 2 BacterialViralGenomics

The Department of Archaeogenetics at the Max Planck Institute for the Science of Human History, Jena, utilizes recent advances in molecular approaches on biomolecules, such as genome wide DNA sequencing, to uncover an entirely new spectrum of information that can be retrieved from sample repositories such as anthropological and archaeological collections. The Molecular Paleopathology and Computational Pathogenomics groups invite applications for a

Post-doctoral position in ancient bacterial genomics (E13)

with a start date as soon as possible.

Job Description We seek to fill a position at the postdoctoral level with a focus on the rectonstruction of ancient bacterial genomes from archaeological contexts. Analyses will involve computational detection of ancient pathogen DNA in large shotgun datasets and genomic reconstruction via either reference-based or de novo assembly approaches, as well as extensive comparative analyses that will integrate data from large collections of modern bacterial genomes. Data will draw upon archaeological samples from the Neolithic to post-Medieval periods, and will cover a broad geographical expanse, with an emphasis on Eurasian and New World populations. Strong bioinformatics skills and literacy in basic statistical procedures are a requirement. Prior experience in working with recombining organisms is preferred though not a requirement. The ideal candidate will hold a PhD in a relevant discipline (microbiology, biology, bioinformatics, computer science, mathematics, population genetics, etc.) and share an interest in the human past. Competency in delivering oral presentations is an asset, and experience with supervising or mentoring students is desirable. This is a full time two-year (renewable) contract position at a pay scale of E13 TVöD, in accordance with the German pay grade system for public employees.

Your application The Max Planck Society is committed to employing individuals with disabilities and relevant candidates are encouraged to apply. The Max Planck Society also seeks to increase the number of women in areas where they are under-represented and thus welcomes applications from female candidates.

Your application should include a CV and a cover letter outlining in detail your qualifications, suitability for the position, and interest in working with our team. Three letters of reference should also be provided.

Please submit your application in English as a single PDF file to our application portal: https://lotus2.gwdg.de/mpg/mjws/perso/shh_p031.nsf/application . Applications will be accepted until July 31, 2020.

Information regarding the Max Planck Institute for the Science of Human History can be found at www.shh.mpg.de . For details about the position, please contact Dr. Kirsten Bos, bos@shh.mpg.de.

The Department of Archaeogenetics at the Max Planck Institute for the Science of Human History, Jena, utilizes recent advances in molecular approaches on biomolecules, such as genome wide DNA sequencing, to uncover an entirely new spectrum of information that can be retrieved from sample repositories such as anthropological and archaeological collections.

The Molecular Palaeopathology, Computational Pathogenomics, and Transmission, Infection, Diversification and Evolution (TIDE) groups invite applications for a

Post-doctoral position in ancient viral genomics (E13)

with a start date as soon as possible.

Job Description We seek to fill a position at the postdoctoral level with a focus on the detection and reconstruction of ancient viral genomes from archaeological contexts. Analyses will involve computational detection of ancient viral DNA in large metagenomic datasets with genomic reconstruction, and comparative analyses that will integrate data from extensive collections of modern viral genomes. Data will draw upon archaeological samples from the Late Pleistocene to post-Medieval periods, and will cover a broad geographical expanse, with an emphasis on Eurasian and New World populations. Strong bioinformatics skills and literacy in basic statistical procedures are a requirement. Prior work on viral genomics is an asset. Wet lab experience is not required. The ideal candidate will hold a PhD in a relevant discipline (microbiology, biology, bioinformatics, computer science, mathematics, population genetics, etc.) and share an interest in the human past. Competency in delivering oral presentations is an asset, and experience with supervising or mentoring students is desirable. This is a full time two-year (renewable) contract position at a pay scale of E13 TVöD, in accordance with the German pay grade system for public employees.

Your application The Max Planck Society is committed to employing individuals with disabilities and relevant candidates are encouraged to apply. The Max

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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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MIIZ Poland DolphinImmunoGenomics

Dear EvolDir subscribers,

A postdoctoral research assistant position is available in a project analysing genome wide variation in striped dolphins in relation to Morbillivirus infection. The work will carried out in the cetacean ecology and evolution research group led by Dr Andre E. Moura at the Museum and Institute of Zoology of the Polish Academy of Sciences (MIZ-PAS). We are re-advertising this position, as the previous round got disturbed by the Covid19 lockdowns. It is still a dynamic situation, so if you are interested in applying but worried about time frame, please do get in touch and we will find a workable solution.

The position is available for 30 months, and includes a three month probation period. The ideal start date is August 2020, although there is of course flexibility to account for the current pandemic situation. The research group is based at the Research Station of the MIZ-PAS in Gdañsk, and maintains strong links with the main research facilities of the MIZ in Warsaw. Therefore, research visits at the main MIZ facilities in Warsaw may be required as part of the job duties. The Research Station also hosts groups working on canid genomics and avian immunogenetics.

The post-doctoral assistant will possess expertise in evolutionary genomics, population genomics or bioinformatics. Candidates can have a background (BSc or MSc degree) in biology, zoology, bioinformatics, computer science, or related fields, and a PhD degree (awarded or to be awarded soon) in a relevant area. The PhD degree should have been awarded no earlier than 7 years before the start of employment. The candidate must be eligible to work in Poland at the time of appointment. A list of required skills can be seen at the end of this message.

To apply, the following documents should be sent to Andre Moura at avmoura@miiz.waw.pl no later than 28.06.2020:

1. Copy of a PhD certificate 2. Curriculum vitae including a publication list, with the following statement provided at the end and signed:

"I give my consent to the processing of personal data provided in my application documents by the Museum and Institute of Zoology PAS for the purpose of the recruitment process, pursuant to the Personal Data Protection Act of 10 May 2018 (Journal of Laws 2018, item 1000) and in agreement with Regulation (EU) 2016/679 of the European Parliament and of the Council of 27 April 2016 on the protection of natural persons with regard to the processing of personal data and on the free movement of such data, and repealing Directive 95/46/EC (General Data Protection Regulation; L 119 from 04.05.2016)".

IMPORTANT: Applications that do not include this statement cannot be processed.

3. Motivation letter (maximum one page) 4. A copy of one research paper to be evaluated in the recruitment process 5. Contact details of two persons who can be contacted for references.

The interviews of shortlisted candidates will take place in early July, and will be held by teleconference (Skype, Zoom, etc.). Interviews in person at the Research Station in Gdańsk-Górki Wschodnie are possible, but only if it is logistically feasible and safe to do so. Informal inquiries can also be addressed to Andre Moura.

Essential skills:

1. Experience with preparing NGS libraries and processing NGS data 2. Good knowledge of evolutionary theory and/or population genetic theory 3. Experience of Linux/Unix environment; 4. Experience with at least one coding language (e.g. Python, Perl, Unix Shell scripts); 5. Good organisational skills; 6. Experience with large databases; 7. Ability to work independently and to communicate with a multi- disciplinary team;

Desirable skills:

8. Experience with analysing whole-genome datasets, aligning to reference genomes, SNP detection; 9. Experience with software for evolutionary genomic analyses; 10. Experience with online genomic databases; 11. Good understanding of natural selection theory; 12. Good understanding of mammalian immune system; 13. Experience of working in an international team.

Research environment

The research at the MIZ is focused on a broad range of themes in animal biology, including systematics, biogeography, evolutionary biology, ecology and population genetics. Andre Moura research group is part of the Laboratory of the Molecular and Biometric Techniques led by Prof. Wieslaw Bogdanowicz, grouping researchers focused on population genetics, phylogeography and evolutionary genomics of a broad range of animal taxa. MIZ laboratories contain modern equipment for genomic analyses, including Pacific Biosciences RSII long-read sequencer and Illumina MiSeq System. The state-of-the-art ancient DNA laboratory carries out work on mammalian palaeogenetics. The Museum zoological collection is among the largest and most valuable in Europe.

"Andre E. Moura" <avmoura@miiz.waw.pl>

MNHN ParisEvolutionGastropods

POSTDOCTORAL RESEARCH POSITION IN EVOLUTIONARY BIOLOGY / GENOMICS

TOPIC: Drivers of diversification in predatory gastropods

One full-time postdoctoral position for 2 years is available at the Muséum National d'Histoire Naturelle (MNHN), located in Paris, France. The position will start the 1 st of October 2020. A one-year extension is negotiable.

The post-doctoral fellow will work in the framework of the ERC project "Hyperdiverse" (ERC-COG-2019, # 865101), which seeks at identifying the drivers of diversification in a group of marine predatory snails, the neogastropods. One of the goals of the project is to sequence 15 genomes of species characterized by various feeding and developmental strategies,that might have influenced the evolutionary success of the group.

In the course of the project the successful applicant will use hybrid assembly strategy to generate first high quality genomes of the Neogastropoda, known to have a large genome size (2-5Gb), with many repeated elements. The post-doc fellow will have to assemble the genomes, combining data from various sequencing technologies (Illumina, Minion, PacBio). In the subsequent annotation step, he will also be in charge of the genome annotation, in particular to identify candidate genes involved in feeding (e.g. toxins, anesthetics, etc) and in larval development, integrating population genomics approaches.

Within the “Institut de Systématique, Evolution et Biodiversité” of the MNHN, the post-doc fellow will work in the team 3E (“Exploration, Espèces, Evolution”), working on the systematics and evolution of benthic marine invertebrates. The team regularly organizes expeditions that the post-doc fellow may join, to enrich the MNHN collections and provide data for a highly active international network of taxonomists and evolutionists with which the fellow will collaborate.

QUALIFICATIONS - PhD in Biology. The candidates are expected to have a good experience in genome assembly and annotation.

SALARY - 2650 euro per month

APPLICATION PROCEDURE: Please submit a CV, detailing your experience in genome sequencing, assembly and annotation. Email your application to [puillandre@mnhn.fr] , before the 3 rd of July 2020.

For informal enquires and more details, email [puillandre@mnhn.fr]

Nicolas PUILLANDRE <nicolas.puillandre@mnhn.fr>

NHM London MacroevolutionOfMarineMammals

Join us at NHM London!

We’re hiring a #postdoc (34 months) for a Leverhulme Trust funded project on #macroevolution of odontocetes and pinnipeds. Taxon-specific expertise not needed. More details here: https://github.com/nhcooper123/-macro-group-info/blob/master/PDRAjobad.md Deadline 13th July.

I recognise this is a terrible time to advertise a job. If you want to apply but will struggle to do so in 6 weeks please let me know. Happy to answer any Qs on Twitter (@nhcooper123) or on email [natalie dot cooper at nhm dot ac dot uk].

Natalie Cooper <nhcooper12@gmail.com>

Oslo EvolutionaryVenomics

Two-year postdoc on venom evolution

A two-year postdoctoral researcher position is available in the Undheim group, based at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences (IBV), University of Oslo, Norway. The Norwegian Research Council-funded project studies the micro- and macroevolution of venom as a complex character, and aims to establish venom as a model that allows integrating quantitative and molecular genetics in examining the evolution of complex traits.

Prior experience with venom research is not a prerequisite, but experience with transcriptome data analysis, biomolecular mass spectrometry, and molecular evolution methods is highly desirable.

Application deadline is August 1st, 2020. Tentative start date is October 1st, 2020.

For more information on the project and how to apply, visit https://www.jobbnorge.no/en/available-jobs/job/187295/postdoctoral-research-fellow-in-evolutionary-venomics Eivind Andreas Baste Undheim <e.a.b.undheim@ibv.uio.no>

Philadelphia EvolutionaryGenomics

Description: A funded postdoctoral position is immediately available in in the laboratory of Dr. Marco Trizzino, in the Department of Biochemistry and Molecular Biology at Thomas Jefferson University, to study evolution of human-specific gene regulation. The laboratory uses a combination of experimental and computational biology to unveil how novel gene regulatory networks evolve. We are particularly interested in the role of Transposable Elements in this process.

The new postdoc will be free to design their project, that could be entirely wet-lab, entirely computational, or a mix of both. Coding skills not required.

More info about the lab can be found here: https://marcotrizzino.wordpress.com/ Our lab is part of the Sydney Kimmel Medical College, offering access to state-of-the-art core resources. Philadelphia is a great place to live, affordable and with a vibrant community. Great music/sport/food/art scene, and excellent location. Thomas Jefferson University is located in the heart of Center City.

Candidates should hold a RECENT (i.e. obtained no more than two/three years ago) Ph.D. Evolutionary Biology, Genomics, Molecular/Cellular Biology, Biochemistry, Developmental Biology or equivalent. Excellent communication and written skills are a must. Funding is available for three years. Starting date is negotiable.

Interested candidates should send a cv, a brief cover letter and contacts of 3 professional references to marco.trizzino@jefferson.edu Review of applications will begin immediately and continue until the position is filled.

Salary will be based on NIH scale for postdoctoral researcher: $50,004 per year for year-1 postdocs. Salary will follow the scale and will be adjusted based on years of postdoctoral experience.

Marco Trizzino <marco.trizzino@jefferson.edu>

RiceU EcolEvolution

HUXLEY FELLOW in ECOLOGY & EVOLUTION: The BioSciences department of Rice University (http://biosciences.rice.edu/) seeks to fill a Huxley Fellow position in ECOLOGY or EVOLUTION. The position is a two-year appointment with a third year extension possible, with a tentative start date of September 1, 2020. The start date is flexible but the Fellow will be expected to start during fall semester 2020.

Our prestigious Huxley Fellow Program aims to recruit outstanding postdoctoral researchers who merge excellence in teaching and research. The Huxley Fellows receive faculty status, employee benefits, competitive salary, and research funds for independent or collaborative research. Collaborative interests with the existing faculty in the EEB research area are a plus. An application (curriculum vitae, statement of research interests and statement of teaching) and three letters of recommendation should be submitted at this link: https://jobs.rice.edu/postings/23761 Application review will begin June 15, and will continue until the position is filled. For further questions and informal inquiries please contact Dr. Julia Saltz (julia.b.saltz@rice.edu), Huxley Fellow Search Committee Chair. Rice University is an Equal Opportunity/Affirmative Action Employer and values a diverse faculty. People from groups underrepresented in STEM are encouraged to apply.

Julia B. Saltz Assistant Professor, Biosciences at Rice University Lab: GRB E309, office: GRB E300E julia.b.saltz@rice.edu Saltzlab.com < http://saltzlab.wordpress.com/ > (she/her)

Julia Saltz <julia.b.saltz@rice.edu>

SaoPauloFederalU BirdAndCactiGenomics

The Amaral Lab at the Department of Ecology and Evolutionary Biology, Federal University of Sāo Paulo has an open post-doc opportunity.

This post-doc fellowship focus on exploring genomes and phenotypes of birds and cacti from the so-called Dry Diagonal area in South America. The selected candidate will work at the Federal University of Sāo Paulo in Diadema (Sāo Paulo State, Brazil) where he/she will develop a research project linked to the Dry Diagonal Dimensions Project, which is conducted jointly by the Biology Institute of the University of Campinas (UNICAMP, Brazil) and Harvard University (US), among other Brazilian (UFSCAR and USP) and US (Cornell, OSU, VSU, AMNH) institutions. Such collaboration is under the aegis of an agreement between the Sāo Paulo Research Foundation (FAPESP) and National Science Foundation (NSF) through their respective programs BIOTA and Dimensions of Diversity.

Adaptation is a central process in evolution, and ecologically diverse groups of species offer opportunities to study adaptive evolution in many levels of biological organization. The Dry Diagonal Dimensions Project will use different types of data in order to understand how adaptation contributes to phenotypic, genomic, and phylogenetic diversification in dry vegetation and neighboring humid forests. Species of Neotropical birds and cacti offer exciting opportunities to explore the genomics of adaptation, as they represent examples of closely related species occupying dry/open and humid forest in areas as Caatinga, Cerrado, Amazonia, and Atlantic Forest biomes. Recent advances in sequencing technology facilitate the task of interrogating hundreds - or even thousands - of loci potentially related to phenotypic variation using both genomes and transcriptomes.

The selected researcher will:

- Collect and process samples of birds and cacti, and occasionally trait data; - Perform sequence capture of candidate genes and sequence complete genomes and transcriptomes; - Perform bioinformatics, genome and trait evolution analyses; - Write scientific reports and manuscripts.

This opportunity is open to candidates of any nationality. The selected candidate will receive a FAPESP's Post-Doctoral fellowship in the amount of R$ 7,373.10 monthly and a research contingency fund, equivalent to 15% of the annual value of the fellowship which should be spent in items directly related to the research activity.

Applications or questions should be sent to amarallab.unifesp@gmail.com. Interested applicants should send a letter of intent, CV and contact information of two references up to June 20th 24h00 GMT.

Fabio Raposo do Amaral Adjunct Professor, Federal University of São Paulo http://www.amarallabunifesp.wix.com/labsite "Fabio R. Amaral" <fabioraposo@gmail.com>

ShaanxiNormalU 2 VisionEvolution

Shaanxi Normal University. Vision Evolution

Two postdoc positions are open in Liu lab at Shaanxi Normal University. The university is located in Xi'an, China.

Liu lab is focusing on the study of animal vision (https://www.researchgate.net/profile/Yang_Liu588). The lab is incorporating genomic analyses and in vitro functional assays to elucidate the molecular mechanisms underlying the evolution of animal vision.

Position 1: Computational and evolutionary analyses on visual genes. The candidate should be skilled in comparative genomics and transcriptomic analyses.

Position 2: Functional evolution of visual pigments. The candidate should be experienced in experimental techniques, such as PCR, cloning, real-time qPCR, cell culture, protein expression and purification, and Western Blot etc. The lab is also encouraging the candidate(s) to propose ideas related to the topic of molecular evolution.

Other requirements Both positions need the candidates have (1) PhD degree, (2) research background in molecular evolution, (3) good English for manuscript writing.

The positions could be 2-3 years, with income around 200,000 CNY per year (before tax and insurance, which is ~25%). The university will also provide a rent-free one-bedroom apartment (on campus) for the positions. The ideal starting date will be this fall, but flexible.

To apply, the candidate(s) could send (1) a cover letter briefly describing backgrounds, research interest, and/or future plan, (2) a CV, and (3) three reference letters to Prof. Yang Liu (yliu@snnu.edu.cn).

Yang Liu, Ph.D Professor College of Life Sciences Shaanxi Normal University 620 West Chang'an Avenue, Xi'an, China. 710119 http://lifesci.snnu.edu.cn/info/1123/5983.htm# https://orcid.org/0000-0002-9258-7237 yliu@snnu.edu.cn

Spain MSCA PopulationGenetics SpeciesCoexistence

The—EvoFlor network—at University of Granada (http://wpd.ugr.es/ ~ evoflor/) and—MESSY lab—at University of Cádiz (https://www.oscargodoy.com/) are seeking a postdoctoral researcher that would be interested in joint development of an application for—Marie—Skodowska-Curie Actions Individual—Fellowships (https://ec.europa.eu/research/mariecurieactions/actions/individual-fellowships_en).

We are seeking a highly motivated biologist (or similar) interested in questions related to evolutionary biology, species coexistence and/or population genetics and willing to combine tools from ecology and genetics to answer broad question on biodiversity evolution. Please find the abstract of the tentative project below. The candidates need to have a PhD degree or four years of equivalent experience.

This year the deadline of the call is September 9th, 2020. To ensure that we have enough time to prepare the application, we would be thankful to receive a letter of interest, stating your interest and experience, and a CV by June 20, 2020, sent by e-mail to—mabdelazizm@ugr.es—and—oscar.godoy@uca.es.

Evoflor is a multidisciplinary network of researchers studying diverse aspects of the evolution of plants, animals and their interactions. We integrate genetic, genomic, and ecological studies from theoretical and experimental perspectives. Our main study system comprises different species of the Brassicaceae family, although we also work in other disparate systems. The University of Granada (UGR), founded in 1531, is one of the largest and most important universities in Spain. Located in Southeast Spain and with over 60.000 undergraduate and postgraduate students and 6.000 staff, the UGR has a powerful presence in a city of 250.000 inhabitants. UGR offers a total of 89 degrees, 110 master's degrees and 28 doctoral programs through its 123 departments and 27 centers. Consequently, the UGR offers one of the most extensive and diverse ranges of higher education programs in Spain. The UGR is a leading institution in research, located in the top 5/10 of Spanish universities by a variety of ranking criteria, such as national R&D projects, fellowships awarded, publications, or international funding. UGR is one of the few Spanish Universities listed in the Shanghai Top 500 ranking (http://sl.ugr.es/0aw0). The edition of the ARWU places the UGR in 201-300 position in the world and as the 2nd highest ranked University in Spain, reaffirming its position as an institution at the forefront of national and international research. With more than 3,500 researchers and technicians engaged in various forms of predoctoral staff, postdoctoral contracts, incorporation of doctors and researchers, the UGR publishes annually more than 2,500 publications, with a percentage higher than 50 % in the first quartile; having a relative growth rate of production well above of the average for Spain and the EU. The UGR stands out especially in production levels in different areas including Earth Science and Instruments Science.

The goal of Mediterranean Ecological and Synthesis lab (MESSY lab) is to understand the ecological and evolutionary processes maintaining biodiversity and their links to ecosystems functioning. For that, we combine detailed field observations and process-based experiments with a unique interface of ecological theory and modelling toolboxes. This interface of theory, modelling and experiments is not specific to any taxonomic group. The University of Cádiz (UCA) is a medium size University close to the gulf of Cádiz in the Atlantic Coast of South West Spain. Although officially established in 1979, UCA can trace its origins back to the 15th century. The University of Cádiz is located in the range of 150-200 European universities in the first edition of Times Higher Education Europe Teaching Rankings (international classification focused on the analysis of excellence in teaching). The UCA stands out in the following sections: teaching & inclusive learning environment, resources for the delivery of the degree certificates effectively and commitment & results. The UCA is above the Spanish average in 9 of the 15 items that appear in the survey made to students. UCA appears in five subjects of the ARWU ranking that selects the 500 best universities in each area of knowledge:—Oceanography—(range 151-200),—Mathematics—(range 301-400),—Chemical Engineering—(range 301-400),—Environmental Science & Engineering—(range 301-400), and—Energy Science & Engineering—(401-500).

Abstract: Geneticists have long recognized the importance of genetic diversity on

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Switzerland Biodiversity

Biodiversity loss is one of the greatest environmental challenges that humanity is facing. Research and action to mitigate the loss of biodiversity and associated ecosystem functions and services are thus critical. To tackle this scientifically and societally urgent topic, the ETH board (Switzerland) has allocated funding to research on Blue-Green Biodiversity (BGB). One goal of this funding initiative is to strengthen interdisciplinary biodiversity research, particularly across ecosystem boundaries. As a result, all funded projects represent collaborations between two Swiss research institutes: WSL (Swiss Federal Institute for Forest, Snow and Landscape Research: www.wsl.ch/en) and Eawag (Swiss Federal Institute of Aquatic Science and Technology: www.eawag.ch/en).

For the first round of calls, BGB2020, is looking to fill 12 1-year postdoc-positions (see the call and description of all positions here:

http://www.anitanarwani.com/uploads/3/1/6/6/31665181/cluster-hire_bgb2020.pdf). All of these positions will be set in a highly collaborative framework at both institutions, and tackle scientific projects for which data are at hand and can be readily used. Application deadlines are soon, so apply quickly!

"Narwani, Anita Julianne Tricia" <Anita.Narwani@eawag.ch>

UCalifornia Berkeley Celegans microbiome

A postdoc position is available at the lab of Michael Shapira at UC Berkeley's department of Integrative Biology (https://ib.berkeley.edu/labs/shapira/). We are using C. elegans to study the role of genetic factors in shaping the gut microbiome, and the changes in microbiome composition that accompany and affect host aging. All motivated researchers are welcome to apply; preference will be given to candidates with experience in genetics/molecular biology/microbiology and/or experience in C. elegans Biology. Some computational skills will also be appreciated. Applications are welcome effective immediately. Please contact Michael Shapira directly: mshapira@berkeley.edu

Michael Shapira <mshapira@berkeley.edu>

UCalifornia Irvine EvolGenomics

Postdoctoral Fellow in Evolutionary Genomics Lab

The Lee lab at the University of California, Irvine invites applications for one Postdoctoral Fellow. Our group works on the interplay between transposable elements and genome evolution by combining population genomics, computational biology, and cell biology. Current projects in the lab include the impacts of transposable elements on epigenome and 3D genome organization, empirical and theoretical population genomics of transposable elements, and broadly how epigenome shapes genome evolution. Candidates will ideally have interests broadly relevant to these topics, and will have opportunities to pursue their own research interests in evolutionary genetics/epigenetics.

Our lab is part of the Department of Ecology and Evolutionary Biology (https://ecoevo.bio.uci.edu/), the Center for Evolutionary Genetics (https://evogen.bio.uci.edu/), and Center for Complex Biological Systems (https://ccbs.uci.edu/). More information about our research interests can be found at http://grylee.science/

The successful candidates will have a Ph.D. in the following or related fields: evolutionary genetics, genetics, genomics, epigenetics, cell biology, bioinformatics or computational biology. We are currently looking for candidates who (1) have extensive experience with high-throughput sequencing and strong quantitative skills or (2) have extensive experience with epigenomics/cell biology. We particularly encourage applications from candidates who have recently completed, or will soon complete, their PhD.

The expected start date is flexible.

To apply, email the following to Grace Lee (grylee@uci.edu) with the subject line "Postdoc application: [Your full name]."

- curriculum vitae, including a full list of publication. Pre-print articles can be included.

- a one-page research statement describing candidates' past experience and future research interests

- contact information for three references

Please contact Grace Lee (grylee@uci.edu) for any questions. Informal inquiries are welcome.

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

Grace Yuh Chwen Lee <grylee@uci.edu>

UEdinburgh BioinformaticsEvolution

We are looking for a bioinformatics or evolutionary genetics postdoc to work with Darren Obbard, Peter Keightley and Susan Johnston.

This is part of a project to quantify variation in mutation rate and other evolutionary parameters across multiple species of Drosophila. The post will be based within the Institute of Evolutionary Biology in Edinburgh (UK), and is funded by the BBSRC for 3 years from August 2020.

Applicants should have (or be about to finish) a PhD in bioinformatics, evolutionary genomics, population genetics, or another relevant field. We're very happy to hear from anyone, whatever their background, but experience with sequence-based bioinformatics (e.g. genome assembly, annotation and/or resequencing data), knowledge of relevant scripting languages (e.g. Python and/or R, Bash, Snakemake etc) and software (e.g. read-mappers, genome-assemblers, variant-callers) is likely to be an advantage.

Please email darren.obbard@ed.ac.uk with any questions or for more details

The full advert, and the link to make a formal application, can be found here: https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id2343 For more information about what we do, see

Obbard http://obbard.bio.ed.ac.uk/ Keightley http://www.homepages.ed.ac.uk/pkeightl/ Johnston https://sejohnston.com/ Darren Obbard darren.obbard@ed.ac.uk The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

OBBARD Darren <darren.obbard@ed.ac.uk>

UFSCarSorocabaU BrazilianBirdLandscapeGenetics

PD fellowship opportunity: Landscape genetics of Brazilian northeastern Atlantic Forest birds

The Thematic Project “Evaluation, recovering, and conservation of the endangered fauna of the Pernambuco Center of Endemism”, financed by FAPESP (São Paulo Research Foundation) and coordinated by Dr. Luís Fábio Silveira (MUZUSP, São Paulo), offers a postdoctoral fellowship for a foreign or Brazilian candidate, who has completed a doctorate not more than six years before the start of the scholarship, to attend the sub-project ”Landscape genetics in areas of the Center of Endemism Pernambuco (CEP)”, under supervision of Dr. Mercival Roberto Francisco, from Universidade Federal de São Carlos, campus de Sorocaba, São Paulo state, Brazil.

The specific objectives are to apply molecular markers to perform genetic variability and gene flow analyses of birds from six Atlantic Forest fragments from Alagoas state, northeastern Brazil, and to correlate genetic metrics to species and landscape characteristics.

This opportunity is open to highly qualified Brazilians and foreigners. It is essential the candidate to have experience and independency to perform both field and laboratorial works, as well as statistical analyses and manuscript preparations. The field work involves capturing birds with the use of mist nets; indentifying and marking the individuals, and collecting blood samples. It requires capability to drive to the study areas and to interact and communicate with local people, that can be hired as field assistants. Laboratory work will involve DNA extraction, and the development and analyses of molecular markers, such as microsatellites and SNPS. To achieve these purposes, the candidate must be available to live from eight to 12 months in Alagoas state to perform the field work (in the first year), and to perform the laboratorial analyses at Sorocaba, São Paulo State, Brazil (Department of Environmental Sciences from Universidade Federal de São Carlos, campus de Sorocaba). The selected candidate will be involved in the planning and execution of the research activities mentioned in this notice and will also work in the administration of the laboratory and co-orientation of graduate and undergraduate students.

Values and conditions:

The scholarship lasts 36 months and includes:

1. Monthly income (free of taxes) of R$ 7,373.10 (Brazilian currency), plus 15% of the annual value for expenses related to research (Technical Reserve);

2. Financial support for travel and installation expenses may be requested for selected applicants and the merits will be analyzed by FAPESP upon acceptance of the concession;

3. The candidate must have completed a doctorate not more than six years before the start of the scholarship; before the start of the scholarship;

4. The scholarship requires full dedication to the research project (except under the conditions described in resolution PR 13/2009 of July 15, 2009);

5. The grantee may not have any formal or informal employment, nor receive, during the period of the fellowship, a scholarship from another entity, salary or remuneration derived from the exercise of activities of any nature.

6. For the implementation of the scholarship the selected candidate must present all the documentation required by FAPESP.

For complete fellowship rules, go to: http://www.fapesp.br/270 How to apply:

The submission deadline is 20 July 2020. Registration exclusively by email (mercival@ufscar.br), with the subject “Post-doctoral ARCA project”. The following documentation, all in PDF format, is required:

1. An English text with a maximum of 2 pages explaining your motivations to work on this project;

2. Summarized CV including all published papers in the area of the project;

3. Two letters of recommendation from researchers;

4. Document attesting PhD/Doctorate conclusion (Diploma).

Selection

The selection of the applicants presenting the complete documentation will be made based on candidate's numbers and quality of publications in the area of the project (ornithology and/or population genetics), and an interview. Only publications on scientific journals will be considered, and the values attributed to each publication will be 0.5, 1.0, 1.5, 2.0, or 2.5 depending on Journal most recent impact factors (0.1-0.5; 0.6-1.0; 1.1-1.5, 1.6-2.0, and > 2.0, respectively). In case of multiple candidates, only the top five ranked applicants based on curriculum analysis will be invited to the interview (via Skype). In the interview, the capacity of communication in English and/or Portuguese; the past experience in the areas of the project, as well as the availability to develop the project will be addressed, and results of this step can imply in the disqualification of the candidate.

The result of the selection will be informed by email to all of the

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UGlasgow Bioinformatician

Postdoctoral Research Assistant

Institute of Biodiversity, Animal & Comparative Medicine, College of Medical, Veterinary & Life Sciences, University of Glasgow

Location: Glasgow Salary: 29,176 - 32,817/35,845 - 40,322 per annum Hours: Full Time Contract Type: Fixed-Term/Contract Placed On: 4th June 2020 Closes: 6th July 2020 Job Ref: 037909

We seek an exceptional post-doctoral candidate to work with Professor Barbara Mable and Dr. Harriet Auty, in the Institute of Biodiversity, Animal Health and Comparative Medicine (IBAHCM). The applicant will make a leading contribution to bioinformatics and statistical analysis of a project recently funded by the Leverhulme Trust, entitled "What can you learn from a fly? Biting insects as noninvasive samplers". Specifically, the job requires expert knowledge in database mining, processing and analysing omics datasets, and a specific focus on methods development. The successful candidate will also be expected to contribute to the formulation and submission of research publications and research proposals, as well as help manage and direct this complex and challenging project, as opportunities allow.

Aims and Approach: The overall aims of this study are to: (i) develop a new generation of genome-wide markers that are sufficiently variable and sensitive to make population genetics inferences from forensic samples; and (ii) using this approach, to test the potential of blood-feeding flies as non-invasive samplers to learn more about population biology of wildlife, which could ultimately be used to inform management decisions that consider levels and patterns of genetic variation in threatened species. The technology now exists but the challenge is the bioinformatics to identify genomic regions that are informative about adaptive and demographic processes and that could be applied across species. We envision that the approach will have broad applicability across a wide range of research questions. Here we will develop and rigorously test the potential of this approach to assess the population genetic structure of vertebrate host populations of conservation value in East Africa.

Please direct informal queries or requests for additional details of the project to barbara.mable@glasgow.ac.uk

This post is full time with funding up to 3 years in the first instance.

Apply online at: my.corehr.com/pls/uogrecruit/erq_jobspec_version_4.jo

It is the University of Glasgow's mission to foster an inclusive climate, which ensures equality in our working, learning, research and teaching environment.

We strongly endorse the principles of Athena SWAN, including a supportive and flexible working environment, with commitment from all levels of the organisation in promoting gender equity and diversity.

The University of Glasgow, charity number SC004401.

Professor Barbara Mable Editor-in-chief, Heredity Rm 404 Graham Kerr Building Institute of Biodiversity, Animal Health & Comparative Medicine University of Glasgow Glasgow, Scotland UK G12 8QQ

Barbara Mable <Barbara.Mable@glasgow.ac.uk>

UGothenburg ModellingSpeciesRanges

Dear All,

At the Department of Marine Sciences, University of Gothenburg, Sweden, we have an exciting Postdoc position “Modelling Species’ Range Expansions in Marine Environments”. The position is for 2 years. The deadline for applying is August 31, 2020.

Please find more information at

https://www.gu.se/english/about_the_university/-job-opportunities/vacancies-details/?id=5615 Yours sincerely, Marina Rafajlovic

Marina RafajloviÄ Assistant Professor/Forskarassistent

UNIVERSITY OF GOTHENBURG Department of Marine Sciences

Visiting address: Carl Skottbergsgata 22 B, room 5119 Postal address: Box 461, 405 30 Gothenburg Mobile: +46 76 580 4288 marina.rafajlovic@marine.gu.se www.marine.gu.se Marina Rafajlovic <marina.rafajlovic@marine.gu.se>

UHelsinki TransGenerationalEffects

POSTDOCTORAL RESEARCHER POSITION at University of Helsinki

in an integrative project to address the role of trans-generational effects in stress tolerance for a fixed term of two and a half years. The starting date is 1.10.2020, but a later starting date can be negotiated. The post doc will join the Life-history Evolution Research group led by Associate Professor Marjo Saastamoinen (https://www.helsinki.fi/en/researchgroups/-life-history-evolution). The overreaching aim of the project is to understand the potential adaptive role of trans-generational impacts and underlying epi(genetic) mechanisms to environmental stress using the Glanville fritillary butterfly as a study organism. The project builds on an on-going work indicating that both individual’Âs own developmental conditions and those experienced by its mother shape its phenotype. Furthermore, epigenetic and transcriptomic analyses suggest that within- and transgenerational responses are mediated by distinct pathways.

We are seeking a post doc to continue this project in order to understand the potential adaptive nature and/or the impact of paternal condition in the trans-generational stress responses. The post doc will participate in planning and conducting the experiment(s), analyse the phenotypic and genomic (transcriptomic and ATAC-sequencing) data, and lead the writing of the resulting manuscript(s). There is also potential for analysing part of the existing data. The successful candidate is expected to have demonstrable experience in bioinformatic analyses of genomic data as well as strong background in evolutionary ecology and experimental approaches. Thus, the postdoctoral researcher will work at the interface of evolutionary ecology and genomics.

Applicants should have completed a PhD in evolutionary ecology or a related field, and have bioinformatics and statistical skills. We seek candidates with excellent written and verbal communication skills, and the ability to conceive, execute and complete research projects, and to think independently and creatively. The post doc will work as a part of a team and thus good social skills are required. For more information, contact assoc. prof. Marjo Saastamoinen by email: marjo.saastamoinen@helsinki.fi

The starting salary will be ca. 3300’V3800 euros/month, depending on the appointee’Âs qualifications and experience.

For more details please use the following link

https://www.helsinki.fi/en/open-positions/-postdoctoral-researcher-in-trans-generational-stress-responses The deadline for submitting the application is 10 August 2020.

Marjo Saastamoinen Associate Professor in Evolutionary Ecology Helsinki Institute of Life Science (HiLIFE)/ Organismal and Evolutionary Biology Research Programme Faculty of Biological and Environmental Sciences University of Helsinki Finland

http://www.helsinki.fi/life-history-evolution https:/-/www.helsinki.fi/en/researchgroups/research-centre-for-ecological-change “Saastamoinen, Marjo A K” <marjo.saastamoinen@helsinki.fi>

UJyvskyl QuantGenetics

We are looking for a postdoctoral researcher to join the group of Ilkka Kronholm at the department of Biological and Environmental Sciences at the University of Jyväskylä. Starting 1st of September 2020 or as soon as possible thereafter, for a fixed term of four years.

Our group studies the properties of spontaneous epigenetic changes, parental effects, and genetic architecture of complex traits. In addition, we do some experimental evolution projects. Our research questions are focused on understanding how different intrinsic and extrinsic factors affect evolutionary adaptation.

We mainly use the filamentous fungus Neurospora crassa as a model system for empirical work. The main approaches used in the lab are quantitative genetics, genomics, association mapping, analysis of mutants using the genetic tools available for Neurospora, etc.

For ideas about epigenetic changes, see: Kronholm & Collins. 2016. Epigenetic mutations can both help and hinder adaptive evolution.Molecular Ecology25: 1856-1868

And a recent paper about and quantitative genetics of thermal performance in Neurospora: Moghadam et al. 2020. Quantitative genetics of temperature performance curves of Neurospora crassa. Evolution, online early: https://doi.org/10.1111/evo.14016 Current projects are focused on estimating rates and phenotypic effects of mutations and epigenetic changes, understanding the mechanisms parental effects in Neurospora, and mapping the genetic basis of thermal performance. The postdoc is expected to contribute to these projects, but the specific project tasks can be tailored according to interests of the candidate. For example, the postdoc can be more wet-lab based or more computationally based.

To be eligible, the candidate needs to have a doctoral (PhD) degree in evolutionary biology, genetics, bioinformatics or a related discipline with strong interest in evolutionary genetics. Previous experience with fungal genetics is not required. Experience in analysis of different types of sequencing (NGS) data, as well as good computational skills and knowledge about statistics, is considered an advantage. Good written and oral communication skills in English are required.

The annual salary range will be approximately 38 000 EUR depending on the qualifications and experience of the candidate.

Finland has a high standard of living, with free schooling (also in English), affordable childcare, good family benefits, and healthcare. Jyväskylä is located in central Finland in the Finnish lakeland, and has excellent opportunities for different nature, outdoor, and sports activities. The city of Jyväskylä is a major educational center and the city has a large student population. As such there is a vibrant cultural scene in the city.

To find useful information about the University of Jyväskylä, the City of Jyväskylä and living in Finland, see the international staff guide:

https://www.jyu.fi/en/workwithus/international-staff-guide Please attach the following documents to the online application form:

1. Curriculum vitae, including contact information of two people willing to provide a reference

2. Cover letter explaining your motivation, research interests, and career plans

3. List of publications

Please submit your application at the latest by 20 July 2020 by using the link found on page:

https://rekry.saima.fi/certiahome/-open_job_view.html?didV00&jc&id Informal inquiries are welcome and should be directed to Ilkka Kronholm

email: ilkka.kronholm(at)jyu.fi

lab website: ikronholm.net

Ilkka Kronholm

"Kronholm, Ilkka" <ilkka.kronholm@jyu.fi>

UKonstanz 6 EvolBiol

Today, we opened our 15th call for applications for Research Fellowships and Postdoctoral Fellowships.

Postdoctoral Fellowships (three to five positions)

We invite researchers in the early stages of their careers who plan to develop and implement an independent research project to apply for a 2-year Postdoctoral Fellowship. The fellowships are open to researchers from all fields represented at the University of Konstanz. We offer three 2-year positions.Furthermore, oneCluster-Zukunftskolleg Fellowshiprelated to the study of collective behaviourcanbefundedby the "Centre for the Advanced Study of

Collective Behaviour"directly. An additionalCluster-Zukunftskolleg Fellowshipcan be funded by the Cluster of Excellence "Politics of Inequality" for projects investigating the political causes and consequences of inequality.

You will find the call for applications as well as information about the eligibility criteria and the application process under: https://www.uni-konstanz.de/-zukunftskolleg/fellowships/postdoctoral-fellowship/ Research Fellowships (three positions)

Researchers with significant work experience at the postdoctoral level are welcome to apply for a 5-year Research Fellowship. The fellows build their own academic profile by leading an independent research group at the University of Konstanz. 5-year Research Fellowships are open to researchers from all fields represented at the University of Konstanz. You will find the call for applications as well as information about the eligibility criteria and the application process under:

https://www.uni-konstanz.de/zukunftskolleg/-fellowships/research-fellowship/ Questions can be directed to Anda Lohan via e-mail:a.lohan@uni-konstanz.de.We look forward to receiving thr applications until15 October 2020, 11:00 am (Konstanz time).

Please feel free to forward this call! Thank you and best wishes, Anda Anda Lohan LLM Programme Director for Research and Fellows Zukunftskolleg P.O. Box 216 Office Y 321 Universität Konstanz 78457 Konstanz

Tel. ++ 49 7531 88 4821 Fax. ++ 49 7531 88 4829 Anda.Lohan@uni-konstanz.de http:/-/www.uni-konstanz.de/zukunftskolleg Prof. Dr. Axel Meyer Lehrstuhl für Zoologie und Evolutionsbiologie 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>

ULausanne 2PDF 2PhD EvolGenomics

2 postdoctoral and 2 PhD positions: Evolutionary genomics/behaviour University of Lausanne, Department of Ecology and Evolution

We are looking for PhD students and postdoctorals to work on three lines of research: 1. Ant behaviour. The idea is to study the evolution of division of labour with a new system based on fiducial identification labels and video tracking. This system which automatically follow all the individuals in a colony allows quantitative studies of behaviour. 2. Ant genetics. We previously identified a supergene influencing social organization in the fire ant Solenopsis invicta. We have sequenced five closely-related species and found that the same genomic element is also responsible for variation in social organization. The aim of the project is to analyse how this large non-recombining region is evolving. 3. Evolutionary genomics. We are sequencing + generating RNAseq data for queens and workers of ca. 80 ant species. These data will be available for all sorts of analyses related to social evolution and the study of the genetic basis underlying differences between castes.

These positions will be funded by an ERC grant and the Swiss NSF. Other topics of research on social behaviour are also possible if they fit the research interests of our group : http://www.unil.ch/dee/keller-group The Department of Ecology and Evolution is a well-funded and vibrant research institution, with superb facilities. Applications should comprise a CV, a list of publications, 1 page describing why you are interested in joining our group and contact information for three referees. Only applications with all these informations will be considered. Applications should be sent to laurent.keller@unil.ch before July 24, 2020.

Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland

http://www.unil.ch/dee/keller-group Laurent Keller <laurent.keller@unil.ch>

ULondon ModellingEvolution

Department of Biological Sciences

Postdoctoral Research Assistant

Full-time Fixed-Term Contract (2 years)

Salary is 35,931 per annum inclusive of London Allowance

Applications are invited for the post of Postdoctoral Research Assistant in the Department of Biological Sciences at Royal Holloway University of London.

We are looking for a highly motivated individual to join the research group of Dr. Francisco Ubeda as a Postdoctoral Research Assistant. We are interested in modelling evolution in general and intra-genomic conflict in particular. The successful candidate will work on a NSF-NERC funded research project which focuses on the evolution of recombination, paternal genome elimination and sperm parasitism in species with sexual reproduction. The project will involve formulating mathematical and computational models and using the predictions of these models to direct empirical work on the evolution of meiosis in sperm parasitic species. This project is an exciting opportunity to understand the circumstances under which natural selection favours different mechanisms of recombination and how intragenomic conflict can transform genomic architectures.

You will be responsible for the formulation and analysis of mathematical/computational models. You will also be responsible for the preparation for publication and presentation of the results from the models. You will work alongside the project's Principal Investigator.

The successful candidate will have a PhD in Biology, Mathematics or Mathematical Biology (it is acceptable to be in the final phase of a PhD programme). A good publication record in peer-reviewed journals is essential, and experience of presenting at international conferences is highly desirable. You will have extensive experience of mathematical modelling in the field of evolution, and be familiar with population genetics and evolutionary theory. We are searching for an experienced, independent and forward-thinking researcher. Royal Holloway University of London is host to a vibrant community of researchers in Evolution.

This is a full time, fixed-contract post, available for 2 years from 1st of August 2020 (although we can accommodate any starting date until 1st of Oct 2020.

For an informal discussion about the post, please contact Dr. Francisco Ubeda on francisco.ubeda@rhul.ac.uk

To view further details of this post and to apply please visit https://jobs.royalholloway.ac.uk .The Human Resources Department can be contacted with queries by email at: recruitment@rhul.ac.uk.

Please quote the reference: 1019-396

Closing Date: Midnight, 10th July 2020

Interview Date: TBC (Mid-July 2020 although some candidates will be interviewed soon after their application is submitted)

The College is committed to equality and diversity, and encourages applications from all sections of the community.

Royal Holloway is committed to equality and diversity, and encourages applications from all sections of the community. Read here about structures and initiatives around equality and diversity, including information on staff diversity networks.

"Ubeda, Francisco" <f.ubeda@rhul.ac.uk>

UmeaU LandscapeGenomicsConiferTrees

Dept of Ecology and Environmental Science, UmeÃ¥ University, Sweden, announces a postdoc fellowship in Landscape genomics of conifer trees. The scholarship is for 2 years, full time, starting in the fall of 2020. The application deadline is 30th June 2020.

Please follow the link for more information about the project and application instruction: https://www.umu.se/en/work-with-us/fellowships-and-grants/6-1180-20/ We look forward to your applications!

Xiao-Ru Wang, Prof. Dept. Ecology and Environmental Science (EMG) UmeÃ¥ University, Sweden

Xiao-Ru Wang <xiao-ru.wang@umu.se>

UNottingham PopulationGenomics

ERC-funded Postdoctoral Position in Population Genomics

Salary: 30,942 to 40,322 per annum (pro-rata if applicable) depending on skills and experience. Closing Date: Thursday 09 July 2020

Our projects employ large scale population genomics, but at the same time have explicitly phenotype-first orientations. In each case we aim to determine the genetic basis and evolutionary repeatability of adaptation to intense, quantifiable selection pressures, both environmental and intracellular. We do this by applying population genomics to wild plant populations that have evolved to overcome demonstrable hazards.

We currently focus on adaptation to genome duplication as well as adaptation to highly challenging, quantifiable environmental stressors in species ranging from Arabidopsis arenosa, to Mimulus guttatus and back throughout the Brassicaceae to A. lyrata and A. thaliana and Cochlearia. We also work on polyploidy in frogs and fish. There is lots of awesome field work in the mountains and chances in interact with international collaborators too.

See https://www.yantlab.net/ for more.

The role: Primary activities will include conducting large-scale population genomic projects. This includes exhaustive demographic and selection analyses of population genomic data. We require candidates who are not only motivated to run with these objectives, but who can also propose new creative project contributions. By the end of your postdoctoral term with us, we expect you to be able to, for example, begin your own group, bringing along your project from our work together. We also expect to engender the development of new directions as a result of discoveries in our group that can spur independent trajectories for your future research.

The ideal candidate: Applicants passionate about evolutionary genetics or population genomics are encouraged to apply. The successful candidate will possess a PhD and a strong relevant publication history. They will also have good knowledge of population genetics and demonstrable use of computational methods in an evolutionary context. The ideal candidate will have initiative, analytical skills, and a drive to push forward on new problems in evolutionary genomics as part of a highly collaborative team.

Candidates must hold a PhD or equivalent in Genetics, Ecology, Evolution, Bioinformatics, or closely related area.

This full-time, fixed-term post is available immediately and will be offered until 30th June 2021. ***Extensions of this term may be possible***

Additional information: To apply for this role please include a covering letter with your application explaining your specific motivations to join the Yant Lab, as well as some specific description of your use of computational genomic or population genetic methods. This is a required element of the application process.

Informal enquiries may be addressed levi.yant@nottingham.ac.uk, but please note that applications sent directly to this email address will not be accepted.

To apply: https://jobs.nottingham.ac.uk/-Vacancy.aspx?id=30371&forced=2 Closing Date: Thursday 09 July 2020 Reference: MED166620

Best wishes, Levi

Levi Yant Associate Professor of Evolutionary Genomics Faculty of Medicine and Health Sciences Future Food Beacon and School of Life Sciences University of Nottingham Room B103 Life Sciences Building University Park Nottingham, UK NG7 2RD | +44 (0)7 966 731 125 https://www.yantlab.net/ https://www.nottingham.ac.uk/-research/beacons-of-excellence/future-food/index.aspx I work flexibly and do not expect a response or action outside of your own working hours.

Levi.Yant@nottingham.ac.uk

UPlymouth 2 EvolutionaryBiol

Two positions are available in evolutionary ecology at University of Plymouth, UK

1. Post-Doctoral Research Assistant in Evolutionary Ecology 2. Research Assistant in Fungal Biology and Evolution

1. Post-Doctoral Research Assistant in Evolutionary Ecology Drs Jonathan Ellis, Mick Hanley, George Littlejohn and Mike Thom (School of Biological and Marine Sciences, University of Plymouth), seek a PDRA to work on a Leverhulme Trust funded project Wherefore

the magic? Investigating the origin of psychedelic compounds in nature. This exciting project will investigate the evolution of psilocybin biosynthesis using molecular and experimental methods.

The Person: You will conduct cutting-edge research to test hypotheses that could explain the evolution of psilocybin biosynthesis. You will lead experiments investigating (1) DNA barcoding of fungal caps; (2) invertebrate avoidance and locomotion in response to psilocybin exposure (slugs, Folsomia and Drosophila); (3) gene expression analyses in response to fungal attack; (4) CRISPR/Cas9 production of fungal mutants and (5) fungal-bacterial interactions. As well as leading laboratory methods and experiments, you will also conduct field sampling. You will work closely with a Research Assistant on a daily basis for the first two years of the project. Consequently, you will have a PhD in Biological Sciences (e.g. molecular ecology, evolutionary or behavioural ecology or a similar discipline). Experience of at least one of the following will be advantageous: high-throughput sequencing technology and analyses of associated data, husbandry and behavioural experimental work using invertebrate systems, knowledge of plant/fungal ? herbivore interactions, including an understanding of the influence of secondary metabolites on invertebrate behaviour. A full UK driving licence (or international equivalent) is desirable. The ability to work independently, plan, design and manage experiments, and convert research data into timely, high-quality publications is essential. You will also need a DBS check to meet licensing requirements for work on psilocybin-containing mushrooms. The PDRA will receive additional career development support, via the annual UoP Performance Development Review process.

For an informal discussion to find out more about the role then please contact Dr Jonathan Ellis by email jonathan.s.ellis@plymouth.ac.uk or by telephone on(+44) 01752 585946

Interviews are likely to take place in September 2020 and you will be notified if you have been shortlisted.

The post will begin in May 2021

FURTHER DETAILS ARE AVAILABLE VIA plymouth.ac.uk/about-us/jobs

2. Research Assistant in Fungal Biology and Evolution

Drs Jonathan Ellis, Mick Hanley, George Littlejohn and Mike Thom (School of Biological and Marine Sciences, University of Plymouth), seek a Research Assistant to work on a Leverhulme Trust funded project Wherefore the magic? Investigating the origin of psychedelic compounds in nature. This exciting project will investigate the evolution of psilocybin biosynthesis using molecular and experimental methods.

The Person: The project will involve experiments investigating (1) DNA barcoding of fungal caps, (2) trials of invertebrate avoidance and locomotion in response to psilocybin exposure, (3) gene expression analyses, (4) CRISPR/Cas9 production of fungal mutants and (5) fungal-bacterial interactions. You will assist in all these work packages, working closely with a Post-Doctoral Research Assistant, assisting the PDRA in field collection of samples and maintenance of fungal and invertebrate cultures. You will support behavioural trials and help in routine laboratory tasks such as DNA isolation, making agar plates, setting up video recording equipment etc. You will also assist in legal compliance and security issues related to the project, for example maintaining meticulous auditing systems regarding access to legally controlled substances. You will help co-author academic publications arising from the project. Consequently, you will have an undergraduate degree in Biological Sciences or a related discipline and experience of working on fungi, invertebrates, molecular methods and/or behavioural experimental work in the lab would be advantageous. A full UK driving licence (or international equivalent) is desirable as is the ability to work independently and under supervision. You will also need a DBS check to meet licensing requirements for work on psilocybin-containing mushrooms. The RA will receive additional project and career development support, via the annual UoP Performance Development Review process.

For an informal discussion to find out more about the role then please contact Dr Jonathan Ellis by email jonathan.s.ellis@plymouth.ac.uk or by telephone on(+44) 01752 585946

Interviews are likely to take place in September 2020 and you will be notified if you have been shortlisted.

The post will begin in May 2021

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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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WageningenU PhD or PostDoc PlantPhylogenomics

PhD or Post-doc -Phylogenomics of Extreme Photosynthesis in Brassicaceae https://www.wur.nl/en/vacancy/PhD-or-Post-doc-Phylogenomics-of-Extreme-Photosynthesis-in-Brassicaceae.htm We are looking for

We are looking for an enthusiastic and motivated plant biologist with either a Msc or PhD who can work in a collaborative and multidisciplinary team. We invite applications from ambitious candidates with relevant research experience and a passion for studying plant trait evolution using phylogenomic approaches.

The PhD or post-doctoral candidate will be the lead researcher for the sub-project "Understanding the genomic and genetic basis of elevated photosynthesis rates of Hirschfeldia incana (Brassicaceae)." You will be part of the larger multidisciplinary "Extremophiles Programme" that combines genomics, genetics, biophysics, physiology, biochemistry and modelling to understand the unique and very high photosynthetic rates in C3 plants in the Brassicaceae family. Specifically, you will be investigating how exceptional photosynthetic properties evolved and is regulated in Hirschfeldia incana, a wild relative of brassica crops such as Brassica rapa and Brassica nigra, by combining genomics and phylogenetics (phylogenomics) and genetic crossing and QTL analyses. If this kind of research would interest you and you enjoy understanding complicated systems then this could be the project for you.

The Biosystematics Group and The Graduate School Experimental Plant Sciences The PhD or post-doctoral position will be under the daily supervision of Prof. Eric Schranz in the Biosystematics Group, Wageningen University & Research. The position will be co-supervised by Prof. Mark Aarts (Laboratory of Genetics) and Prof. Dick de Ridder (Bioinformatics group). You will be part of the Biosystematics group, with ~30 employees, including technicians, PhD students, post-docs, junior and senior scientists working on fundamental questions about biological diversity. The group research themes are: (1) origin and maintenance of plant and insect biodiversity, (2) speciation, domestication and plant-animal interactions, and (3) applying phylogenetic patterns to test hypotheses on underlying evolutionary processes. The Biosystematics Group is part of the Plant Science Group and works closely together with other groups (such as Genetics and Bioinformatics) within Wageningen University. The position will be part of the Dutch inter-university Graduate School Experimental Plant Sciences (EPS). The mission of EPS is to organize the training of PhD students and postdocs to become self-reliant researchers.

We ask

* A MSc or PhD in plant genomics, genetics, or related fields with an interest in the evolution of plant traits (e.g. photosynthesis). * Expertise and experience with generating and analysing plant comparative genomic and genetic datasets. * A collaborative worker with good interpersonal communication skills. * a good command of both spoken and written English language is critical (i.e. as demonstrated by published work). This position requires an excellent English language proficiency (a mininum of CEFR C1 level). For more information about this proficiency level, please visit our special language page < http://www.wur.nl/upload_mm/d/7/b/fa964c14-bf33-4148-8722-002cb3b1bef9_Common%20European%20Framework.pdf >.

Applications should include: a cover letter including a statement about your motivation to apply and your suitability for the position (either as a PhD candidate or post-doctoral researcher); a curriculum vitae including contact information for two references; and copies of your University MSc or PhD degree. We offer

We offer a meaningful and challenging position with, depending on your experience, a competitive salary from a minimum of 'Ã 2.325 to a maximum of 'Ã 2.972 for PhD, or 'Ã 3.123 to a maximum of 'Ã 4.274 for Post-Doc, for a full working week of 38 hours in accordance with the Collective Labor Agreement Dutch Universities. The job is for a period of 3 years (1 year and after a positive evaluation extension for another 2 years) at an international leading organization. The candidate will be based at the Biosystematics group.

In addition, we offer:

* 8% holiday allowance; * a structural year-end bonus of 8.3%; * excellent training opportunities and secondary employment conditions; * flexible working hours and holidays can possibly be determined in consultation so that an optimal balance between work and private life is possible; * excellent pension plan through ABP;

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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

WashingtonStateU Pullman 2 MicrobeEvolution

Postdoctoral Position: Washington State University (Pullman, WA)

Microbial Adaptation to Serpentine Soil

The labs of Maren Friesen (Washington State University, Pullman) and Stephanie Porter (Washington State University, Vancouver) are seeking a postdoctoral research associate to study the evolutionary and ecological genomics of environmental adaptation in wild Mesorhizobium bacteria. These Mesorhizobia are nitrogen-fixing bacterial symbionts that inhabit the root nodules of a native west coast legume. We have identified a Mesorhizobium genomic island associated with nickel tolerance in generalist lineages that grow on and off nickel-enriched serpentine soil (Porter et al. 2017 ISME), and have expanded this project to encompass ~700 strains. The system has multiple specialist and generalist clades and is poised to address questions about the ecological and genomic determinants of adaptation in wild microbes. This NSF project also includes Joel Griffitts (Brigham Young University) who is testing the molecular genetic basis of nickel tolerance.

Our ideal candidate would have a strong quantitative background, firm understanding of evolutionary ecology, excellent written and verbal communication skills, and ability to work well in a collaborative team. Training in at least one of genomics, bioinformatics, phylogenetic methods, and/or biostatistics is desirable. The position will be based in Pullman WA and the successful applicant will have access to the excellent facilities at WSU for plant growth, phenomics, genomics, biochemistry, and microscopy. There is a strong intellectual community in the Palouse spanning WSU and our neighbor 7 miles to the east, the University of Idaho in Moscow, ID. Pullman and Moscow are vibrant small towns with a strong sense of community and ready access to outdoor activities. The postdoc will have regular virtual meetings with co-advisor, Dr. Porter, and will visit collaborators at the Vancouver campus twice a year to the extent that travel is safe.

Job Duties: Development, organization and implementation of protocols to evaluate the mechanisms of bacterial adaptation; bioinformatic analysis of -omics data including TNseq, bacterial genomes (Illumina and PacBio) and transcriptomes; population and evolutionary genomics analysis; construction and testing of evolutionary ecological models using empirical data; training and supervision of temporary employees; development of experimental designs; summarization, and statistical analysis of data; manuscript preparation and the opportunity to write grant proposals in conjunction with the principal investigators; contribute to an inclusive, collaborative and inspiring lab environment.

Qualifications: Required: A Ph.D. degree in evolution, ecology, microbiology, modeling, genomics, or a related discipline at the time of hire. Applicants must have a demonstrated track record of creative, productive research as well as excellent skills in quantitative methods, written and verbal communication, and organization. Applicants must also demonstrate the ability to work in a collaborative and interdisciplinary environment. Preferred: Apparent background in some aspect of microbial genomics, evolution, ecology, physiology, biochemistry.

Availability: The position start date is flexible and is a temporary, 12 month, full-time position. Initial appointment is for one year and may be renewable dependent upon satisfactory performance and continued funding. Salary is commensurate with experience and includes medical benefits. For more information about the position contact Maren Friesen at m.friesen@wsu.edu and/or Stephanie Porter at stephanie.porter@wsu.edu . Screening of application materials will begin June 1 and continue until the position is filled; please apply by June 15 for priority consideration.

Apply online: https://wsujobs.com/postings/51840 I am social distancing to the greatest extent possible. By all acting together we can flatten the epidemic curve of COVID-19 and reduce the impacts on our communities.

< https://inboxwhenready.org/?utm_campaign=signature&utm_medium=email&utm_source=signature > I'm using Inbox When Ready < https://inboxwhenready.org/?utm_campaign=signature&utm_medium=email&utm_source=signature > to protect my focus.

Maren Friesen <maren.l.friesen@gmail.com>

Postdoctoral Position: Washington State University (Pullman, WA)

Plant-microbe interactions in bioenergy rhizosphere nitrogen cycling

The lab of Maren Friesen (Washington State University, Pullman) is seeking a postdoctoral research associate to study interactions between the bioenergy crop switchgrass and the rhizosphere microbiome, particularly

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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

WorkshopsCourses

Online AvidaED Jul1-2

The 6th annual Avida-ED Active LENS Workshop will be held July 1 'V 2, 2020. This year, responding to COVID-19 pandemic restrictions, we are holding an on-line workshop using Zoom.

The purpose of the Active LENS workshop is to train instructors in the use of the Avida-ED software package, developed to help students learn about evolution and the nature of science, so that workshop participants can both implement classroom interventions using this software and also train other educators.

Avida is a digital evolution software platform used to study evolutionary processes, and harness evolution to solve engineering problems. Avida-ED is a free, browser-based, user-friendly version of Avida developed specifically for educational purposes, with a graphical user interface and visualizations that allow the user to observe evolution in action. (Seehttp://avida-ed.msu.edu/for more information and to run the software in your web browser.) Organisms within this software (Avidians) are self-replicating computer programs, competing for computational resources supplied by the environment. Their replication is imperfect, resulting in mutations in some of their offspring, which may alter the ability of those organisms to make use of their environmental resources. Populations studied over the course of generations therefore display all of the elements necessary for evolution by natural selection: variation, inheritance, selection, and time. Avida-ED thus provides not a simulation of evolution, but an actual instance of it.

Avida-ED has been developed for undergraduates and advanced placement high school students to learn about the nature of science and evolution in particular. Users have significant control of the environment and are able to change parameters such as the world size, the mutation rate, and what resources are available. Individual organisms can be saved in a virtual freezer, analyzed individually to watch how they perform tasks and replicate themselves, and used to start new evolutionary runs. Because digital organisms grow and divide much faster than even the fastest microbes, Avida-ED allows users to test evolutionary hypotheses over the course of hours or minutes. By generating hypotheses, collecting data, and analyzing results, users will gain experience not just with concepts in evolution, but with the nature and practice of science as a whole.

Workshop participants will join a growing community of educators using digital evolution to let their students directly observe evolutionary processes through inquiry-based exercises that advance reform-oriented active learning.

The application form for the Active LENS Workshop must be completed online on the following page:

https://avida-ed.msu.edu/active-lens-train-the-trainers-workshop-2020-edition/ Registration for the course is $50. (Note: Participants who complete the course will receive a certificate and a refund of the course fee.) All applications received by June 15th will receive full consideration, but late applications will be considered if room is available. If you have any questions or difficulties with the application, contact Diane Blackwood (blackwo5@msu.edu).

Louise S. Mead, PhD Education Director BEACON Center for the Study of Evolution in Action Michigan State University 567 Wilson Rd., 1441 Biomedical and Physical Sciences

East Lansing, MI 48824 517-884-2560

"Mead, Louise" <lsmead@msu.edu>

Online BayesianPhylogeneticsUsingRevBayes Jul13-Aug15

We are offering a free, virtual short course on Bayesian phylogenetic inference using RevBayes.

This course will be held during July and early August of 2020 (exact dates are tentative), with particular focus on (1) tree inference from molecular data, (2) analyses combining fossil and extant taxa, and (3) evaluating MCMC performance, with advanced topics including assessing model adequacy and macroevolutionary analyses. Additional topics may be added depending on the interests of the selected participants. Participants in the course will interact with the instructors and one another as they complete tutorials (detailed lessons on different RevBayes analyses with pre-recorded video guides). Additionally, we will hold 5 or more interactive sessions to discuss and review tutorials and to consult with researchers interested in applying the methods available in RevBayes to their own data. The dates for the interactive sessions are currently tentative and may be adjusted depending on the schedules of the participants and instructors.

We are hoping to identify up to 15 participants for this online course. While we hope we are able to accommodate everyone who applies, we realize that this may not be possible because of time-zones and availability. If the number of applicants exceeds our capacity, we hope to organize a second round of sessions later in the year. Participants will not be charged for the course, but we will request that they commit to completing the tutorials and attending a majority of interactive sessions.

For more details about the Stay-at-Home RevBayes Workshop and a link to the application form, please go to: https://revbayes.github.io/workshops/-online2020.html Tracy Heath <trayc7@gmail.com>

Online DataSci PopGenet Jun29-Jul3 Sep14-18

ONLINE COURSE 'V Reproducible Data Science using RMarkdown, Git, R packages, Docker, Make & Drake, and other tools (RDRP01) This course will be delivered live

29th June - 3rd July

https://www.psstatistics.com/course/reproducible-data-science-and-r-package-design-rdrp01/ Course Overview: This course provides a comprehensive introduction to doing reproducible data analysis, which we define as analysis where the entire workflow or pipeline is as open and transparent as possible, making it possible for others, including our future selves, to be able to exactly reproduce any of its results. We cover this topic by providing a thorough introduction to a set of R based and general computing tools such as RMarkdown, Git & GitHub, R packages, Docker, Gnu Make and Drake, and show how they can be used together to do reproducible data analysis that can then be shared with others. After a general introduction on Day 1, where we introduce the core concept of a research compendium, we will begin by covering RMarkdown, knitr and related tools. These are vital tools for reproducible research that allow us to produce data analysis reports, i.e. articles, slides, posters, websites, etc., by embedding analysis code (R, Python, etc) within the text of the report that is then executed, and the results it produces are inserted into the final output document. On Day 2, we provide a comprehensive introduction to version control using Git, including using GitHub. Git and GitHub are vital tools for the organization, maintenance, and distribution of our code, especially for large scale and long term projects involving multiple collaborators. On Day 3, we cover how to create, maintain, distribute R packages. R packages are obviously the principal means of distributing reusable R code generally, and here, we will also look at how R packages can be used also to create, maintain, and distribute research compendia. On Day 4, we cover Docker, which is a now very popular means for producing reproducible computing environments across different devices, platforms, and operating systems. On Day 5, we cover build automation tools, particularly Gnu Make and Drake, which are used for automatically running complex analysis code that involves multiple inter-dependencies between files. Gnu Make is a general purpose build automation tool, while Drake is specifically designed for complex data analysis pipelines in R. On each day, therefore, we aim to provide a comprehensive and thorough introduction to a set of valuable and generally useful computing tools, each of which plays a key role in allowing us to do reproducible data science.

Any questions please email oliverhooker@prstatistics.com

AND

ONLINE COURSE 'V Fundamentals of populations genetics using R (FOPG01) This course will be delivered live

14th - 18th September

https://www.prstatistics.com/course/fundamentals-of-populations-genetics-using-r-fopg01/ Course Overview: The aim of the course is to introduce you to the fundamentals of population genetics theory, through quantitative visualizations of the dynamic of genetic elements within and between populations, using the R statistical programming language. We will be using a mixture of lectures, exercises, and case studies to increase the intuitive understanding of population genetics concepts and facilitate conceptual experimentation and visualization in R.

By the end of the course participants should: 1. Understand the fundamentals of population genetics theory 2. Be able to use R to visualize data sets and write simple functions 3. Know how to import different data types into and out of R 4. Create simple population genetics simulations in R 5. Understand essential summary statistics from the population genetics literature (e.g. FST , D, pi, theta, etc.) 6. Be able to generate publication quality figures from population genetic data

Any questions please email oliverhooker@prstatistics.com

– Oliver Hooker PhD. PR statistics

2020 publications; Parallelism in eco-morphology and gene expression despite variable evolutionary and genomic backgrounds in a Holarctic fish. PLOS GENETICS (2020). IN PRESS

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53 Morrison Street Glasgow G5 8LB +44 (0) 7966500340 +44 (0) 7966500340

Oliver Hooker <oliverhooker@prstatistics.com>

Online GenomeAssemblyPacBioHIC Nov9-13

Course: Eukaryotic genome assembly USING Pacbio (Hifi and CLR) and Hi-C

When and where: ONLINE - 9th-13th of November 2020

Instructor: Dr. Marcela Uliano-Silva (Wellcome Sanger Institute, UK)

Teaching assistant: Joāo Ferreira Nunes, MSc (Wellcome Sanger Institute, UK)

Course website: (https://www.physalia-courses.org/-courses-workshops/pacbio/)

This course will introduce the audience to a spectre of methods which are present in a usual assembly workflow, starting from raw data and finishing with a fully assembled genome. We will see how to manipulate raw reads, analyse their quality, how to run different assembly algorithms, how to run Hi-C scaffolding algorithms and how to analyse assembly quality.

Both beginners and more advanced users will find useful information in this course. Course attendees must have a laptop with either macOS or any Unix version. Background in using mentioned operating systems via the command line is highly desirable. We will, however, cover the essentials throughout the hands-on sessions.

Should you have any questions, please feel free to contact us at: (mailto:info@physalia-courses.org)

All the best, Carlo

(https://scholar.google.com/citations?user=-pbVcB7AAAAAJ&hl=EN)

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 GEOMEDatathon

GEOME Datathon - Data Wranglers Needed!

The GEnomics Observatory MEtadatabase (GEOME < https://geome-db.org/ >; geome-db.org), the Diversity of the Indo-Pacific Network (DIPnet < http://diversityindopacific.net/ >; diversityindopacific.net) and Ira Moana Project (Genes of the Sea < https://sites.massey.ac.nz/iramoana/ >; https://sites.massey.ac.nz/iramoana/) are seeking graduate students from US institutions whose research has been idled or who have lost income due to the COVID19 pandemic to participate in a distributed (remote) datathon.

GEOME (geome-db.org) is a web-based database that captures the who, what, where, and when of biological samples and associated genetic sequences. The goal of the datathon will be to upload to GEOME the geospatial (latitude and longitude) and collection metadata (habitat, date of sample collection, etc.) that are associated with biosamples from natural eukaryotic populations in the Sequence Read Archive of NCBI/INSDC. This will be accomplished through literature searches, or by directly contacting the owners/authors of each dataset we have identified in NCBI.

Interested graduate students who are currently studying at US universities are invited to fill out a short application form < https://forms.gle/8omcKCbbV9o2gS3j8 >, which will include confirmation of their advisor's support for this activity. We encourage applications from a diversity of backgrounds. Attention to detail and strong organizational skills are absolutely essential. Basic skills with spreadsheets and text files, literature searches, and writing professional emails are also required, and preference will be given to applicants with an interest or experience in population genomics and genetic biodiversity research. No specific coding skills are required. Preference will be given to applications received by midnight PDT on June 29th, and selected applicants will be informed on July 1st.

Selected applicants will be paid $1500 to handle between 50 and 150 datasets (NCBI BioProjects), equivalent to 100 hours of work. Students will gain skills in data curation, familiarity with standards in biodiversity research, and will be able to develop their professional network through this opportunity. Work will commence on July 6th, 2020 and must be completed by August 21st, 2020. Students will be expected to attend a 1-2 hour Zoom training on July 6th, and a brief weekly Zoom check-in with GEOME personnel, but otherwise will be able to work according to their own schedule.

Please direct any inquiries to Eric Crandall, ecrandall@psu.edu

Application Link: https://forms.gle/8omcKCbbV9o2gS3j8 Eric Crandall - University of Hawai'i and Pennsylvania State University Michelle Gaither - University of Central Florida Libby Liggins - Massey University Rachel Toczydlowski - Michigan State University

Deck J, Gaither MR, Ewing R, Bird CE, Davies N, Meyer C, Riginos C, Toonen RJ, Crandall ED. 2017. The Genomic Observatories Metadatabase (GeOMe): A new repository for field and sampling event metadata associated with genetic samples. PLoS Biol. 15(8):e2002925. doi:10.1371/journal.pbio.2002925.

ecrandall@psu.edu

Online IntroductionToFloraOfAlaska Jun22-Jul20

Dear all,

There are a few spaces left if you are interested in learning about the Flora of Alaska as well as getting familiar with some unique approaches to delivering a systematic botany course online, this might be one for you. One of the hallmarks of systematic botany courses is the hands-on learning experience in a laboratory setting. To create a similar lab experience for the online offering, we have carefully chosen technology that will allow students from all over the state (and even outside Alaska) to collect data in their home communities, perform plant dissections and have a hands-on learning experience within the flora's native environment. Instead of traditional course materials like textbooks, students will purchase an inexpensive wide-angle macro lens that connects to their smartphone or tablet. This 2-inch lens lets students take high-resolution, detailed photos of flora on the go with classifying metadata, such as GPS location attached. The technology not only lets students mimic lab spaces in their own natural areas but also expands their digital networks through the submission of images to iNaturalist, enabling them to share and collaborate with enthusiasts around the world and contribute citizen science data to research. Students don't just sit at their computers in this class, they go outside, touch with their hands and share what they discover. The course design includes carefully videotaped lectures using the Learning Glass platform, video dissection demonstrations, virtual biome exploration using a 360 camera, and selected interactive reading materials. This course is an exciting intersection of curiosity for wild plants, an exploration of Alaska's plant communities and an accessible introduction to the science of botany.

Class URL: https://introtoflora.community.uaf.edu/ Where: University of Alaska Fairbanks (USA)

Instructor: Dr. Steffi Ickert-Bond (Professor of Botany and Curator of the Herbarium (ALA) at the University of Alaska Fairbanks)

Course goals:

The objective of this class is to introduce you to several aspects of Alaska's unique flora. Class modules and hands-on exercises are designed to familiarize you with the identification, description, and morphology of our local flora. In addition, you will get familiar with dissection of flowers, using technical keys, seeing scientific (Latinized) names, and learn vocabulary that comes with describing and talking about plants, and curate images that you will take of the plants in your immediate surroundings.

Student learning outcomes:

On completion of this class, you will be able to identify and describe several common plant families and species that are native and common to Interior Alaska and be more comfortable with floral dissection and taking photographs of flowering plants that will aid in their identification and classification.

Dates: The 1-credit class will run from 22 June- 20 July and is fully asynchronous.

Registration: You can register at https://ecampus.uaf.edu/register/summer-2020-registration/ and select 52841 BIOLF195. The class costs $273.

More info: You can read more about the class and watch a video dissection of Brassicaceae at https://news.uaf.edu/online-botany-course-utilizes-student Best, Steffi

Steffi Ickert-Bond, Ph.D.

Professor of Botany and Curator of the Herbarium (ALA), UA Museum University of Alaska Fairbanks 1962 Yukon Drive Fairbanks, AK 99775-6960, USA

Phone: 907-474-6277 (office) 907-474-5285 (WRRB lab) Fax: 907-474-5469

Ickert-Bond lab website http://www.frontierbotany.info Herbarium website and Facebook http://www.uaf.edu/museum/collections/herb/ https://www.facebook.com/ALAHerbarium/ Search 270,000 digitized ALA specimens: http://arctos.database.museum/home.cfm Steffi Ickert-Bond <smickertbond@alaska.edu>

Online MicrobialMetabarcoding Nov23-27

Dear all,

registrations are now open for the Physalia course "16 S/ITS Metabarcoding of microbial communities" - ONLINE - 23rd -27th November

Course website: (https://www.physalia-courses.org/courses-workshops/course30/)

Instructors: Dr. Daniel Pass (University of Cardiff, UK); Dr. Xavier Harrison (University of Exeter, UK); Dr. Bruno Fosso (CNR, Italy); Dr. Anna Sandionigi (University of Milan Bicocca, Italy)

This course will provide a thorough introduction to the application of metabarcoding techniques in microbial ecology. The topics covered by the course range from bioinformatic processing of next-generation sequencing data to the most important approaches in multivariate statistics. Using a combination of theoretical lectures and hands-on exercises, the participants will learn the most important computational steps of a metabarcoding study from the processing of raw sequencing reads down to the final statistical evaluations. After completing the course, the participants should be able to understand the potential and limitations of metabarcoding techniques as well as to process their own datasets to answer the questions under investigation.

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/=0A=0ATwitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/#!forum/physalia-courses info@physalia-courses.org

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ONLINE Paleogenomics Nov16-20

Dear all,

the 3rd edition of our course “Paleogenomics - from metagenomics to phylogenomics” will take place ONLINE from the 16th to the 20th of November.

Course website: (https://www.physalia-courses.org/-courses-workshops/course27/)

Instructors: Dr. Amine Namouchi (CEES, University of Oslo, Norway) and Dr. Claudio Ottoni (University of Rome Sapienza, Italy)

This course will introduce biologists to the main bioinformatics tools for the analysis of Next Generation Sequencing (NGS) data from ancient samples. Through a series of theoretical and practical hands-on sessions, this course will give you a clear understanding of the most common bioinformatics methods adopted in a wide range of paleogenomics projects. During the course we will cover various steps from metagenomics screening of ancient samples and taxonomical assignment, to NGS reads mapping, authentication through post-mortem damage analysis, variants calling and filtering, and phylogenomics.

Should you have any questions, please feel free to contact us: (info@physalia-courses.org)

Best regards, Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/#!forum/physalia-courses “info@physalia-courses.org” <info@physalia-courses.org>

Online Phylogenomics Nov23-27

Dear all,

the 3rd edition of the Physalia course on Phylogenomics will take place online from the 23rd to the 27th of November.

Instructors: Dr. Michael Matschiner and Dr. Milan Malinsky (University of Basel (Switzerland))

Course website: https://www.physalia-courses.org/-courses-workshops/course21/ Overview: While genomic data promise unprecedented insights into the evolution of the tree of life, they also pose new challenges that must be addressed to avoid misleading results and to fully leverage the potential of the genome-scale data sets. These challenges include the identification of orthologuous sequences that are suitable as phylogenetic markers, the selection of appropriate models of sequence evolution, and the detection of gene-tree discordance due to incomplete lineage sorting and introgression. In this workshop we will present theory and exercises to infer time-calibrated phylogenies from multi-locus, RADseq, and whole-genome data sets while accounting for these confounding factors.

Programme: (https://www.physalia-courses.org/-courses-workshops/course21/curriculum-21/)

Other upcoming Physalia courses: (https://-www.physalia-courses.org/courses-workshops/)

Should you have any questions, please feel free to contact us at (mailto: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 RNAseqNonModelOrganisms Dec7-11

Dear all,

registrations are now open for our 5-day ONLINE course “RNA-seq Analyses in non-model organisms”: https://www.physalia-courses.org/courses-workshops/course11/ When: 7th-11th December 2020

Instructors: Dr. Nicolas Delhomme and Dr. Bastian Schiffthaler (Umea Plant Science Center, Sweden)

Course overview:

This course provides an overview of modern applications of transcriptome sequencing and popular tools and algorithms for exploring transcript reconstruction and expression analysis in a genome-free manner, leveraging the Trinity software and analysis framework. Attendees will perform quality assessment of Illumina RNA-Seq data, assemble a transcriptome using, among others, Trinity, quantify transcript expression, leverage Bioconductor tools for differential expression analysis, and apply Trinotate to functionally annotate transcripts. In parallel to the short-read assembly, participants will perform the pre-processing of 3rd generation sequencing data (PacBio IsoSeq) and the resulting assemblies will be compared. Additional methods will then be explored for characterizing the assembled transcriptome and revealing biological findings.

For the full programme, please see: (https://www.physalia-courses.org/courses-workshops/course2/curriculum2/)

For the full list of our courses and Workshops, please see: (https://www.physalia-courses.org/courses-workshops/course11/)

Should you have any questions, please feel free to contact us at: (mailto:info@physalia-courses.org)

Thanks and best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

ULisbon cE3cAdvancedCourses

cE3c Advanced Courses 2020/2021 - List already available

The detailed program of the Advanced Courses organized by cE3c - Centre for Ecology, Evolution and Environmental Changes - http://ce3c.ciencias.ulisboa.pt/ - for the academic year 2020/2021 is already available. There are 20 courses in total, of which four are new.

IMPORTANT NOTE: Most courses are intended to be presential, but if needed (e.g. due to COVID-19 security measures by the time of the course) they may be adapted to be given remotely (online)

These courses are aimed for students enrolled in Doctoral Programmes in Biology or related area. They can also be attended by post-graduate students of other Doctoral Programmes or Masters in Biology, or others with basic biology formation (such as BSc in Biology or related areas).

These courses are free for 1st year PhD students of several Doctoral Programmes of the Faculty of Sciences of the University of Lisbon (FCUL) or institutions in partnership with FCUL, counting credits for their formation: - Biology, Ciências do Mar or other PhD programmes at FCUL; - Biodiversity, Genetics and Evolution - BIODIV (ULisboa and UPorto); - Biology and Ecology of Global Changes - BEAG (ULisboa and UAveiro).

The courses have in general an intensive format, with one week of duration, with 5-6 ECTs recognition for the above mentioned Doctoral Programmes. Some have a shorter format (see details in each course's programme).

We detail below the list of courses, teachers and calendars. More details (including programmes, fees and procedures for applications) can be found at:

https://ce3c.ciencias.ulisboa.pt/training/ (shorturl.at/jJXY5)

Advanced Courses cE3c 2020/2021

November 2nd - 6th 2020 - Stable isotopes in Ecology and Environment: a tool to integrate scales and complexity (Cristina Máguas). Deadline for applications October 2nd 2020.

November 2nd - 6th 2020 - EvoS-2 - Evolutionary Studies - applying evolutionary thinking outside the biology realm (Filipa Vala). Deadline for applications October 2nd 2020.

November 9th - 13th 2020 - Production of Science Communication Activities (Cristina Luís, Filipa Vala & Patricia Garcia Pereira). Deadline for applications October 16th 2020.

November 16th - 20th 2020 - Natural History Collections and Biodiversity (Maria Judite Alves et al.). Deadline for applications October 16th 2020

January 6th - 8th 2021 - Reproducibility in science (Inês Fragata). Deadline for applications December 8th 2020 (NEW; this is an online course) NEW

January 11th-15th 2021 - Hands on Functional Diversity: from Ecological Indicators to Ecosystem Services (Alice Nunes, Paula Matos, Laura Concostrina-Zubiri et al.). Deadline for applications December 11th 2020.

January 18th-22nd 2021 - Scientific Writing and Communication (Gabor Lövei). Deadline for applications November 20th 2020.

January 25th - 29th 2021 - Soil ecology and ecosystem services (Teresa Dias & Cristina Cruz). Deadline for applications: December 28th 2020.

February 8th - 12th 2021 - Until death do us apart: living in a symbiotic world (Silvana Munzi, Cristina Cruz & Lourdes Morillas). Deadline for applications December 15th 2020.

February 15th-19th 2021 - Urban Ecology: the green within the city (Ana Catarina Luz, Pedro Pinho, Cristina Branquinho et al.). Deadline for applications January 15th 2021.

March 1st-5th 2021 - Strategies for citizen engagement in science communication (Cristina Luís, Esther Marin et al.). Deadline for applications February 2nd 2021. NEW

April 7th - 9th 2021 - Science and the Media: bringing together scientists, journalists and society (Marta Daniela Santos). Deadline for applications February 27th 2021.

April 12th-16th 2021 - Ecohydrological modeling for climate change impact assessment (Joāo Pedro Nunes, Luís Dias, Amandine Pastor et al.). Deadline for applications January 31th 2021. NEW

May 5th-7th 2021 - Introduction to R programming and biological data analysis (Inês Fragata & Vitor Sousa). Deadline for applications April 2nd 2021.

May 10th - 14th 2021 - Advanced R for Ecology and Evolutionary Biology (Inês Fragata & Vitor Sousa). Deadline for applications April 2nd 2021.

June 14th - 18th 2021 - Applied Methods in Community Ecology and Functional Ecology (Paulo Borges & François Rigal). Deadline for applications April 23rd 2021.

June 22nd - 25th 2021 - Island Biogeography (Ana Margarida Santos et al.). Deadline for applications May 14th 2021 (only if presential).

June 28th - July 1st 2021 - Measuring Biodiversity: How to get data, assess its quality and measure different aspects of diversity (Joaquín Hortal). Deadline for applications: May 14th 2021.

July 12th-16th 2021 - Speaking "Nature": Methods for measuring the impact of environmental pollution on ecosystems (Silvana Munzi, Pedro

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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

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.