EvolDir

April 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

Anchorage PlantEvolution Jul18-22

PLANTS Undergraduate travel awards enhancing diversity at BOTANY 2020 meetings, July 18-22, 2020, Anchorage, Alaska http://2020.botanyconference.org/ Target date for travel grant applications: Mar 30, 2020. Apply soon!

Information: cms.botany.org/home/awards/travel-awards-for-students/plants-grants.html

PLEASE SHARE THIS ANNOUNCEMENT WITH COLLEAGUES AND STUDENTS!

PLANTS Grants: Undergraduate Travel Awards Enhancing Diversity at the Botanical Society of America Conferences PLANTS (Preparing Leaders and Nurturing Tomorrow's Scientists: Increasing the diversity of plant scientists) is a program to bring diverse and talented undergraduates to the BOTANY 2020 meeting July 18-22, 2020, in Anchorage, Alaska. Funded by the National Science Foundation and Botanical Society of America, the program will support up to 12 undergraduates to attend the entire meeting, discuss scientific talks with mentors (grad student, postdoc, professionals), and participate in networking, professional development, and career-oriented events. The program covers the normal costs of travel, registration, food and accommodation at the meeting. An overview of the scientific conference is available at: 2020.botanyconference.org Topics at the conference range across all levels of botany and include presentations on conservation, biodiversity, plant genomics, evolution, plant systematics, and botanical education. There are also several social functions specifically targeted at students for networking and fun. The meetings are a great way to understand the breadth of botanical research and education, to meet undergraduate and graduate students with similar interests, and to network with professionals in your area of interest. This is really a friendly community, so please consider joining us!

DEADLINE: Target date of Mar 30, 2020. Apply soon!

APPLICATIONS: Applications will be accepted with a target date of MARCH 30, 2020. The application includes completion of the online form providing your statement of interest, a letter of recommendation, and unofficial transcripts. Applications are welcome from all domestic undergraduates from the US and Puerto Rico (we are unable to accept applications from international students) who have interest in plant science; the admissions goal is to create a diverse pool of students attending the conference. The application form is located online at https://awards.botany.org/-

awards/award/2020-plants-grant We encourage you to review the online instructions and application form thoroughly before filling it out. Have letters of reference and unofficial transcripts sent directly to Amelia Neely aneely@botany.org

CONTACTS: For further inquiries, please contact one of the organizers: Anna Monfils – anna.monfils@cmich.edu Heather Cacanindin – hcacanindin@botany.org Ann Sakai aksakai@uci.edu

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Asilomar California ForestGenetics Jun16-18

North American Forest Genetics Society Biennial Meeting Asilomar Conference Center, Pacific Grove California June 16-18, 2020

The time is approaching for the first biennial meeting of the North American Forest Genetics Society (NAFGS) at the Asilomar Conference Center (https://-treegenesdb.org/nafgsconference). A block of 125 beds (single or double rooms) has been reserved at Asilomar but once this is reached it may not be possible to enroll for the meeting. Thus, it is timely to register for the meeting and book your accommodation.

Aside from the program and field trip shown at the conference web site, there will be ample opportunity for ad hoc groups to meet while at the conference. Asilomar is a world class facility for this type of creative opportunity. For example, see (https://en.wikipedia.org/wiki/-Asilomar_Conference_on_Recombinant_DNA), Asilomar holds a very special place for an important moment in the history of genetics/genomics research. So please make your plans to attend the NAFGS conference and make your contribution to the history of forest genetics research in North America. We encourage everyone to be a member of the NAFGS and there are no membership fees (https://treegenesdb.org/user/registermulti/step1).

Emily Grau <esgrau@gmail.com>

Budapest MathStatMolBio Apr18-19

Due to uncertainties regarding COVID19, we plan to extend the abstract submission and registration deadlines for MASAMB 2020.

For recent updates, or if you have questions about the event, please use #masamb2020 on twitter or email ssolo@elte.hu!

The 30th Workshop on Mathematical and Statistical Aspects of Molecular Biology (MASAMB) will be held in Budapest on April 18 and 19, 2020.

For details see http://masamb2020.elte.hu and below.

Bioinformatics and statistical genetics, twin themes of the long-running series of annual MASAMB meetings, have gained huge impetus from large-scale genome sequencing projects and development of high-throughput biological assay systems, including gene-expression, proteomic, metabolomic and single-cell genomics technologies. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunities for numerate scientists.

With typically around 80-120 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchanging ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome and encouraged to submit abstracts. Details of previous meetings are available at the MASAMB archive: https://www.ebi.ac.uk/goldman-srv/masamb/ Gergely J SzöllÃµsi <sszolo@gmail.com>

Budapest MathStatMolBio POSTPONED

Due to escalating uncertainty regarding COVID19, we have decided to postpone MASAMB 2020 to a fall date that is to be determined at a later time.

For updates, or if you have questions about the event, please see http://masamb2020.elte.hu, #masamb2020 on twitter or email ssolo@elte.hu.

Dr. Gergely J SzöllÃµsi

MTA-ELTE ,,Lendület" Evolutionary Genomics Research Group ERC "GENECLOCKS" Research Group head researcher http://ssolo.web.elte.hu Tel: 00 36 30 725 35 32

Gergely J SzöllÃµsi <sszolo@gmail.com>

Cleveland Evolution2020 Cancelled

Evolution 2020 Cancelled

The councils of SSB, ASN and SSE have made the difficult decision to cancel the 2020 Evolution meeting in Cleveland. Our highest priority is the health and well-being of our communities. Full refunds have been issued to all attendees and sponsors who registered. Societies are discussing how to adjust plans for Evolution 2021 and the possibility of having some virtual events later this year.

BUT...

Get your Evolution 2020 "The meeting that never happened" fundraising t-shirt here: https://www.customink.com/fundraising/evolution-2020-the-meeting-that-never-happened On sale now for four weeks only. Proceeds to the tri-society (ASN/SSB/SSE) joint meeting fund to cover expenses related to cancellation of the meeting. Combine orders within your lab to save shipping costs (international shipping is a flat fee).

"hrundle@uottawa.ca" <hrundle@uottawa.ca>

Evolution 2020 Cancelled

Evolution 2020 Cancelled

The councils of SSB, ASN and SSE have made the difficult decision to cancel the 2020 Evolution meeting in Cleveland. Our highest priority is the health and well-being of our communities. Full refunds will be issued to all attendees and sponsors who have registered thus far. These refunds will start being processed on Monday, March 23. The three societies' leadership groups are discussing how to adjust plans for Evolution 2021 and the possibility of having some virtual events later this year.

If you would like to make a donation to help defray cancellation costs for the three societies, you can now do so through SSE. All funds will go to the conference accounts. https://payments.evolutionsociety.org/donate Please pay attention to and implement best practices during these stressful times, and stay healthy. < https://payments.evolutionsociety.org/donate >

communications@evolutionsociety.org

ICE Helsinki InsectDiseaseEvolution Jul19-24

We would like to invite submissions to our symposium addressing the field of self-medication in social and solitary insects. The symposium will be held during the International Congress of Entomology (ICE 2020), Helsinki, Finland, July 19-24, 2020.

Symposium: Self-medication in insects (organised by Michael Lattorff and Silvio Erler): Insects show remarkable abilities to choose and balance their diet. They are avoid the uptake of pathogens from the environment with their food. When becoming infected insects are able to shift their diet and use plant derived chemicals to therapeutically heal themselves. Some insect species might even be able to use such secondary plant products as prophylactic medication to prevent any infection. There is the need to identify common mechanisms across insect orders that promote prophylactic or therapeutic self-medication.

Submissions through this link: https://submit.peerageofscience.org/conference/ICE_2020/109489 Deadline for submission of abstracts: March 30, 2020.

More information about the conference: https://ice2020helsinki.fi/ Dr. Michael Lattorff and Dr. Silvio Erler

"Erler, Silvio" <silvio.erler@julius-kuehn.de>

Makarska Croatia RupicapraConservation Apr21-23 2021

Dear friends and colleagues,

We are happy to announce that the "*III International Rupicapra Symposium*" will be held in *Makarska, Croatia, 21-23 April 2021*.

The Symposium aims to disseminate and exchange scientific knowledge on chamois species and subspecies and to promote their conservation and sustainable management. The two-days scientific programme will cover topics related to Genetics and Systematics, Physiology and Disease, Behaviour and Ecology as well as Management and Conservation.

We encourage the participation of early career scientists and we aim at inclusive collaboration with a good gender balance and wide geographical representation. The Symposium is open to researchers, experts, managers and to everybody interested in this species, hoping to bridge the gap between science and practical implementation.

Please forward this email to anyone who might be interested!

We hope to see you in Makarska!

Nikica Âprem & Luca Corlatti

– Website: Facebook page: https://www.facebook.com/RupicapraSymp/ Twitter page: https://twitter.com/RupicapraSymp Rupicapra Symposium <rupicaprasympiii@gmail.com>

Marseilles 24thEvolBiology Sep22-25

24th Evolutionary Biology Meeting at Marseilles September : 22-25 2020

The Evolutionary Biology Meeting at Marseilles is an annual congress which gather together International scientists interested in the mechanisms of evolution that generate the incredible diversity of living things found on Earth (and possibly beyond)

If the congress was initially a local meeting, it quickly gained an important weight in the scientific life. Indeed, whereas the number of participants has been increasing, the geographical origin of the researchers has been diversifying and widening year by year.

Today, the Evolutionary Biology Meeting at Marseilles has reached a worldwide dimension and plays a paramount role in the international scientific life: allowing the gathering of high level specialists, it encourages the exchange of ideas and stimulates the works of the researchers all through the world.

The following subjects will be discussed:

* Evolutionary biology concepts and modeling; * Biodiversity and Systematics; * Comparative genomics ans post-genomics (at all taxomic levels); * Functional phylogeny; * Environment and biological evolution; * Origin of life and exobiology; * Non-adaptative versus adaptative evolution; * The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge; * Convergent evolution * Evolution of complex traits (Evo-Devo)

contact Marie-Hélène Rome

marie-helene-rome@univ-amu.fr

registration abstract submission see also : web site aeeb.fr or https://ebm24.sciencesconf.org/ EvolBiolMeetingMarseilles

best regards

Pierre Pontarotti DR CNRS

< https://ebm24.sciencesconf.org/ >

< https://twitter.com/pontarotti >

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

Montpellier InfectiousDiseases Jun14-17 cancelled

Dear All,

We regret to announce that we have decided to cancel the EEID 2020 due to the Covid-19 pandemic.

People who have paid can obtain a refund from the event organisers. Please send an email to coeeid@services.cnrs.fr if you have any questions. We will post any news updates on our website, and hope to see you at the next EEID meeting.

With best wishes,

The Organising Committee.

alison duncan <Alison.Duncan@umontpellier.fr>

Montpellier InfectiousDiseases Jun14-17 update

Dear All,

We would like to inform everyone that at this point, the EEID2020 meeting is going ahead as planned and registration remains open (www.eeidconference2020.org). Please note that attendees can cancel their meeting registration with a full refund (minus a 10% fee) until the 4th May.We are monitoring the situation as it develops and will post updates on our website as soon as they are available.

The Organising Committee

alison duncan <Alison.Duncan@umontpellier.fr>

Napoli EvoDevo COVID-19 information

Dear Evo-Devo community,

In light of the worldwide COVID-19 situation, the abstract submission and early-bird registration dates for the 8th EED conference in Naples have been extended to the 15th of April 2020. Payments for the EED2020 are temporarily suspended, but you are still able to register for the conference.

If you have already proceeded with a bank transfer, the paid amount will still be kept for your registration. We currently cannot say whether the meeting will take place as planned or will be postponed to another date. As soon as the situation in Europe is clear and we have government directions on how to proceed, you will receive an update.

You can also check the conference website for updates on deadlines and other information: https://-www.evodevo2020.eu/ Feel free to contact the conference agency (info@evodevo2020.eu) should you require further assistance.

Kind regards,

Rainer Melzer on behalf of the Executive Committee

EuroEvoDevo <eed.soc@gmail.com>

Novosibirsk Bioinformatics Jul6-10

Dear colleagues! The deadline for abstract submission on the 12th International Multiconference on "Bioinformatics of Genome Regulation and Structure/Systems Biology"'VBGRS/SB-2020 https://bgrssb.icgbio.ru/-2020/ is coming. Click for registration

The conference will be held on06-10 of July 2020in Novosibirsk Academgorodok: the first day devoted to plenary lectures will be held at the House of Scientists, the remaining four days will be held at Novosibirsk State University, sections of the conference and symposia will go in 5 streams. Chair of the Multiconference program committee: Academician of the Russian Academy of Sciences Nikolay Kolchanov, ICG SB RAS. Important dates:

- Last date of submission the abstracts for the conference BGRS/SB-2020 'V March 14, 2020
- Notification of inclusion in the conference program BGRS/SB-2020 'V April 7, 2020
- Last date of fee payment 'V May 1, 2020
- Dates of the conference 'V 06-10 July, 2020
- Dates of the tour to the Altai mountains 'V July 11 'V 15, 2020
- Dates of the tour to Baikal Lake 'V July 11-19, 2020

For foreign participants it is important to start visa process, please, follow the instructions(https://-bgrssb.icgbio.ru/2020/visa/). Organizing committee suggests publication of abstract in regular Conference Proceedings (up to 2 pages) and publication of extended thesis in IEEE Xplore Digital Library (4 pages). Rules and conditions of publication are on the website https:/-/bgrssb.icgbio.ru/2020/abstract/ . Submission rules in Russian.

After the Multiconference, the abstracts recommended by the Program Committee will be published as full-text articles in special issues in:

1. Frontiers in Genetics
2. International journal of Molecular Sciences (MDPI IJMS)
3. PeerJ

4. Journal of Molecular Biology (Russian)
5. Applied Sciences (MDPI)
6. Journal of Bioinformatics and Computational Biology
7. Current Bioinformatics
8. Frontiers in Cell and Developmental Biology
9. Cells

Details on journals, information about quartiles could be found here.

Multiconference BGRS/SB-2020will include the following symposia and sections: - Section "Genomics, transcriptomics and bioinformatics" - Section "Systems Computational Biology" - Section "Structural biology and Computational pharmacology" - Section "Biodiversity, molecular evolution and bioinformatics" - Section "Biotechnologies: experimental and computer approaches" - Symposium "Systems biology, bioinformatics and biomedicine" (SbioMed-2020) - Symposium "Cognitive Sciences, Genomics and IT" (CSGI- 2020) - Symposium "Mathematical methods and high-performance computing in the life sciences, biomedicine and biotechnology" - Section "Bioinformatics and systems biology of plants" - Symposium"Animal Genetics" - Symposium "Systems biology of DNA repair processes and programmed cell death"(SbPCD-2020) - Section "Systems Biology of Aging" - Section "Organization of education process for research in the field of bioinformatics and systems biology"

Yours faithfully, Conference Organizing Committee BGRS/SB-2020 Contact:bgrs2020@bionet.nsc.ru Website of BGRS/SB-2020:https://bgrssb.icgbio.ru/2020 Site of the Institute of Cytology and Genetics SB RAS:www.bionet.nsc.ru BGRSSB2020 Organizing Committee <bgrs2020@bionet.nsc.ru>

QuebecCity SMBE Cancelled

We have decided to cancel SMBE 2020 dueto concerns about COVID19. The wellbeing of our communities is always the most important consideration. Please join me in thanking an outstanding local organizing committee in Québec City, particularly Nadia Aubin-Horth and Christian Landry. We hope to see you at a future SMBE meeting.

We will provide more details on refund process in the near future. In the meantime, be well wherever you are.

With best wishes,

Marta L. Wayne President, SMBE

–

Dr Lulu Stader

Executive Administrator, Society for Molecular Biology and Evolution

smbe.contact@gmail.com

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

Snowbird Utah GenesAsEnvironment May31-Jun2

Early Registration till MARCH 31ST is now open for AGA2020: Genes as Environment: Indirect Genetic Effects in Evolution, Agriculture, and Medicine The American Genetic Association 2020 President's Symposium May 31 through June 2 in Snowbird, Utah

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

Student and postdoc members receive free registration if they submit a poster abstract by March 31st, and have the chance to be selected for an oral presentation and $300 travel award. Poster abstracts from all registrants will be accepted.

We hold the friendliest symposia - small meetings in lovely settings that provide great opportunities to interact with the best in the field.

AGA members receive significant discounts on symposium registration.

Check out our speaker lineup: Key Distinguished Lecture: Allen J. Moore Nathan Bailey Amelie Baud Piter Bijma Butch Brodie Nancy Chen Niels Dingemanse Kathleen Donohue Courtney Fitzpatrick Maren Friesen Andrew McAdam Joel McGlothlin Stephanie Porter David Rand Julia Saltz Michael Wade Alastair Wilson

Join us in Snowbird! https://www.theaga.org/agatwentytwenty.htm theaga@theaga.org

Anjanette Baker <theaga@theaga.org>

YosemiteNatlPark Symbiosis May15-17 CANCELLED

CONFERENCE CANCELLED DUE to the COVID-19 PANDEMIC

Dear Colleagues,

Registration is NOW CANCELLED for the 10th Annual Yosemite Symbiosis Workshop.

The TENTH annual Yosemite Symbiosis Workshop will NOT take place on May 15-17, 2020 at the Sierra Nevada Research Institute, Yosemite National Park.

Keynote speaker 2020: Martin Kaltenpoth Professor, Johannes Gutenberg University, Mainz

WE APOLOGIZE and WE ARE SORRY TO BE MISSING THE MEETING.

See you next year!!! Yosemite 2021!

Joel L. Sachs *Professor & Vice Chair, *Department of Evolution Ecology & Organismal Biology

*Director of UCR Microbiome Initiative (https://microbiome.ucr.edu/ Department of Botany & Plant Sciences (Cooperating Member) Department of Microbiology & Plant Pathology (Cooperating Member) University of California, Riverside

Mailing Address: Sachs Lab - UC Riverside 3401 Watkins Dr., 1229 Spieth Hall Riverside, CA 92521

Office (951) 827-6357 / Fax (951) 827-4286 www.sachslab.com http://www.biology.ucr.edu/people/faculty/Sachs.html Joel Sachs <joels@ucr.edu>

GradStudentPositions

Antwerpen CichlidGenomics

Application deadline extended due to the current situation. New application deadline: 25 March 2020

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

The hundreds of closely related but ecologically diverse species of Lake Malawi cichlid fishes provide an exceptional model to study the genomic mechanisms involved in rapid adaptation and diversification. We have recently shown that hybridisation in an ancestral population of Lake Malawi cichlids promoted their adaptive radiation

https://doi.org/10.1093/molbev/msz294 In this project you will use genomics and transcriptomics to investigate the mechanisms behind this phenomenon. You will apply these techniques in hybrid crosses of divergent cichlid species in our fish facilities. Furthermore, you will investigate short and long-read whole-genome sequencing data of wild populations. You will use these data to test for the role of different genomic mechanisms in adaptation and diversification.

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

You will need to apply through the University of Antwerp Job portal providing a cover letter (1 page), an academic CV and the name of two references. The cover letter should clearly lay out your motivation to engage in this project.

https://www.uantwerpen.be/en/jobs/vacancies/-ap/2020bapfwetex073/ Looking forward to your application. Best wishes,

Hannes Svardal

Hannes Svardal <Hannes.Svardal@uantwerpen.be>

BielefeldU TheoreticalEvolutionaryEcology

PhD position in Theoretical Biology at Bielefeld University, Germany (application deadline: April 23, 2020)

The Theoretical Biology group and SFB/TRR 212 are looking for a new PhD student to join in mid-August 2020. The goal of the research project will be to contribute to a better understanding of the causes and consequences of intraspecific trait variation, with particular focus on traits that are under density-dependent selection. Specific research questions include: How do trait variation and multi-scale density-dependence affect a population's ability to persist in the face of habitat loss or habitat fragmentation? What are the eco-evolutionary causes and consequences of intraspecific trait variation in two or more interacting species? And what patterns of genetic variation do we expect around loci underlying such intraspecific trait variation?

Until December 31st, 2020, the position will be located in the collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC^3, https://www.uni-bielefeld.de/biologie/crc212/) and for the remaining term in the research group for theoretical biology at Bielefeld University.

Research tasks (95 % in 2020, then 75 %): - development of eco-evolutionary models - mathematical analysis of models - implementation in a programming language (e. g. R, C++, Python) - simulation studies - interdisciplinary collaboration, e. g. with other research groups in the collaborative research centre - writing scientific publications

Teaching tasks (0 % in 2020, then 20 %): - teaching courses in ecology, including advising Bachelor and Master projects

Organizational tasks in the research group (5 %)

Your Profile

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

Preferable qualifications - experience with mathematical modeling - working knowledge of ecology and evolution - experience in leading exercise sessions/tutorials

Remuneration Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L). As stipulated in ç 2 (1) sentence 1 of the WissZeitVG (fixed-term employment), the contract will end by August 14th , 2023. In accordance with the provisions of the WissZeitVG and the Agreement on Satisfactory Conditions of Employment, the length of contract may differ in individual cases. The employment is designed to encourage further academic qualification. The position is advertised as 65 % part-time job. In individual cases, this percentage may be reduced on request, as long as this does not conflict with official needs. Bielefeld University is particularly committed to equal opportunities and the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application Procedure For full consideration, your application (containing a cover letter detailing your motivation and relevant experiences, CV, copies of certificates, and contact details for at least one reference) should be received via email (a single PDF document) sent to meike.wittmann@uni-bielefeld.de by April 23, 2020. Please mark your application with the identification code: wiss20077.

Contact Jun. Prof. Dr. Meike Wittmann Fakultät für Biologie, Theoretical Biology P.O. Box: 10 01 31 33501 Bielefeld, Germany Phone: +49 521 106-67627 Email: meike.wittmann@uni-bielefeld.de https://www.uni-bielefeld.de/biologie/theoreticalbiology meike.wittmann@googlemail.com

BournemouthU FoxPopulationDynamics

A funded PhD position in population dynamics of the fox in Dorset is available at Bournemouth university.

We are seeking an outstanding PhD candidate to lead on this exciting project which aims to understand how the predation pressure experienced locally by bird species of conservation concern may be determined by the population dynamics of a key predator across a large region.

Studies of declining wading bird populations throughout Europe have typically found that, because of breeding-season predation, productivity is insufficient to replace natural mortality of older birds (Macdonald & Bolton 2008). Several of the predator species such as the fox implicated are generalists that thrive in modern human-dominated landscapes to become disproportionately numerous relative to individual prey species.

This is a fully-funded PhD studentship which includes a stipend of 15,225 each year to support your living costs.

More info can be found here : https://www.bournemouth.ac.uk/study/courses/phd-studentship-population-dynamics-fox-dorset Best regards,

Emilie Hardouin

Dr. Emilie Hardouin Principal academic in Conservation Genetics Deputy Head of Department - Life & Environmental Sciences Bournemouth University Faculty of Science and Technology Christchurch House Talbot Campus Poole, Dorset BH12 5BB United Kingdom Tel: +0044 (0)1202 962402

Open hours Monday from 9h to 12h, please book an appointment

Emilie Hardouin <ehardouin@bournemouth.ac.uk>

FUBerlin InsectImmunEvolution

Freie Universitaet Berlin, Germany Open PhD position: Damage, immune defence and pathogen virulence evolution Application deadline: 30th March 2020

The Evolution and Ecology of Insect Defences group at the Institute of Biology, Freie Universitaet (FU) Berlin, Germany, would like to invite applications for a German Research Foundation (DFG) funded doctoral candidate position (TV-L E13, 65%) for the research project: “Damage, immune defence and pathogen virulence evolution: From the wild to the lab”. The position is fixed-term and available for 4 years and it will start in June 2020, or as soon as possible thereafter.

Project background Our research lies in the field of eco-evo-immunology (https://armitagelab.com/). To fully understand immune defence variation and function it is essential to consider the ecological context in which defences are used and the evolutionary pressures placed on them. Much of our extensive knowledge is from carefully controlled laboratory-based studies, which is quite different from the complex environments under which the defences have evolved. Given rapid adaptation rates to lab conditions in short-lived insects, it is relevant to connect insight from the lab with that from wild organisms. To address this, in this project, the successful candidate will sample flies (Drosophila melanogaster) from the wild and examine their "natural state", in terms of the degree of wounding that they have been subjected to and their cuticular microbiota. The latter will be identified and quantified using e.g. 16S rRNA metabarcoding. They will also ask how immune defences of wild- and lab-bred D. melanogaster differ in terms of resistance to bacterial pathogens, and whether their associated cuticular microbiota affect the virulence evolution of bacterial pathogens. A mathematical/statistical analysis will provide an understanding of the drivers of the virulence data. The results will give insight into variation in the natural selection pressures placed upon the host, and inform us about how they affect insect defences and pathogen virulence evolution.

The position is part of the "Insect Infect" Research Unit funded by the DFG. The Research Unit will give the opportunity for the candidate to interact with a diverse group of doctoral candidates, post-docs and PIs, to obtain methodological training, to collaborate with theoreticians, and to receive bioinformatics support. There will be yearly retreats for Research Unit members and access to a graduate training programme.

Requirements A completed University Master's degree in biology.

Desirable - We would like applications from enthusiastic and highly motivated students with a background/strong interest in evolutionary ecology. - Laboratory experience with bacteria and insects. - Good basic knowledge of statistics and experimental design. - Proficient in spoken and written English. - Good team-working and communication skills. - Ability to work independently. - A European driving licence would be an advantage. - Experience in collecting insects from the wild. - Experience in molecular biology. - Completed projects/internships on topics relevant to the research area are advantageous.

How to apply Applications should be written in English and include the following documents: (1) a cover letter detailing your suitability and motivation to join the research project (no more than one page), (2) a CV including details of your research experience, the abstract of your MSc thesis, and any publications, (3) the names of 2-3 potential referees. Please send the application as one single PDF document, to sophie.armitage@fu-berlin.de, with the following identifier in the subject field: WiMi InsectInfect_SA. The deadline for applications is the 30th March 2020. Interviews will take place as soon as possible after this date. The working language of the group is English. For further information, please contact Sophie Armitage.

Sophie Armitage <saoarmitage@zedat.fu-berlin.de>

Iceland 2 AquaticBiol

Please find below 2 MSc of research opportunities in Iceland for 2020:

"What shapes diversity within a species? Insight from an Arctic fish

Organisms in the Arctic and sub-Arctic areas are faced with unprecedented frequent fluctuations in their environment. In those geographical areas, diversity is mostly seen within a species (also called intraspecific diversity) rather than across species. Arctic charr (Salvelinus alpinus), a Northern freshwater fish, has colonised rapidly freshwater ecosystems after the last glaciation, and populations of Arctic charr can be found in various forms inhabitaing very various habitats (from anadromous type to small benthic fish living underground). Bulk of our work at Hólar University (North Iceland) has been to understand the interactions between the environment and development in shaping phenotypic variation in this species (e.g. SkÃºlason et al. 2019).

We conducted a plasticity experiment manipulating the diet (benthic versus pelagic) of juveniles fish originating from 5 populations of Icelandic Arctic charr, as well as some of their hybrids. Individual growth trajectories and behaviour of this fish are also known.

We are looking for two motivated students at the MSc level to characterise brain size/shape and meristic characters differences (gut length, gut complexity, sex, etc...) in these fish. Ideally the two students will work hand in hand collecting data, but each will have a separate project:

- The interplay of genetic and environmental factors in shaping brain size and shape in fish

- The interplay of genetic, developmental and environmental factors in shaping fish phenotypes (focusing on internal organs and anatomy)

Knowledge on the analysis of shape (geometric morphometrics) and basic coding in R software are good assets, but not compulsory.

MSc study:

These two research projects are ideal research projects for a Master in Aquatic biology at Hólar University. This Master is taught in English, with courses available on site as well as in other Icelandic universities. The Master is 120ECTS divided into 90ECTS of research and 30ECTS of courses. We preferably look for MSc students that will start in the Fall 2020 in our Department of Aquaculture and Fish Biology, SauÃ°arkrókur Iceland. These two projects are self-funded but there are opportunities to secure some small fundings once the studies have started.

Application: please send a CV and a cover letter indicating why you want to pursue a MSc of research and why this research topics motivates you? Please indicate the name of one or two previous supervisors that have directly worked with you. The application should be sent to

camille@holar.is and

ssteele@hi.is

-Our webpage:

https://www.holaraquatic.is/ -information on the MSc in Aquatic Biology at Holar:

https://ugla.holar.is/kennsluskra/index.php?tab=nam&chapter=namskra&Namsleid_=12&Namsleid__=20206&Namsleid___=62001520206&Namsleid=62001520206&submit=View -This is where most students and employees from our department live:

http://holar.is/en/location Thank you Camille

Camille Leblanc, lektor (Assistant Professor) Hólar University, Department of Aquaculture and Fish Biology Háeyri 1, 550, Saudárkrókur Iceland

Tel: +00 354 455 6387/ mobile +00 354 868 3689

Camille Leblanc <camille@mail.holar.is>

MasarykU 2 HostParasiteCoevolution

Evolutionary ecology of congeneric monogeneans One of the research topic of the group of evolutionary ecology of host-parasite interactions represents the studies of host-parasite coevolution using the systems of monogenean parasites and their associated fish hosts. Phylogenetic and cophylogenetic approaches have been applied to infer the patterns of parasite speciation and diversification and to reveal historical routes of dispersion of freshwater fish with current fragmented dispersion. The actual project of A. VeteÃÂnÃÂ’kovÃÂ Ã—imkovÃÂ focused on the investigation of diversity and phylogeny of host-specific congeneric monogeneans parasitizing cyprinid fish in Middle East representing the important place of historical contacts of fauna among three continents. Actually there is the open position for PhD student within the above mentioned project. The main objective of the PhD thesis will be to analyze the diversity and phylogeny of monogeneans exhibiting different level of host specificity (Dactylogyrus, Gyrodactylus and Diplozooidae). These parasites will be used as supplementary tool to infer the historical contacts of cypriniform fish between Middle East and Mediterranean areas using cophylogenetic approach.

Funding: fellowships of Masaryk University and partial salary covered by a grant project of supervisor. The successful candidate will follow PhD program at Masaryk University in Brno. The starting date is second half of September 2020. Qualification: Applicants with master degree in biological fields preferably with the previous experiences in parasite determinations (more specifically, working with fish monogeneans) and molecular analyses are invited to apply. The PhD study with the above mentioned topic is open by Masaryk University (program Evolutionary and Ecological Biology, specialization: Parasitology). Before submitting an official application to Masaryk University (deadline 30 April, 2020), the candidates are requested to contact Andrea VeteÃÂnÃÂ’kovÃÂ Ã—imkovÃÂ (simkova@sci.muni.cz) to discuss the specification of the topic. If interested, please, send (1) CV including a list of publications, (2) motivation letter, and (3) recommendation letters of two reviewers (including their e-mail contacts).

Coexistence of hybrid and polyploid forms of cyprinids: the role of parasitism

One of the research topic of the group of evolutionary ecology of host-parasite interactions represents the studies of genetic disruption in hybrid and polyploid fish hosts. Even natural hybridization in cyprinids is common phenomenon, the frequency of hybrids are relatively low. In contrast, the coexistence of the forms with different ploidy level is extraordinary evolutionary phenomenon in fish. Basically,research group of A. VeteÂ¹níková Â©imková focused on genetic disruption in fish hybrids hypothesizing the potential broken host-parasite co-adaptation especially for host specific parasites missing their closely associated hosts. However, the genes involved in metabolism and reproduction are in obvious interest as their pattern of expression may explain the mechanisms of current coexistence of hybrid and polyploid forms in cyprinids.

Actually there is the open position for PhD student within the above mentioned research topic. More specifically, the aim of the PhD thesis will beto analyze the transcriptome profile of diploid-polyploid complex of cyprinid fish and to search for the over expression and under expression of genes involved in growth, metabolism, reproduction and immunity. The PhD project will also include the experimental parasite infection; the quantification of the differentially expressed genes associated with parasites will be analyzed in diploid, triploid and tetraploid forms of hosts. Funding: fellowships of Masaryk University and partial salary covered by a grant project of supervisor. The successful candidate will follow PhD program at Masaryk University in Brno. The starting date is second half of September 2020. Qualification: Applicants with master degree in biological fields preferably with the previous experiences in molecular analyses including library preparation, qPCRand NGS bioinformatics analyses (fish transcriptome) are invited to apply. The PhD study with the above mentioned topic is open by Masaryk University (program Evolutionary and Ecological Biology, specialization: Parasitology). Before submitting an official application to Masaryk University (deadline 30 April, 2020), the candidates are requested to contact Andrea VeteÂ¹níková Â©imková (simkova@sci.muni.cz) to discuss the specification of the topic. If interested, please, send (1) CV including a list of publications, (2) motivation letter, and (3) recommendation letters of two reviewers (including their e-mail contacts).

Prof. Andrea VeteÅníková Åimková, Ph.D.

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MaxPlanck EvolutionaryOptimization

The research group Olfactory Coding headed by Dr. Silke Sachse in the Department of Evolutionary Neuroethology at the Max Planck Institute for Chemical Ecology offers a 3-year PhD position. The project is funded by the new priority program 2205 ÂEvolutionary optimization of neuronal circuits Â of the DFG. In tandem with the lab of Prof. Dr. Veronica Egger, University of Regensburg, the project aims to unravel the cellular basis of anisotropic lateral inhibition in the rat olfactory bulb and fly antennal lobe, a feature that is highly relevant for olfactory coding. As a key technique, we will employ 2-photon functional imaging combined with the MARCM technique to monitor odor-evoked activities of individual inhibitory neurons in the Drosophila antennal lobe. We ultimately aim to assign specific inhibitory interactions to defined neuronal types in both rat and fly and integrate these result into a new generic network model of the convergent olfactory system.

Payment will be based on the tariff contracts for the public service (65% E13). We provide an excellent research environment with enthusiastic scientists from different nationalities at the Max Planck Institute for Chemical Ecology in Jena, Germany (http://www.ice.mpg.de).

Candidate requirements:

- Master degree in Biology or related subject
- Strong interest in Neuroscience
- Interest in method development/refinement; ideally, prior experience in fly genetics and neurophysiology
- Very good skills in English (both in speaking and writing)

How to apply: The Max-Planck Society is an equal opportunity employer and strives to employ both genders equally, as well as to employ more individuals with disabilities. Please send your application as a single pdf in English including a letter of motivation, CV, list of publications and relevant certificates (degree certificates, etc.) and the names of two referees (including email address) to Dr. Silke Sachse (ssachse@ice.mpg.de).

Dr. Silke Sachse Research Group Leader Max Planck

Institute for Chemical Ecology Department of Evolutionary Neuroethology Hans-Knoell-Strasse 8 D-07745 Jena Germany

phone: 49 - 3641 - 57 - 1405 fax: 49 - 3641 - 57 - 1402 email: ssachse@ice.mpg.de web: http://www.ice.mpg.de/ext/olfactory-coding.html Silke Sachse <ssachse@ice.mpg.de>

MNHN Paris SocialEvolutionInsects

Sociality and convergent evolution: insights from ecomorphology and transcriptomics in cockroaches

The Museum national d'Histoire naturelle in Paris invites applications for a 3-year PhD position in evolutionary biology. The PhD project will be conducted under the supervision of Frédéric Legendre and Philippe Grandcolas within the Institut de Systématique, Evolution, Biodiversité (http://isyeb.mnhn.fr).

Description Despite progresses made in particular through kinship selection, understanding the circumstances of the emergence of integrated social systems remains a major challenge. In diploid organisms, unlike haplo-diploid organisms, kinship selection is, however, not the primary evolutionary cause. Ecological or morphological factors may have played a major role in the origin of sociality, but their relative importance remains suggested rather than quantified, without any formal phylogenetic test. This project aims to study, in a comparative framework, the influence of ecomorphological factors on the evolution of eusociality in the Blattodea (cockroaches and termites), a group of diploid insects with several subsocial convergent lineages and a single eusocial lineage. These tests will be conducted in the shift-in-dependent-care hypothesis framework, which emphasizes the importance of a wood diet and a subsocial behaviour. In parallel, transcriptomic analyses will be carried out on four targeted species, in order to assess the differential gene expression between wood-eating (or not) and subsocial (or not) species. Those transcriptomic data will also be used to assemble the genomic data acquired elsewhere (out of the scope of the PhD project) in the framework of the ANR PRCI SOCIOGENOMICS (PIs: F. Legendre and E. Bornberg-Bauer; 2020-2024). The PhD student will thus work in collaboration with our partner, specialized in comparative genomics of insects.

Methods The ecomorphology of the cockroach species and their social behaviours will be defined on the basis of literature and natural history collections. Several morphological features will be characterized: general shape, shape and ornamentation of the pronotum, leg ornamentation, shape of the mandibles, eye size, presence and length of wings. Parental behaviours will be identified from a pre-established list of 11 behaviours. Due to the broad comparative framework, an initial focus will be made on four essential lineages (and their sister-groups) and then progressively extended to other lineages, starting with those present in our 2015 phylogeny, which will serve as a basis for comparative phylogenetic analyses. For the latter, state-of-the-art methods will be used (e.g. phylogenetic path analysis, morphospace, ancestral state modeling).

Skills required - Master degree in evolution, systematics, biodiversity or any project- related discipline. - Established knowledge in phylogenetics and modern comparative methods (including skills in R). - Ability to work in an international collaboration. - Knowledge in comparative anatomy (of insects). - Expertise in transcriptomic analysis or in the evolution of sociality would be an asset, as would a naturalist background.

Application submission Applications must be submitted before the 5th of April 2020. The PhD will begin between May and October 2020. Please send your applications to both supervisors: detailed resume, motivation letter, grades (including M2 if possible), contact details of your current and previous surpervisors. Do not hesitate to contact us before sending your application if you want to talk about the project.

Contacts frederic.legendre@mnhn.fr philippe.grandcolas@mnhn.fr

Frédéric Legendre Associate Professor, HDR Curator of Dictyoptera Institut Systématique, Evolution, Biodiversité (ISYEB) Muséum national d'Histoire naturelle UMR 7205, MNHN, CNRS, Sorbonne Université, EPHE CP50, 45 rue Buffon 75231 Paris Cedex 05, FRANCE tel: +33 1 40 79 81 26 Fax: +33 1 40 79 56 79 Email: frederic.legendre@mnhn.fr

Frédéric LEGENDRE <frederic.legendre@mnhn.fr>

NHM UOslo ComparativeGenomics

For the following PhD (Jobbnorge ID:184791) please apply at https://www.jobbnorge.no/en/available-jobs/job/184791/doctoral-research-fellowship-in-comparative-genomics .The deadline for the deadline is at 14.04.2020.

Job description Applications are invited for a 4 year position in a Research Fellowship as a PhD Candidate in Comparative Genomics to be based at the Natural-History Museum, University of Oslo. The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD program at the Faculty of Mathematics and Natural Sciences. Appointment to a research fellowship is conditional upon admission to the Faculty's research training program. A plan for the research training must be submitted no later than two months after taking up the position, and the admission approved within three months. Compulsory service, duty work, shall represent 25% of the total hours of work.

More about the position The subject of the PhD project will part of the recently founded RCN-project "InvertOmics - Phylogeny and evolution of lophotrochozoan invertebrates based on genomic data". The origin and evolution of Bilateria is controversially discussed in several biological disciplines such as systematics or evolutionary developmental biology. In one hypothesis, evolution in Bilateria advances from a simple body organization similar to flatworms towards more complex forms several times independently. In the other one, the evolution progresses in the opposite direction from a complex ancestor more like an annelid to simple organizations by several separate reductions. Support for one or the other depends on the phylogeny and evolution of Lophotrochozoa, one of the major bilaterian taxa, but a robust phylogeny is still lacking despite recent phylogenomic studies. This is due to both low coverage by genomic data and misleading biases in data of lophotrochozoan taxa. In this project, high-quality reference genomes shall be generated and new procedures to both ameliorate negative effects of biases and establish a new support measurement, which is entirely different from all recent support measurements. Due to both the large genomic dataset and these thorough analyses, a robust phylogeny of Lophotrochozoa shall be provided allowing contributions to discussions about the origin and evolution of Bilateria as well as of lophotrochozoan taxa and character traits. The aim of this PhD project as part of InvertOmics is to concentrate on the problem of reconstructing the phylogeny of Lophotrochozoa from the data side. Therefore, new high-quality genomes for 50 lophotrochozoan species covering all 16 lophotrochozoan phyla shall be generated. Modern genome sequencing strategies combining long and short reads will be employed. As several lophotrochozoan species have very small body sizes ($<$ 500 length) this is challenging, but existing protocols for single-cell genomics shall be optimized for single small-sized individuals collected from natural populations as part of the project. These data together with publicly available genomes will be used to reconstruct the phylogeny of Lophotrochozoa and address possible biases in the dataset using newly developed approaches as part of this project (see the accompanying advertisement for a PostDoc position). The phylogenetic reconstructions will be used to trace the evolution of different character traits within Lophotrochozoa and Bilateria, which also take into account the uncertainty of relationships. Therefore, modern macroevolutionary tools to reconstruct ancestral states will be used. The Natural History Museum has a modern DNA laboratory as well as access to the Norwegian Supercomputer facilities. The PhD will be associated with the research group "Frontiers in Evolutionary Zoology", specifically Torsten Struck (Professor of Evolutionary Genomics).

Qualification requirements - Applicants must hold a Master's degree or equivalent in biology or related disciplines like bioinformatics. - A good command of English is required. - We seek a person with strong motivation for research in genomics. - The candidate must be skilled in general molecular laboratory practices. - Experience with next-generation sequencing of genomes is required and working with small amounts of tissue material (i.e., whole genome amplification) is preferable. - Computing skills and background in bioinformatics to assemble and annotate genomes are expected.

Evaluation of the application In assessing applications, particular emphasis will be placed upon the academic and personal ability of the candidate to complete the project within the given timeframe and write a PhD thesis under supervision. Interviews with selected candidates will be arranged. Please

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NorwegianUSciTech ConservationGenetics

PhD position in conservation genetics: The importance of inbreeding and genetic drift in conservation of fragmented populations

A fully-funded 4-year PhD position in basic conservation genetics research is available at the Centre for Biodiversity Dynamics, Department of Biology, Norwegian University of Science and Technology (http://www.ntnu.edu/cbd).

About the position: A major challenge in conservation biology is the lack of information needed to properly evaluate genetic risks of population extinction. Specifically, there is great need for a better understanding of the mechanisms underlying inbreeding depression and loss of genetic variation in nature, and how these processes affect the dynamics and viability of fragmented populations. The PhD project is part of a research project recently funded by the Research Council of Norway (RCN) that aims to provide such insight. First, the PhD candidate will integrate genomic analyses of inbreeding and genetic drift with high-quality demographic data to identify the causes of spatio-temporal variation in inbreeding and inbreeding depression, and examine the occurrence and strength of drift load in subdivided house sparrow (Passer domesticus) populations at the coast of Norway. Second, data from both natural and experimentally-manipulated populations will be used to examine the genetic architecture of inbreeding depression and heterosis. Third, novel quantitative genetics and genomics approaches will be used to quantify the effect of inbreeding and drift for the adaptive potential in subdivided populations. These results will be combined with results from other parts of the RCN project to evaluate the importance of genetic processes and spatial structure for the short- and long-term viability of fragmented populations.

The PhD student will work closely with two postdocs and national and international collaborators and will be supervised by Professor Henrik Jensen (main supervisor), Professor Jane Reid and Associate Professor Stefanie Muff (co-supervisors) at CBD, NTNU.

Job description: The PhD project will involve sophisticated statistical analyses of extensive genomic data (genome-wide high-density SNP genotypes and whole genome sequences) and field data (individual data on phenotypes, survival and reproduction). The PhD student is expected to participate in fieldwork and further research training in house sparrow populations at the coast of mid- and northern Norway. The project would suit a highly motivated and numerate student with enthusiasm for working on fundamental questions in conservation genetics using empirical data. Full training in key aspects of the project, and associated transferable skills, will be provided. The position provides an excellent opportunity for students who wish to qualify for future work in both basic and applied research positions and/or wish to pursue a career in academia.

Qualification requirements: We seek candidates with a keen interest in conservation genetic questions and a strong academic record in quantitative evolutionary ecology and/or population genetics (including quantitative genetics and genomics). Good competence in R and/or other statistical programming languages is also important. The qualification requirement is completion of a master's degree or second degree (equivalent to 120 credits) in biology or equivalent education, with a grade of B or better in terms of NTNU's grading scale. Applicants with no letter grades from previous studies must have an equally good academic foundation. Applicants who are unable to meet these criteria may be considered only if they can document that they are particularly suitable candidates for education leading to a PhD degree. MSc students who expect to complete their master's degree studies by summer 2020 are also encouraged to apply. Employment will then be postponed until the master's degree is finished.

Other desired qualifications: - Fundamental knowledge or very strong interest in relevant topics in conservation genetics and evolutionary biology, for example inbreeding depression, heterosis, genetic rescue, quantitative genetics - Willingness to learn and use novel statistical and/or mathematical analysis methods - Good written and oral English - Some experience with fieldwork and/or molecular genetic laboratory work is favourable - Experience working with large genomics data sets would be advantageous

Personal characteristics: - Highly motivated and enthusiastic about conservation genetics - Excellent teamworking and written and verbal communication skills - An independent, self-driven working style

We offer: - An exciting and stimulating project that is part of a strong international academic research environment - An open and inclusive work environment with dedicated and interactive supervisors and colleagues, fostering gender equality and international mobility in science

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Stockholm ButterflyPlantEvolution

PhD position in Evolutionary genomics of butterfly-plant associations (deadline April 23)

A PhD position has been announced at the Department of Zoology, Stockholm University, Sweden, as part of the project "Evolving modularity in the adaptations of phytophagous insects to their host plants", newly funded by the Swedish Research Council.

The Department of Zoology is a vibrant international community, consisting of five interactive and collaborative divisions: Ecology, Ethology, Functional Morphology, Population Genetics, and Systematics and Evolution. The advertised PhD will be part of the Division of Ecology.

The project aims to improve our understanding of the causal mechanisms behind the evolutionary patterns observed in insect-plant associations, and is based on the idea that adaptations to specific host plants can best be understood as "modules" of co-expressed genes and the corresponding phenotypes – in particular larval performance on different hosts.

Work in the PhD project will focus on butterflies, and will involve field collection and laboratory rearing of insects, including short-term selection experiments, as well as genomic analysis of in particular RNA-sequencing data. Experience from rearing and genomics of non-model insects is thus particularly meriting.

The position is for four years full time, with salary and social security. To be eligible you need a degree corresponding to at least four years of higher education, including an independent project at an advanced level in animal ecology, evolutionary biology or similar subject (i.e. a Master's degree or similar).

The project will be supervised by Prof. Sören Nylin:

https://www.su.se/english/profiles/snylin-1.183643 and co-supervised by Prof. Niklas Janz:

https://www.su.se/english/profiles/janz-1.182966 Informal inquiries and expressions of interest are welcome to soren.nylin@zoologi.su.se.

Formal advertisement and link to application (deadline April 23):

https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=11873&rmlang=UK –

Soren Nylin Professor i Zoologisk Ekologi/Professor of Animal Ecology Biology Section Dean

Department of Zoology Stockholm University S-106 91 Stockholm SWEDEN

Soren.Nylin@zoologi.su.se

Soren Nylin <soren.nylin@zoologi.su.se>

StockholmU YeastExperimentalEvolution

Fully funded 4-year PhD position available in Population Genetics: Dynamics of Adaptation using Experimental Evolution with Yeast, Fitness Landscape Theory, and Machine Learning

Supervisor: Rike Stelkens Start date: October 2020 (negotiable) Application deadline: 23 April 2020

A PhD position in experimental evolution with the budding yeast Saccharomyces cerevisiae is available in the Stelkens lab. We are generally interested in the role of hybridization - the interbreeding of individuals from genetically divergent populations or species - in adaptive evolution. Hybridization instantly increases the genetic variation of the populations, which can be exploited for adaptation through natural selection, and help hybrids succeed in ecological niches where parents cannot survive. At the same time, hybridization is a serious conservation concern because hybrid offspring usually have poor fitness. We are excited by this 'double agent' role of hybridization with both detrimental and beneficial effects on biodiversity, especially under environmental stress.

Topics of this PhD thesis include (but are not limited) to 1) the dynamics of adaptation to changing environments with and without hybridization, 2) the construction of empirical fitness landscapes using DNA barcodes to track the evolution of lineages over time, 3) understanding the genetic architecture of (hybrid) fitness using machine learning and statistical modelling. This position is part of a paired PhD programme between the Zoology and Mathematics Department at Stockholm University. The goal of this programme is to scrutinize mathematical theory with experimental data, and to combine population genetics, machine learning and statistical modelling.

Qualifications: We are looking for a highly motivated person with a strong interest in evolutionary biology, ideally with experience in experimental evolution and quantitative/molecular/population genetics. Prior training in Saccharomyces yeast cultivation, statistics and programming (e.g. R, Python, Perl) is a plus. Applicants should be able to think quantitatively, be well-organized, good communicators, and happy to work in our very international team. The applicant is expected to be fluent in English. Training will be provided in experimental evolution, forward and reverse molecular genetics, statistics, bioinformatics, genomic data analysis, and microbiology. There is flexibility within the project for the student to develop their own interests. The graduate program covers four years of full-time study. The position can be combined with teaching (maximum 20%), which prolongs the employment with the corresponding time. The successful candidate will receive salary and full social benefits according to local agreements.

Environment: The campus is located four metro stops from the center of Stockholm, one of the most beautiful and dynamic capitals in Europe. The campus is home to a vibrant scientific community, including the Science for Life Laboratory (genomics and bioinformatics core facility) and the Swedish Museum of Natural History. Sweden is a free and open society, and strives to be one of the world?s most innovative and research-intensive nations. We enjoy a respected system of democracy and individual rights, free health care, freedom of speech, a free press, the right to scrutinize those in power, and access to beautiful nature. Most Swedes speak English.

Application: Please send formal application, including a statement of motivation, relevant expertise, a CV and the contact details of at least two references through the official Stockholm University job portal: https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=11782&rmlang=UK It is strongly recommended that you read relevant literature and tailor your cover letter and application accordingly. Applications without this will not be considered. Literature to read before applying: https://academic.oup.com/mbe/article/37/1/167/5569557 https://www.ncbi.nlm.nih.gov/pubmed/31199875 https://onlinelibrary.wiley.com/doi/full/10.1111/-eva.12214 More details on research and teaching in the department: https://www.su.se/zoologi/english/ Enquiries to: rike.stelkens@zoologi.su.se

Rike Stelkens Assistant Professor Division of Population Genetics Department of Zoology Stockholm University, Sweden lab website: stelkenslab.com

Rike Stelkens <rike.stelkens@zoologi.su.se>

UCopenhagen AncientEnvironmentalDNA

PhD fellowship in ancient environmental DNA at the Globe Institute, University of Copenhagen

We are offering a PhD fellowship in ancient environmental DNA commencing 1 June 2020 or as soon as possible hereafter.

The successful candidate will be part of the Copenhagen group of the ERC Synergy project, Seachange, in which a cross-disciplinary approach is adopted to assess the impact of major cultural transitions on marine ecosystem functioning and biodiversity. Apart from ancient environmental DNA analyses, the overall project includes classical zooarchaeology, isotope analyses, dating methods, marine historical ecology and ecosystem modeling. The PhD candidate will take an active part in the overall Seachange project. In the Copenhagen group, the student will work alongside a Postdoctoral Fellow, specifically on metabarcoding and shotgun sequencing of environmental DNA time-series in midden, bulk-bone and/or marine sediment core samples from Australia, Antarctica and/or Iceland. The main focus will be on fieldwork and subsampling from already collected samples, development, optimization and validation of laboratory protocols, ecological analyses of the generated environmental DNA time series in relation to cultural transitions in one or more sites and on data integration across disciplines.

Further details: https://employment.ku.dk/phd/-?show=151462 Best wishes,

Kristine

Kristine Bohmann Associate Professor

University of Copenhagen Faculty of Health and Medical Sciences eDNA Group / DNAmark DNA reference database Section for Evolutionary Genomics, GLOBE Institute

Ãster Farimagsgade 5, CSS Building 7, 2nd floor 1353 Copenhagen K, Denmark

Tel.: +45 40750521 Skype: kristinebohmann

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Kristine Bohmann <kbohmann@sund.ku.dk>

UGeneva Evolution

The PhD School of Life Sciences at the University of Geneva is pleased to announce the Winter Call 2020 for PhD applications, deadline April 15th, 2020.

The newly created school strives to educate tomorrow's innovative, independent scientists. The PhD School offers the opportunity to perform research in one of the most innovative universities in the world.

Students will join a multidisciplinary environment, uniting over 140 research groups in 6 competitive programs:

§Ecology and Evolution

§Biomedical Sciences

§Molecular Biosciences

§Pharmaceutical Sciences

§Physics of Biology

§Genomics and Digital Health

Students benefit from core training in their home program and any other training of their choice, including opportunities offered at the partner universities in Lausanne, Fribourg, Neuchâtel, and Berne. The School encourages scientific and social exchange among students in all programs through annual PhD retreats and the PhD Forum.

The PhD School invites applications from motivated candidates all over the world. Applicants should hold or expect to obtain shortly a Master's degree or equivalent from a university in a field of Life Sciences.

Geneva rates among the top ten cities for quality of life, and offers many cultural and sportive opportunities outside PhD life. Students in the research groups of the School are guaranteed a stipend commensurate with the cost of living in Geneva.

Website: https://lifesciencesphd.unige.ch/ Email contact: phd-lifesciences-sciences@unige.ch

Application link: https://apply.lifesciencesphd.unige.ch/login phd-lifesciences-sciences <phd-lifesciences-sciences@unige.ch>

UGroningen 9 Evolution

9 PhD Scholarship positions in Evolutionary Life Sciences

Host organization

The University of Groningen is a comprehensive research university with a global outlook, deeply rooted in Groningen, City of Talent. Quality has been our top priority for over four hundred years, and with success: the University is currently in or around the top 100 on several influential ranking lists.

The Faculty of Science and Engineering (FSE) is the largest faculty within the University. We offer first-rate education and research in a wide range of science and engineering areas, from astronomy and biology to nanoscience and mechanical engineering. Our community has an open and informal character with students and staff from around the world.

GELIFES, the second largest institute of the Faculty of Science and Engineering fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches, aiming to understand adaptation on all levels of biological organisation. Researchers pursue fundamental questions while collaborating with partners from industry, medicine and other realms of society. For its research programme, called Adaptive Life, which is one of the six focus themes of the FSE and celebrates its first lustrum this March, the institute is looking to contract 9 new PhD students .

Our research fields include behavioural biology, chronobiology, ecology, evolutionary biology, genetics and genomics, neurobiology, physiology and theoretical modelling, using a wide array of research tools. Research levels range from molecular and organismal to population and community, performed under laboratory, semi-natural and field conditions. Studying the framework of evolutionary adaptation allows for a large diversity of model organisms, for which we have extensive facilities. A wide array of species are studied, from microbes, algae, plants and insects to vertebrates such as fish, birds, rodents, marine mammals and humans.

We offer 9 full scholarships for PhD projects within our research theme Adaptive Life.

PhD project description

GELIFES offers 9 four-year scholarship PhD positions for the most talented and motivated national and international students, starting between July and September 2020. All PhD positions are integrative by nature, spanning across different expertise groups or institutes. Upon selection, PhD candidates will receive expert supervision and mentoring, and excellent training through cutting-edge research projects, advanced courses and training opportunities, complemented by workshops on generic research, transferable skills and teaching. The home base for GELIFES' research is the spectacular Linnaeusborg at Zernike Campus, Groningen. Research is performed with state of the art equipment and in well-equipped facilities.

As a PhD candidate, you are committed to conduct independent and original scientific research, to report on this research in international publications and presentations, and to present the results of the research in a PhD dissertation, to be completed within four years. After thesis completion, many of GELIFES' PhD students move on to top positions in academia or industry.

For an overview of currently available supervisors and potential topics, please check the Adaptive Life website < https://www.rug.nl/research/fse/themes/adaptive-life/research/phd-projects-3 > . On this website you will also find a description of projects started in the 1st and 2nd round of the programme.

Here you will also find the link <https://www.rug.nl/education/phd-programmes/phd-scholarship-programme/phd-scholarships?details to the vacancy website detailing all information pertaining to the application procedures, the application link, conditions of the scholarship programme, English language requirements and time line as indicated below in brief. We recommend all candidates to contact potential supervisors prior to applying.

Qualifications

We are looking for highly motivated, proactive and diligent researchers with good communication skills and the ability to work in an interdisciplinary team. Demonstrable command of the English language is a prerequisite. Successful candidates have completed a Master's degree (or equivalent) that is relevant to the topic of interest.

Conditions

The position is offered within the UG PhD Scholarship Programme. This programme is issued by the Dutch Ministry of Education, Culture, and Science (OCW) within the framework of the national PhD Scholarship Programme. PhD scholarship students receive a scholarship (stipend) of Â¿ 2,181 per month (gross) from the University of Groningen for a period of four years. PhD scholarship students are not employed by the university. PhD scholarship students

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UGuelph FishGenomics

Fully-Funded M.Sc. & Ph.D. Opportunities in Fish Stress Genomics: Genomic Network for Fish Identification, Stress and Health

Project summary: The Bernier Lab at the University of Guelph is looking for highly motivated MSc and PhD candidates to join the Genomic Network for Fish Identification, Stress and Health—(GEN-FISH). This large scale, multi-lab, research project funded by Genome Canada aims to develop, optimize and field test an integrated genomic "toolkit" to accurately assess and monitor the health status of fish for the management of Canada's freshwater fish resources on a broad geographic and taxonomic scale.

Position summary: As a member of GEN-FISH (www.gen-fish.ca), you will be involved in developing, testing, and validating a high throughput universal gene expression panel for fish health. Specifically, validation experiments performed at the Alma Aquaculture Research Station will assess the responsiveness of the gene expression panel using multiple species x stressor interactions. Parallel evaluation of standard and novel stress biomarkers will complement the gene expression profiling results and provide an integrated molecular to organismal view of fish health.

How to apply: Anyone wishing to apply should send their CV, unofficial transcript, names and contact information of 2 references, and a letter of interest to Dr. Nick Bernier.— Interested candidates should have a strong interest in stress physiology and preferably research experience in molecular biology.— Further information on the graduate program and stipends for MSc & PhD students in the Dept. of Integrative Biology can be found at—https://www.uoguelph.ca/ib/grad_program_overview . Start date: May 2020, but this date is flexible and the positions will remain open until filled.

Contact:—Nick Bernier: nbernier@uoguelph.ca

Sara Jamieson <saraj@uwindsor.ca>

ULethbridge Avian Paleoneurology

The Iwaniuk lab at the University of Lethbridge currently has an opening for a MSc or PhD student interested in avian paleoneurology. The successful applicant will work on a collaborative project with the National Museum of Natural History (Smithsonian Institution) on the brain and sensory system anatomy of extinct birds. The project will rely primarily on micro-CT scanning of fossil and subfossil specimens, with the aim of understanding the sensory ecology of extinct bird species. There will also be opportunities to learn histology and digital microscopy techniques as well as using our extensive comparative brain collection, now housed within a brand new science building.

Potential applications should have research experience in ornithology, paleontology, comparative anatomy, or neuroanatomy. Previous experience with Avizo, Mimics or R is desirable, but not essential.

The University of Lethbridge offers competitive scholarship funding, including tuition waivers, for applicants based on grades and research experience. Students in the Iwaniuk lab typically attend international conferences annually and support is available for workshops relevant to thesis work.

Start dates are flexible, but the next deadline for the School of Graduate Studies for applications is May 1st 2020.

To apply, send: 1) a c.v.; 2) unofficial copies of academic transcripts; and 3) a brief description of your research interests to: andrew.iwaniuk@uleth.ca. More information about our lab can be found at: http://scholar.ulethbridge.ca/iwaniuk/home. Additional information on scholarships and deadlines can be found at: https://www.uleth.ca/graduate-studies/ Andrew N. Iwaniuk Associate Professor Canada Research Chair in Comparative Neuroanatomy Canadian Centre for Behavioural Neuroscience University of Lethbridge Lethbridge AB T1K 3M4 Canada office: +1 403 332 5288 http://scholar.ulethbridge.ca/iwaniuk/home Bird-brain (bÃ≫rd brān)1. a person regarded as silly or stupid.

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

ULisboa EvolutionaryBiology

PhD opportunity in Evolutionary Biology at the Universidade de Lisboa, Portugal

We are seeking one PhD candidate to apply to the 2020 Doctoral Program of the Portuguese Science and Technology Foundation (Fundação para a Ciência e Tecnologia) to conduct research on the mechanisms underlying divergence and speciation of a seabird complex that has seasonal breeding populations isolated by time.

Project: A possible mechanism of sympatric speciation is allochrony, in which differences in breeding times lead to temporal assortative mating and limit gene flow among asynchronous breeders. With this project we propose to characterize the genomic architecture of regions of evolutionary significance in temporal divergence and speciation. The project will focus on the Madeiran Storm-petrel complex, which showcases one of the only known avian example with divergence and cryptic speciation driven by isolation by time (Friesen et al. 2007, Silva et al., 2016, Taylor et al. 2017, 2019). The sympatric but allochronic populations of this species complex span the speciation continuum from complete reproductive isolation in the Azores, where seasonal (ie, summer and winter) populations have speciated, to those weakly differentiated in Madeira, and genetically admixed in Cape Verde and the South Atlantic. The pattern of replicated pairs of populations diverging along this continuum provides an outstanding opportunity to investigate the mechanisms underlying parallel allochronic divergence.

Supervision: Research will be co-supervised by Dr. Mónica Silva, Research Associate at the Center for Ecology, Evolution and Environmental Changes, Universidade de Lisboa (http://ce3c.ciencias.ulisboa.pt/member/moacutenica-c-silva) and Prof. Vicki Friesen, Queens University, Canada (https://biology.queensu.ca/people/department/professors/vicki-friesen/).

Application: Applicants must have a good scholar record and hold a Masters degree in a relevant field (Evolutionary Biology, Biology, Bioinformatics). It is mandatory that students have good analytical skills and previous training in population genomics or comparative genomics. The candidate should be fluent in written and spoken English. At least one publication(s) significantly increases the competitiveness of the applicant.

The applicant is expected to apply to a PhD scholarship by Fundaçāo para a Ciência e a Tecnologia which will cover both tuition fees and living expenses (more info here: https://www.fct.pt/apoios/bolsas/concursos/individuais2020.phtml.pt). The call will be open between the 2nd and 31st March (17h00 local time). Applications will be submitted in English. The candidate will write and submit a grant proposal working closely with both supervisors.

Candidates should soon send their CV and a detailed motivation letter demonstrating the fit for the position to Monica Silva, mssilva@fc.ul.pt.

Mónica C. Silva, Ph.D Centro de Ecologia, Evoluçāo e AlteraçÃµes Ambientais (cE3c) Faculdade de Ciências, Universidade de Lisboa

Monica Silva <mssilva@fc.ul.pt>

ULouisiana ConservationEvolutionaryGenomics

Graduate Position in Conservation and Evolutionary Genomics

University of Louisiana at Lafayette

The Cassin Sackett Lab at the University of Louisiana is looking for a highly motivated graduate student to study population and conservation genomics in prairie dogs or associated species (e.g., other rodents and fleas). We use ancient DNA, field sampling, next-generation sequencing and bioinformatic approaches to answer fundamental questions in evolutionary biology, especially those with practical conservation applications. Some major questions being asked in the lab are:

§How do humans influence the evolution of wildlife? We study the ways in which climate change, habitat alteration, and introduced diseases impact the distribution of genetic variation, rates of gene flow, and the probability of adaptation.

§What is the genomic basis of rapid adaptation to novel pathogens? We examine the demographic and environmental constraints to adaptation and whether genomic architecture of rapid adaptation differs from that of more gradual adaptation (e.g., to climate).

Please visit the lab website for more details on current projects: www.cassinsackett.com The student will work in a collaborative environment on aspects of a project that uses genomic approaches to investigate the potential for resistance to *Yersinia pestis*, the bacteria causing plague. Projects could include: 1) systematics, co-evolution and vector competence in fleas, 2) landscape genetics, phylogeography and adaptation in prairie dogs, 3) molecular evolution in prairie dogs, 4) evolution in co-occurring rodent species, or 5) other relevant topics.

The position is supported by a teaching assistantship, with the possibility of future RA support pending funding. The position will be based in UL's Department of Biology (https://biology.louisiana.edu/). Interested applicants should contact cassin.sackett@gmail.com for inquiries. The desired start date is spring 2021.

Qualifications:

Applicants should have a bachelor's degree in biology, computer science, or a related field. We are looking for a student who is motivated, hard-working, and passionate about topics in evolutionary biology. The student should have or be willing to develop excellent organizational and communication skills, computing skills, and the desire/willingness to engage in outreach. The Cassin Sackett lab is committed to increasing diversity in STEM, and we especially encourage applications from women, minorities, veterans and other underrepresented groups.

How to apply:

Interested candidates should apply by October 1 (but earlier applications are encouraged) following the guidelines at https://gradschool.louisiana.edu/admissions . – Loren Cassin Sackett, Ph.D. Fulbright Scholar, Colombia Research Affiliate, Smithsonian Institution Assistant Professor, Biology University of Louisiana Lafayette, LA 70504 www.cassinsackett.com Latest paper: https://onlinelibrary.wiley.com/doi/abs/10.1111/1755-0998.13122 Loren Cassin Sackett <cassin.sackett@gmail.com>

UNaples 2 PlantEvolBiology

TWO PHD POSITIONS IN PLANT EVOLUTIONARY BIOLOGY AT THE UNIVERSITY OF NAPLES

1. PROJECT DESCRIPTION: The selected student will work with Dr. Salvatore Cozzolino (https://www.docenti.unina.it/salvatore.cozzolino) on a research project entitled "The contribution of plastic and hereditable components in scent emission for shaping species distribution and speciation in sexually deceptive or-

chids"

We are interested in how diversity evolves and understanding the processes and factors that determine the spatial distribution of species on the planet. By using one of the most evolutionary successful families of flowering plants, the orchids, as a study system, we are addressing a set of inter-related questions about species sorting/species coexistence and competition. In particular, by focusing on sexually orchids, floral scent traits modulating adaptations to pollinators as well as their molecular bases will be studied using selection analysis, phenotyping (particularly for floral volatiles) and segregation analyses. We are particularly interested in how plasticity and hereditability of scent emission in sexually deceptive Ophrys allows the potential for rapid adaptation to local pollinator. This is a central issue for species radiation but also for rapid adaptive response to climate changes. POSITION CHARACTERISTICS: The Department of Biology in Naples (http://www.dipartimentodibiologia.unina.it/) offers excellent research facilities and a stimulating working environment for graduate students in plant ecology and evolution. The project will also involve strict collaboration with orchid researchers in Germany (Prof. Philipp Schlueter) and Switzerland (Prof. Florian Schiestl). Salary is according to the University of Naples PhD guidelines. Funding, including for laboratory and field costs, is available for 3 years.

REQUIREMENTS: Applicants should hold a Master degree in plant systematics, biodiversity, plant ecology or evolutionary biology. Prior experience with plants and/or pollinators is an advantage, expertise in profiling scent emission by GC-MS and solid preparation in biostatistics are highly appreciated. Proficiency in English both orally and written is a must; for a project including field work a driver license is desirable.

PhD candidate should apply to the 2020 Doctoral Program in Biology. As pre-application

: i) PhD candidate should apply to the 2020 Doctoral Program in Biology. As pre-submission a two-page application letter describing your research interests, clearly stating why are you interested in a Ph.D. position in evolutionary botany and your career goals; ii) your CV, including a list of publications (if applicable); iii) a copy of your undergraduate and graduate academic record; iv) names and contact details of at least two referees selected from your academic advisors. HOW TO APPLY: Send the following documents by email AS A SINGLE PDF FILE to Dr. SALVATORE COZZOLINO (cozzolin@unina.it). DEADLINE FOR APPLICATION: Applications will be screened from March 15th 2020 to April 15th until the position is filled.

STARTING DATE: 1st november 2020.

2. PROJECT DESCRIPTION: The selected student will work with Dr. Salvatore Cozzolino (https://www.docenti.unina.it/salvatore.cozzolino) on a research project entitled " The potential for rapid pollinator niche diversification is fueled by ancestral lineage hybridization"

We are interested in how diversity evolves and understanding the processes and factors that determine the rapid sorting of species in some radiating clades. By using one of the faster flowering plant radiating group, as the Mediterranean sexually deceptive Ophrys, we are addressing a set of inter-related questions about species sorting/radiation by ancestral hybridization. In particular, we focus on two recent species groups that presumable sorted out and quickly radiated following hybridization of ancestral lineages. The PhD project will focus on testing the tempo and mode of origin by hybridization of the these radiating Ophrys lineages by using genomic tools and in-depth phylo-/population-/pan-genomics analytical approaches.

POSITION CHARACTERISTICS: The Department of Biology in Naples (http://www.dipartimentodibiologia.unina.it/) offers excellent research facilities and a stimulating working environment for graduate students in plant genomics and evolution. The project will also involve strict collaboration with orchid researchers in Germany (Prof. Philipp Schlueter) and Switzerland (Prof. Alex Widmer). Salary is according to the University of Naples PhD guidelines. Funding, including for laboratory and travelling, is available for 3 years.

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UOrleans France InvasiveXylophagousBeetles

A fully-funded Ph.D. position is available at INRAE Unité de Recherche de Zoologie Forestiere, Orléans on "Surveillance of invasive xylophagous beetles using DNA metabarcoding" Biological invasions represent the third most important global threat to biodiversity and a major risk for the economy, the environment and society.

A major finding in the last few years is the sharp increase in interceptions of emerging exotic species, not previously known as invasive and sometimes unknown to science. It is therefore essential to develop genomic tools that will allow to detect and identify exotic species potentially invasive to be able to set up measures to eradicate them at an early stage.

The main aim of this thesis is to develop a nondestructive metabarcoding approach to detect newly arrived exotic xylophagous cerambycid beetles collected with automatic pheromone traps set up across the major European ports of entry. We will develop DNA barcoding reference libraries for Holarctic Cerambycidae beetles with a focus on China as a major source of invasive species into Europe.

This thesis is part of the European project HOMED (http://homed-project.eu/) The position is available from 1st October 2020 and limited to 3 years. We are seeking a student who is highly motivated and passionate about Genomics and Entomology. Preferred candidates will have experience in DNA metabarcoding and forest entomology, although experience in these areas is not necessary. The successful candidates will be supervised by Dr Geraldine Roux (Univ Orléans), Professor Stephane Boyer (Univ Tours) and Dr Carlos Lopez-Vaamonde (INRAE, URZF, Orléans) and will be based at Unité de Recherche de Zoologie Forestiere, Orléans and registered at University of Orléans. International students are welcome to apply. Interested applicants should submit a CV, a copy of their academic transcript and a cover letter outlining their research interests before the 27th March 2020 to : geraldine.roux@inra.fr ; carlos.lopezvaamonde@inra.fr ; stephane.boyer@univ-tours.fr

Carlos LOPEZ-VAAMONDE Research Scientist INRAE-Centre Val de Loire, Unité de Zoologie ForestiÂÂre 2163 Avenue de la Pomme de Pin CS 40001 Ardon, 45075 Orléans Cedex 2, France. Tél. : +33 247367349 email: carlos.lopezvaamonde@inrae.fr https://www6.val-de-loire.inra.fr/entomocentre/ https://pollen.univ-tours.fr/lequipe/ Carlos Lopez Vaamonde <carlos.lopezvaamonde@inra.fr>

USouthBohemia NeoSexChromosomes

PhD position in Molecular Biology & Genetics

We are looking for excellent & highly motivated candidate for a PhD position in the* Laboratory of Comparative Cytogenetics and Genomics* (http://bit.ly/-2Vvhc50) lead by *Petr Nguyen*.

Project:* Neo-sex chromosome evolution in Lepidoptera* Sex chromosomes, their differentiation, and role in speciation belong to the most intriguing questions of evolutionary genetics. It was proposed that comparison of patterns in sex chromosome evolution between male and female heterogametic taxa could be informative for identification of general features of this process. Moths and butterflies (Lepidoptera) represent the most speciose lineage with female heterogamety (WZ/ZZ). Unlike in other WZ/ZZ taxa, sex chromosome-autosome fusions are common in Lepidoptera, which makes them ideal model system for investigations into establishment and differentiation of neo-sex chromosomes. The project aims at investigating drivers of lepidopteran neo-sex chromosome evolution and a role of sex chromosome turnover in species divergence. It will encompass generating genomic resources, expression profiling, and cytogenetic and population genetic analyses in several non-model taxa such as ghost moth chromosome races and butterflies of the tribe Danaini.

Offer: > PhD study for 4 years 2020-2024 (possible start in Aug/Sep 2020; http://bit.ly/2TrFSK1) > research campus with a strong tradition in biosciences > professional career development in science & soft skills > access to the state-of-the-art research infrastructure & equipment > focus on activity, creativity & innovativeness > international collaboration & visibility, international short-term research visits > English speaking, stimulating and friendly environment > PhD fellowship & part-time job employment on research grants > administration support with relocation & settlement in the Czech Republic > participation in annual PhD retreat > meals allowance, full health insurance, student benefits > work-life balance in a middle-sized university city offering options for outdoor, sport & cultural activities

Requirements: > MSc in Molecular Biology, Genetics or similar > proficiency in English 'V oral and written > openness to learn new techniques, active attitude to problem-solving > ability to work in a team > independent thinking & passion for science

How to apply: Please submit your structured CV including list of publications, motivation letter, name & contacts of two academic referees via e-mail to *jobs@prf.jcu.cz* by *Wed 15 Apr 2020*. Interviews with selected applicants will be held in April 2020.

For more information, contact Petr Nguyen Assistant Professor Department of Molecular Biology and Genetics Faculty of Science, University of South Bohemia Ceske Budejovice, Czech Republic petr.nguyen@prf.jcu.cz; http://bit.ly/2Tq4uSn Petr Nguyen <petr.nguyen@prf.jcu.cz>

UTurku AvianMicrobiome

A funded PhD position in host-microbiome associations in wild birds (University of Turku, Finland)

We are seeking an outstanding PhD (graduate) student to lead an exciting project exploring the causes and consequences of variation in gut microbiome in a wild bird populations.

All organisms on our planet carry microorganisms in their gut. Human and animal model studies show that gut microbiome is strongly linked to health. Host and its full microbial community have been suggested to form an inseparable entity ’V the holobiont, yet the importance of gut microbiome is poorly understood in wild populations, for example in birds. The project goals are to understood the causes and consequences of variation in microbiome composition in wild populations, and whether microbiome can contribute to local adaptation and allow animals to respond to changing environment. The study system is the wild populations of the passerine great tit (Parus major), a well-known ecological model system.

The work will include (1) collecting and coordinating microbiome data collection at large spatial scale across European populations, (2) conducting experimental microbiome manipulations in wild populations of great tits and common-garden experimental designs (3) laboratory analyses of microbiome and physiological biomarkers (4) statistics and bioinformatics of microbial data (5) dissemination of project results via high-quality journal publications and conference presentations.

Requirements - MSc degree in ecology, evolutionary biology, physiology, genetics or microbiology. - Background knowledge in ecology, physiology and microbial ecology. - High motivation to learn molecular, statistical and bioinformatic skills is essential. - Experience laboratory work/ experimental designs and working in wild populations/ knowledge on avian ecology is a bonus. - Excellent English writing and verbal communication skills are essential.

We offer - Funding for 3 years (25000pounds /year, partly tax-free). A further grant for the 4th year can be applied (high success). - Resources for travel to conferences or workshops abroad. - Well equipped labs and state-of-the-art scientific equipment, software, access to journals and scientific databases - Supervision in all aspects of the work (from field to lab to computational skills), possibility to join workshops to cement the skills in e.g. bioinformatics - International, enthusiastic working environment (the working language is English), large collaborator network. - Starting date: Sept-Nov 2020 The PhD student will be positioned at the University of Turku, Finland, and supervised by Dr. Suvi Ruuskanen (Turku), and Dr. Kirsten Grond (University of Alaska Anchorage, USA).

Application deadline is 2nd April 2020. Please email your applications as a single merged PDF (up to 10 MB) to Suvi Ruuskanen (skruus@utu.fi). The .pdf should contain:

1) A cover letter summarizing your motivation, research interests, experiences and qualifications 2) Curriculum vitae, including an account of relevant technical skills/prior experience. 3) Information for three references; 4) Proof of completion of the master’Âs degree (diploma) + list of grades received in the master’Âs program (diploma supplement / transcript of records). If pending, please provide the expected date of graduation ’V before the start of this position ’V with an explanation of the current status.

After reviewing all applicants, I will ask for reference letters from top candidates.

More information on the Ruuskanen Group: https://-sites.utu.fi/ruuskanengroup/ Suvi Ruuskanen, Academy research fellow Department of Biology 20014 University of Turku, FINLAND

Mobile +358503256547

Suvi Ruuskanen <skruus@utu.fi>

Vienna InsectGenomics

Graduate position: Insect Genomics in Vienna Boku, University of Natural Resources and Life Sciences, Vienna Ph.D. Research Fellow in Insect Genomics

30 h/week

Fixed-term contract 3 years

A Ph.D. position is available at the Department of Forest and Soil Sciences, Boku, Vienna in the lab of Christian Stauffer.

Apple proliferation is a disease caused by a phytoplasma. These bacteria are transmitted by different insect species. While several phloem feeders occur on apple, only a small number is able to acquire and transmit phytoplasma. This project aims to address the question of the phytoplasma transmission efficiency of different insect species. Whole genome sequencing of different insects will be performed to study the interaction between the phytoplasma and of various vector populations.

We are looking for an enthusiastic candidate with a strong background in whole genome sequencing and bioinformatics of insects. To investigate factors affecting transmission efficiency the candidate will perform genomic analyses of the insects.

The project is in close collaboration with Hannes Schuler (University of Bolzano). Other partners in the project are Katrin Janik (Research Centre Laimburg), Rosemarie Tedeschi (University of Turin) and Omar Rota-Stabelli (Fondazione Edmund Mach).

The salary is according to the standard personnel costs of the FWF https://www.fwf.ac.at/en/research-funding/-personnel-costs/ . General requirements for the position: The candidate should hold a Master degree in Entomology, Bioinformatics, Biotechnology, Biology or Evolutionary Biology with a multidisciplinary profile. The candidate should have excellent communication skills and should be fluent in English. German skills, although helpful, are not essential.

Please send applications to christian.stauffer@boku.ac.at within April 7th including your CV, a list of publications, cover letter with your research background and contact information of two supervisors/mentors for references. Please indicate ???Insect Genomics??? as subject of the mail.

Christian Stauffer, Institute of ForestEntomology, Forest Pathology and Forest Protection; Department of Forest and Soil Sciences, Boku, University of Natural Resources andLife Sciences,Vienna, Peter Jordanstrasse 82-I, SCHW 01/124 1190-Austria

Tel: +43 1 47654-91631 http://www.wabo.boku.ac.at/ifff/ E-mail:christian.stauffer@boku.ac.at

Christian Stauffer <christian.stauffer@boku.ac.at>

Jobs

Biose Idaho 3 PlantEvolution

Hello Colleagues Three associated positions have open up at Chicago Botanic Garden which will be based in Boise Idaho. Qualifications are Bachelor's degree in ecology, botany, biology or equivalent with appropriate experience; Knowledge of plants.

Title: COORDINATOR, BOTANICAL OUTREACH AND COMMUNICATION (Regular-Full time) located at the Bureau of Land Management Headquarters Office in Boise, Idaho. Position Overview: To assist with outreach efforts related to Seeds of Success and the Plant Conservation and Restoration Program of BLM, communicating with a wide variety of audiences including federal, state, local, and tribal agencies and elected officials; non-governmental organizations and interest groups; industry; traditional and new media outlets; public land users; and other stakeholders.

Title: CURATOR, SEEDS OF SUCCESS NATIONAL COLLECTION (Regular-Full time) located at the Bureau of Land Management Headquarters Office in Boise, Idaho. Position Overview: To coordinate and implement seed collection and banking activities nationally for Seeds of Success and provide curation for the National Collection, within the Plant Conservation and Restoration Program of BLM, communicating with a wide variety of audiences including federal, state, local, and tribal agencies and elected officials; non-governmental organizations and interest groups; industry; traditional and new media outlets; public land users; and other stakeholders.

Title: GIS ANALYST (Regular-Full time) located at the Bureau of Land Management Headquarters Office in Boise, Idaho. Position Overview: Coordinate and implement data analysis and mapping for the Seeds of Success National Collection and the BLM Plant Conservation and Restoration Program.

For more information please go to https://www.chicagobotanic.org/jobs to apply. Please include a c.v. and cover letter with your application. Review of applications begins March 30, 2020 and will continue until a suitable candidate is hired. Contact Kayri Havens at khavens@chicagobotanic.org with any questions.

Genetics Lab <Lab@chicagobotanic.org>

BrighamYoungU Bioinformatics

job:

The Department of Biology at Brigham Young University invites applications for a continuing faculty status (BYU's equivalent to tenure) track position in bioinformatics. Individuals committed to excellence in teaching, preferably using evidence-based teaching approaches, are encouraged to apply. Candidates are expected to have a demonstrated commitment to teaching and mentorship at both the undergraduate and graduate levels.

The applicant is expected to teach courses in the bioinformatics core and potentially develop courses in their area of expertise. Faculty in the Department of Biology have diverse research interests (e.g genetics, systems biology, ecology, systematics, and evolution). Successful applicants will have a Ph.D., experience in methods and/or research applications of high-throughput biological data and a commitment to establishing a collaborative, externally-funded, nationally recognized research program.

The Department of Biology offers competitive start-up packages, reduced first-year teaching loads for new faculty, and generous funds for providing experiential learning opportunities to students. Additionally, faculty have access to the campus super computer in the Office of Research Computing, and opportunities for collaborations and interdisciplinary work through the Simmons Center for Cancer Research, BYU DNA Sequencing Center, and the Monte L. Bean Life Science Museum.

Inquiries should be directed to Dr. Perry Ridge, Bioinformatics Faculty Search, 4102 LSB, Department of Biology, BYU, Provo, UT 84602, USA (or email perry.ridge@byu.edu)

Information required at the time of application 'V Interested persons should apply online at https://yjobs.byu.edu. Complete applications will include a cover letter, curriculum vitae, teaching statement, research statement. Applicants should provide names and contact information for three references: letters of recommendation will be requested for those candidates that make our short list. The initial review process will begin on March 20 and continue until the position is filled.

Equal Opportunity Employer: m/f/Vets/Disability

Brigham Young University is an equal opportunity employer. All faculty are required to abide by the university'Âs Honor Code and Dress and Grooming Standards. Preference is given to qualified candidates who are members in good standing of the affiliated church, The Church of Jesus Christ of Latter-day Saints. Successful candidates are expected to support and contribute to the academic and religious missions of the university within the context of the principles and doctrine of the affiliated church.

Steve Leavitt <steve_leavitt@byu.edu>

CEA Genoscope France BioinformaticsMetagenomics

A permanent research position in environmental genomics is open at the Genoscope research center in France.

Job title: Bioinformatics researcher in metagenomic data analysis for the study of ecosystems and microbial metabolism

URL: http://bit.ly/3cA9ZXi Type of contract: CEA permanent position (CDI)

Location: Genoscope, Evry, France (30 km south of Paris)

Context: The Genoscope (CEA, François Jacob Biology Institute) is a French reference centre in environmental genomics that conducts large-scale analyses for the understanding of ecosystems, particularly in the context of major environmental changes. Its research unit (UMR8030 Genomics Metabolics of the CEA, CNRS and Paris-Saclay Evry University) brings together several laboratories composed of researchers and engineers with expertise in genomics, bioinformatics, microbiology and biochemistry. This strong interdisciplinarity makes it possible to finely characterize the species, functions and interactions present in an ecosystem, but also to focus on the metabolism of these microorganisms. The exploration of biodiversity in terms of chemical potential offers applications in bioremediation, biomass valorization and in the discovery of new catalysts for sustainable chemistry.

Missions: The researcher will join the LABGeM laboratory which develops bioinformatic methods and performs analyses for the study of prokaryotic genomes and metabolism.

He/She will be able to undertake research in environmental genomics and will be in charge of : - conducting bioinformatics analyses of metagenomic samples (assembly/binning, taxonomic assignation, functional analyses, biotic interactions) - implementing innovative strategies for the exploration of metabolic pathways based on comparative (meta-)genomics and associated with experimental characterizations of enzymatic activities - developing academic and industrial research projects -promoting analyses and methods through scientific publications -supervising the work of engineers, postdocs and PhD students.

The research projects being conducted will be part of the scientific strategy of our research unit, which combines computational and experimental approaches for the characterization of new metabolic functions.

Candidate profile: The candidate must have a PhD in bioinformatics and at least one postdoctoral experience. He/She will have a strong background in metagenomics but also in functional analyses of proteins. Naturally curious, with a strong interest in microbiology but also in computer science and statistics, the ideal candidate would be able to conduct research in environmental genomics through bioanalysis in relation with wet labs while being involved in bioinformatics methodological developments.

To apply: Please send to David Vallenet (vallenet@genoscope.cns.fr): - a detailed CV - a summary of your past research activities and your motivation for the position - the contacts of at least two referees

– CEA-DRF-Jacob-Genoscope Laboratoire d'Analyses Bioinformatiques pour la Génomique et le Métabolisme – LABGeM – 2, rue Gaston Crémieux 91057 Evry Cedex | Tel : (33) 1 60 87 84 53

Vallenet David <vallenet@genoscope.cns.fr>

CIBIO-InBIO Portugal HumanMicrobialDiversity

Research Scientist Position at the CIBIO-InBIO, Portugal

Application Review Begins April 30th, 2020

The CIBIO-InBIO (https://cibio.up.pt) in Vairāo, Portugal, is seeking a highly motivated Research Scientist (RS). The work performed by the RS will contribute to our diverse research program devoted to the investigation of the role of microbial infection and host immunity in the etiology of respiratory disorders. The RS will mainly focus on Omic-based research (metagenomics, metatranscriptomics and transcriptomics) on the impact of microbial diversity and function on human heath (host-microbe interactions). However, candidates with experience in Omic research applied to microbial ecology (e.g., microbe-environment interactions) are welcome to apply. This research is part of ongoing collaborations between CIBIO-InBIO, the George Washington University (Washington DC, USA) and University of Vigo (Spain). The selected candidate will be based on the CIBIO-InBIO, but could also temporarily work at the Computational Biology Institute (CBI) in Washington DC (https://cbi.gwu.edu).

Applications can be submitted by any national, foreign and stateless candidate(s) holding a doctorate degree in Biology, Computational Biology, Bioinformatics, Microbial Ecology or related area. General requirements: 1. Experience in Omic analyses (metagenomics and transcriptomics) and an understanding of the key issues and relevant tools in the field. 2. A good quantitative background and good programming skills (R, Python and Perl) and Big Data managing. 3. Proficiency in English (written and spoken)

Monthly remuneration to be paid is the one set by article 23 (3) of RJEC, corresponding to level 33 of the Single Salary Table, approved by Order no. 1553-C/2008 of December 31st, i.e. 2.128,34 Euros. A contract will be offered for one year with the possibility of extension for another year upon performance.

A detailed description of the position and information to submit your application can be found at: http://www.eracareers.pt/opportunities/index.aspx?task=showAnuncioOportunities&jobId=123357&idc=1 For questions relating to this opportunity, please contact Dr. Pérez-Losada at mlosada323@gmail.com.

“mlosada323@gmail.com” <mlosada323@gmail.com>

ColbyC Maine VisitingProf Genetics

Colby College is seeking a visiting assistant professor of genetics for the 2020-21 academic year. The position will begin on September 1, 2020. Candidates should have a Ph.D. in biology and a strong commitment to undergraduate education. Desirable characteristics include familiarity with teaching in a liberal arts setting and use of non-mammalian animal models. The position involves teaching the equivalent of five courses per year, with laboratories constituting a portion of that load. The successful candidate will teach the genetics course and a course in the area of expertise of the candidate.

Please submit a cover letter, curriculum vitae, undergraduate and graduate transcripts, three confidential letters of recommendation, and statements of research interests and teaching philosophy including evidence of commitment to the value of diversity and inclusive teaching on Interfolio link

http://apply.interfolio.com/74771

Review of applications will begin on April 1, 2020 and will continue until the position is filled. The search committee is especially interested in candidates who will contribute to the diversity and excellence of the campus community.

Colby is a private, coeducational liberal arts college that admits students and makes employment decisions on the basis of the individual’s qualifications to contribute to Colby’s educational objectives and institutional needs. Colby College does not discriminate in its educational programs or employment on the basis of race, color, gender, sexual orientation, gender identity, disability, religion, national origin, age, marital status, genetic information, or military or veteran’s status. Colby is an equal opportunity employer and operates in accordance with federal and state laws regarding non-discrimination. Colby complies with Title IX, which prohibits discrimination on the basis of sex in an institution’s education programs and activities. Questions regarding Title IX may be referred to Colby’s Title IX coordinator or to the federal Office of Civil Rights. We encourage inquiries from candidates who will contribute to the cultural and ethnic diversity of our college.

For more information about the College, please visit our web site: www.colby.edu . Dave Angelini <drangeli@colby.edu>

IGFL Lyon GroupLeaderEvoDevoPhysio

Dear friends and colleagues,

Our institute the Institut de Génomique Fonctionnelle de Lyon (IGFL), in Lyon, France is recruiting a new group leader. The IGFL is a great place for those interested in integrative animal biology, especially for teams working at the interfaces of evolution, development and physiology. The working environment is great, with very friendly, international atmosphere.

http://igfl.ens-lyon.fr/calls/igfl-group-leader-2020.pdf all best,

Michalis

Michalis Averof Institut de Génomique Fonctionnelle de Lyon (IGFL) CNRS and Ãcole Normale Supérieure de Lyon tel. +33 4 26731364 www.averof-lab.org

Michalis Averof <michalis.averof@ens-lyon.fr>

IzTech Turkey BioinformaticsComputationalBiology

The Graduate School of Engineering and Sciences at Izmir Institute of Technology (IzTech) invites applications for faculty positions at assistant or associate professor levels to participate in interdisciplinary graduate programs. We seek highly qualified and motivated investigators at early- or mid-career levels with a strong research program in the fields of bioinformatics, computational and systems biology. The successful candidates are expected to be involved in the growth of the program, demonstrate capability for establishing a strong, externally funded research program, and commitment to excellence in graduate education.

IzTech, one of the top-tier research universities in Turkey, was established in 1992 aiming to offer a high level of education, and carrying out exemplary research in scientific and technological fields. The campus is located in Gulbahce near Urla with ready access to local beaches and attractive sites. The instruction language at the Institute is English. Further information can be found at www.iyte.edu.tr. Interested individuals may submit their curriculum vitae, and a description of proposed research area to Dr. Efe Sezgin at efesezgin@iyte.edu.tr

Efe Sezgin, PhD. Ãzmir Ãnstitute of Technology Gülbahce köyü Urla, Izmir - Turkey 35430 Phone: (90) 232 750 6910 Fax: (90) 232 750 6196 efesezgin@iyte.edu.tr efeszgn0@gmail.com

efeszgn0@gmail.com

SouthDakotaStateU FisheriesBiologist

South Dakota State University'Âs Department of Natural Resource Management (NRM) is offering an exciting career opportunity for an Assistant/Associate Professor 'V Fisheries Science. This is a 9-month, full-time, benefits-eligible, tenure-track position with research, teaching, advising, and service responsibilities. The preferred start date is August 2020. This appointment is 55% research and 45% teaching, along with acknowledgement of a service component. The candidate will be expected to be active in both our undergraduate and graduate training programs, conduct research in their area of expertise and be able to contribute to an applied research program but also obtain competitive research funding to address basic ecological questions. Candidates should have a strong quantitative research background in fisheries science with an emphasis on the management and ecology of freshwater fish populations in streams, rivers, and/or natural lakes.

SDSU is especially interested in candidates that can contribute to and/or coordinate course offerings that address the experiences of underrepresented minorities in organizations. Women, minorities, veterans, and people with disabilities are especially encouraged to apply.

RESPONSIBILITIES: - Teach undergraduate courses in areas focused on fisheries management, ecology and conservation; and develop a graduate course in area of specialty. - Periodically teach Seminars and Special Topics, and mentor Independent Study as needed. - Advise and mentor undergraduate and graduate students. - Contribute to a nationally- recognized research program which includes developing extramural sources of funds and publishing in peer-reviewed national and international journals. - Obtain and administer outside research funding, including support for graduate students. - Participate in University, College, and Department governance and service; participate in professional service and outreach activities.

MINIMUM QUALIFICATIONS: - Completed Ph.D. in fisheries science, aquatic ecology, or closely related area by application date. - Demonstrated record of research and scholarly activities, including a strong quantitative skill set. - Excellent oral and written communication skills and strong interpersonal communication skills. - A valid driver'Âs license is required. - Must be authorized to work in the United States. Sponsorship is not available for this position.

PREFERRED QUALIFICATIONS: - Postdoctoral experience, employing quantitative approaches for understanding the dynamics of fish populations, their ecological interactions, and the impacts of natural and anthropogenic stressors on the sustainability of natural fish populations and fisheries resources. - Teaching experience, experience in grant writing, and involvement in professional society activities. - Demonstrated collaboration with natural resource agencies. - Desired commitment to a highly collegial working environment. - Experience working with diverse groups or cultures.

BENEFITS: South Dakota State University offers a wide range of benefits including medical, dental, and flexible benefits, retirement plans, compensation packages, paid holidays, and vacation leave. Employees also have access to internal and state-sponsored training as well as reduced tuition for state-supported courses at all State of South Dakota academic institutions

DATE OF FIRST CONSIDERATION: 27 March 2020 CONTACT: Further inquiries may be directed to the Search Chair, Steve Chipps, at 605-688-5467, or by email: steven.chipps@sdstate.edu

JOB POSTING: https://yourfuture.sdbor.edu/postings/18780 Maribeth.Latvis@sdstate.edu

TexasAMU Conservation

The Department of Life Sciences at Texas A&M University-Corpus Christi (TAMU-CC) invites applications for a tenure-track Assistant Professor of Biology in terrestrial ecology and conservation. Appointment will begin Fall 2020. We seek a motivated and talented person who can work in coastal watershed ecosystems and whose research focus is mainly on terrestrial organisms. We seek a colleague whose expertise is complementary to that of existing faculty and who can fill known gaps in the department (among others, reptiles, mammals, birds, or insects).

The successful candidate will be expected to develop a vigorous, externally funded research program, supervise graduate students, and teach undergraduate and graduate courses in conservation biology as well as their individual expertise. This position will further expand and complement our M.S./Ph.D. programs in Marine Biology (http://sci.tamucc.edu/departments/life-sciences/marine-biology/index.html), Coastal and Marine Systems Science (http://sci.tamucc.edu/departments/physical-sciences/coastal-marine/index.html), and M.S. Biology (http://sci.tamucc.edu/academics/biol-ms/index.html).

Required Qualifications: * Ph.D.in Biology or closely related discipline. * A strong publication record in leading, high impact, journals. * Post-doctoral experience.

Preferred Qualifications: * Individuals with active, externally funded research programs and collaborations who can take advantage of our research laboratories and equipment including Core Genomics Facility, High Performance Computing clusters, Isotope Core Lab, microscopy and other analytical facilities, and potential faculty collaborators. * Applicants whose research focus is complementary to existing faculty in the department are especially encouraged to apply.

TO APPLY: http://hr.tamucc.edu/Job_Opportunities/index.html All required documentation must be submitted to be considered for the position. A completed application will include: 1. Cover letter 2. Curriculum vitae 3. Statement of research interests 3. Teaching and diversity statement that details a) how you will foster inclusion and diversity in your program and b) your preferred teaching interests. 4. Four professional references including name, address, title, telephone number, and email addresses.

The position will remain open until a finalist is selected. Applicants are encouraged to apply prior to March 31, 2020.

For more information, please contact: Dr. Kim Withers Search Chair, Department of Life Sciences Email: kim.withers@tamucc.edu

David S Portnoy

Associate Professor Ruth A. Campbell Professor of Marine Biology Texas A&M University Corpus Christi 6300 Ocean Dr. Unit 5892 Corpus Christi, TX 78412 (361)-825-2859

"Portnoy, David" <David.Portnoy@tamucc.edu>

UAlabama Birmingham TeachingEvolution

The Department of Biology at the University of Alabama at Birmingham (UAB) invites applications for a full-time Assistant Teaching Professor (non-tenure earning). The primary responsibility of the successful candidate will be to teach a range of introductory biology courses for biology majors and non-majors.

Candidates must have a Ph.D. in biological sciences or a related field, plus demonstrated experience in teaching and in course development. The successful candidate will be comfortable teaching high enrollment courses and have a track record of teaching excellence as well as a strong interest in innovative pedagogies including online instruction.

Review of Applications will begin March 31, 2020 and continue until filled.

Questions about the position should be directed to Dr. Nicole Riddle (riddlenc@uab.edu).

UAB is an Equal Opportunity/Affirmative Action Employer committed to fostering a diverse, equitable and family-friendly environment in which all faculty and staff can excel and achieve work/life balance irrespective of, race, national origin, age, genetic or family medical history, gender, faith, gender identity and expression as well as sexual orientation. UAB also encourages applications from individuals with disabilities and veterans.

sakh@uab.edu

UCDavis LabManager GenomicVariationLab

The Genomic Variation Laboratory (GVL) is looking to hire a new laboratory manager to start in June or July 2020. The GVL is a large and dynamic group of PIs, students, and technicians who are passionate about using genetic and genomic tools to advance the management and conservation of wild populations. The GVL provides a supportive, inclusive environment that values both rigorous science and work-life balance.

The laboratory manager is integral to the structure of the GVL; the candidate chosen for this position will manage supply budgets and inventories, maintain equipment, and work with vendors. As a scientist, the laboratory manager will have opportunities to innovate methods, steer experimental design, and produce & analyze data for funded research projects. As a mentor to students and technicians, the GVL lab manager will be able to participate in a wide range of conservation genetics studies focused on various fish and wildlife species.

The ideal candidate will have a Masters or PhD in genetics, genomics, or a related field and have demonstrated proficiency in molecular techniques, including preparation of high throughput sequencing libraries. Strong written and verbal communications skills, and the ability to manage multiple projects at a time are a must.

For more information or to apply for the position, visit https://recruit.ucdavis.edu/JPF03441 Best,

Andrea

– Andrea Schreier, PhD Adjunct Assistant Professor Director, Genomic Variation Lab Meyer Hall 2235 University of California Davis Office (530) 752-0664 Lab (530) 752-6351 https://gvl.ucdavis.edu/ < http://genome-lab.ucdavis.edu/People/Drauch/index.htm >

Andrea Schreier <amdrauch@ucdavis.edu>

UFlorida MicrobialEvolution

Assistant Professor in Microbiology and Cell Science

Microbiology and Cell Science Department University of Florida Institute of Food and Agricultural Sciences (IFAS) Gainesville, Florida USA

Salary commensurate with qualifications and experience

For full consideration, candidates should apply and submit additional materials by April 1, 2020. The position will remain open until a viable applicant pool is determined.

This is a 9-month tenure-accruing position that will be 30% teaching (College of Agricultural and Life Sciences), 70% research (Florida Agricultural Experiment Station) and 0% extension (Florida Cooperative Extension Service), available in the Microbiology and Cell Science Department, Institute of Food and Agricultural Sciences, at the University of Florida. Tenure will accrue in the Department of Microbiology and Cell Science. This assignment may change in accordance with the needs of the unit. Duties will include the development of a strong extramurally funded research program in an area broadly related to microbiology and cell biology, including bacteriology, fungal biology, parasitology, and/or virology that can include but is not limited to microbial pathogens, symbionts, and natural products and can span from molecular to ecosystem studies. The incumbent will be expected to develop a successful teaching program that includes teaching one undergraduate course in either cell biology, virology, or a related course. The faculty member will participate actively in graduate education by chairing graduate committees, serving on graduate committees, supervising thesis and dissertation research, supervising undergraduate research, and publishing the results with his/her graduate students. The faculty member will actively seek contract and grant funding to support his/her program.

A doctorate (foreign equivalent acceptable) in microbiology (including bacteriology, mycology, parasitology, or virology), cell biology, molecular biology, or a closely related discipline is required with published experience in the field of study. At least two years of postdoctoral experience is required. Candidates should have demonstrated skills in verbal and written communication, interpersonal relationships, and procurement of extramural funding. Candidates must be supportive of the mission of the Land-Grant system. Candidates must also have a commitment to IFAS core values of excellence, diversity, global involvement, and accountability. Strong data analysis and computer skills are important.

The University of Florida (http://www.ufl.edu) is a Land-Grant, Sea-Grant, and Space-Grant institution, encompassing many academic and professional disciplines, with an enrollment of more than 54,000 students. UF is a member of The Association of American Universities. The Institute of Food and Agricultural Sciences (http://ifas.ufl.edu) includes the College of Agricultural and Life Sciences (http://cals.ufl.edu), the Florida Agricultural Experiment Station (http://research.ifas.ufl.edu), the Florida Cooperative Extension Service (http://extension.ifas.ufl.edu), the College of Veterinary Medicine (http://www.vetmed.ufl.edu), the Florida Sea Grant program (http://www.flseagrant.org/), and encompasses 16 on-campus academic departments and schools, 12 Research and Educational Centers (REC) located throughout the state, 6 Research sites/demonstration units administered by RECs or academic departments, and Florida Cooperative Extension Service offices in all 67 counties (counties operate and maintain). The School of Natural Resources and Environment is an interdisciplinary unit housed in IFAS and managed by several colleges on campus. IFAS employs over 2500 people, which includes approximately 900 faculty and 1200 support personnel located in Gainesville and throughout the state. IFAS, one of the nation's largest agricultural and natural resources research and education organizations, is administered by a Senior Vice President and four deans: the Dean of the College of Agricultural and Life Sciences, the Dean for Extension and Director of the Florida Cooperative Extension Service, the Dean for Research and Director of the Florida Agricultural Experiment Station, and the Dean for the College of Veterinary Medicine. UF/IFAS also engages in cooperative work with Florida A&M University in Tallahassee.

The Microbiology and Cell Science Department includes 25 tenured and tenure-track faculty as well as five non-tenure faculty members who serve as instructors. Our faculty are located primarily in one building, but we also have four faculty members at the Genetics Institute building, two at the Ft. Lauderdale Research and Education Center, two at the Florida Space

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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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UIceland MarBio FishEvol

Dear all,

The Department of Biology in the Faculty of Life and Environmental Sciences at the University of Iceland seeks engaging and motivated applicants for a position of assistant professor in Marine Biology, Fish biology or Fisheries Sciences.

Field of work: The assistant professor is expected to develop courses in marine and fisheries science at the Bachelor level and participate in a joint Master program with the Marine and freshwater Institute in Iceland and to conduct research in this area of science. This is a tenure-track position with an option of an appointment of five years. A successful applicant with sufficient qualifications is eligible to apply for promotion to associate or full professorship upon appointment. In addition to research, the successful applicant is expected to supervise MSc and PhD students, attract third-party funding, teach courses at the undergraduate and graduate level, and participate actively in departmental activities.

Qualification requirements

- A Ph.D. degree in marine sciences, fish biology, fisheries sciences or a closely related field
- An excellent record of research, according to the applicant's academic age
- Substantial teaching experience and motivation for teaching development
- Organizational skills is a crucial advantage
- Strong communication and interpersonal skills
- Proficiency in written and spoken English

The hiring process will focus on identifying candidates who are best suited to the circumstances and needs of the Faculty of Life and Environmental Sciences.

Application process: Please include the following with the application: a copy of the PhD certificate, a CV, a list of publications, a teaching statement, and an outline of research plans. Applicants are expected to name three persons who are willing to give references about their research and/or teaching. Additionally, applicants should select up to eight of their publications which they regard as most relevant to their application, provide either copies of those articles or information about electronic access, and describe their contribution to multi-author publications.

Applications and documents not submitted online shall be submitted in duplicate to the University of Iceland Division of Science and Innovation, SÃmundargata 6, 101 Reykjavík.

The successful candidate will be hired for five years with the possibility of a permanent contract at the end of this period, cf. paragraph 3, Article 31 of the Regulation for the University of Iceland no. 569/2009.

Processing of applications, evaluation of applicants' competence and hiring shall be in accordance with the Act on Public Higher Education Institutions no. 85/2008 and the Regulation for the University of Iceland no. 569/2009. In accordance with Article 38 of the Regulation for the University of Iceland no. 569/2009, the rector may promote a new employee to the position of senior lecturer or professor if the individual in question meets requirements.

Salary will be in accordance with the current collective wage and salary agreement between the Union of University Teachers and the Minister of Finance.

All applications will be answered, and applicants will be informed about the appointment when a decision has been made. Applications may be valid for six months.

Appointments to positions at the University of Iceland are made in consideration of the Equal Rights Policy < http://english.hi.is/university/equal_rights_policy > of the University of Iceland.

https://english.hi.is/university/equal_rights_policy The University of Iceland has a special Language Policy < http://english.hi.is/university/university_iceland_language_policy >.

https://english.hi.is/university/university_of_iceland_language_policy Further information

For further information, contact Arnar Pálsson, head of the Department of Biology, +354 5254265, apalsson@hi.is.

The School of Engineering and Natural Sciences employs approximately 360 people in academic positions. The School offers an international working environment, with the number of international employees and students increasing each year. Currently about quarter of all employees and graduate students are international. There are around 2900 students at the School, divided into six faculties, including approximately 350 MS students and 150 doctoral students. Research institutes at the School are the Science Institute that divides into the Institute of Earth Sciences and Institute of Physical Sciences, Institute of Life and Environmental Sciences, Engineering Research Institute and the Institute

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ULisbon 2yr GenomicDataAnalysis

The Computational Biology and Population Genomics Group of the Center for Ecology Evolution and Environmental Change (cE3c) (http://ce3c.ciencias.ulisboa.pt/) is hiring for a two year contract an highly motivated researcher for working in genomic data analysis. The project is the extension of our recent paper on Global Change Biology

https://onlinelibrary.wiley.com/doi/full/10.1111/gcb.14497 see details at: http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=123341 Octávio S. Paulo Assistant Professor Computational Biology and Population Genomics Group cE3c - Centre for Ecology, Evolution and Environmental Changes

Departamento de Biologia Animal Faculdade de Ciências, Universidade de Lisboa P-1749-016 Lisboa Portugal

Tel: 00 351 217500614 direct Tel: 00 351 217500000 ext22359 Fax: 00 351 217500028 email: octavio.paulo@fc.ul.pt skype: octaviopaulocobiggroup facebook.com/pages/Cobig2/

"Octavio S. Paulo" <ofpaulo@fc.ul.pt>

UMainz EvolutionaryPlantSciences ExtendedMay1

Job Advertisement

The Faculty of Biology - Institute of Organismic and Molecular Evolution (iomE) - invites applications for a

Professorship in Evolutionary Plant Sciences

(Bes.Gr. W 3 LBesG)

available at the earliest opportunity.

We are seeking an internationally renowned scientist in the field of plant organismic and molecular evolution, focusing on processes of evolutionary adaptation and/or speciation. Research foci may include genomics, gene regulation, epigenetics, biotic interactions and aging, in an evolutionary context.

The successful candidate is expected to develop an independent and internationally visible research program, supported by sustained extramural funding. She/he will be embedded in a highly collaborative environment including the three institutes of the Faculty of Biology (http://www.bio.uni-mainz.de/-33_ENG_HTML.php), the Institute of Molecular Biology (IMB; www.imb-mainz.de), the Institute of Biotechnology and Drug Research (IBWF; www.ibwf.de), and other faculties of the natural sciences at Johannes Gutenberg University, as well as the Rhine Main Universities alliance (RMU) with Frankfurt and Darmstadt. Participation in the research training group GenEvo ("Gene Regulation in Evolution: From Molecular to Extended Phenotypes"; https://www.bio.uni-mainz.de/-koordinierte-forschungsprojekte), the CRC1361 ("Regulation of DNA Repair and Genome Stability" https://-/www.sfb1361.de/) and in the State'Âs strategic research initiative ReALity ("Resilience, Adaptation and Longevity") is encouraged. Teaching in botany and evolutionary biology in the Bachelor and Master programs is expected with the ability to teach basic classes in German within five years.

Applicants must meet the general requirements according to public services law and the Higher Education Act of Rhineland-Palatinate (" 49 Hochschulgesetz 'V Higher Education Act) including the relevant university and doctoral degrees, and an outstanding scientific track record. The State of Rhineland-Palatinate and JGU put particular emphasis on intensive student support. We expect the University'Âs faculty to reflect this in their presence at the University.

JGU aims at increasing the number of female faculty members and therefore explicitly encourages applications by female scientists. Disabled applicants with adequate qualification will be favored.

Applications including the usual documents (e.g. CV; copies of certificates; lists of publications and teaching activities; funding record; current research and future research plans; teaching concept) as a single PDF file and separately the form available at www.bio.uni-mainz.de/-1517_ENG_HTML.php should be submitted in electronic form not later than May 1st 2020 to the

Dean, Faculty of Biology (biologie@uni-mainz.de)

Informal requests can be directed to Prof. Dr. Susanne Foitzik (foitzik@uni-mainz.de) or Prof. Dr. Andreas Wachter (wachter@uni-mainz.de).

The information on data protection in handling your application can be found at: https://-www.verwaltung.personal.uni-mainz.de/files/2019/10/-Datenschutz- Bewerber.pdf

Job offers and further information also on the Internet: www.verwaltung.uni-mainz.de "Foitzik, Susanne" <foitzik@uni-mainz.de>

UOklahoma NHM Director

The University of Oklahoma seeks a Director for the Sam Noble Oklahoma Museum of Natural History

The Sam Noble Museum at the University of Oklahoma is seeking a visionary leader to serve as Director and to work collaboratively with an outstanding professional staff and faculty curators. The Museum is the state's natural history museum and an organized research unit of the university. It is also a space for celebrating the state's rich cultural and natural heritage, and engages in significant outreach and educational activities designed to serve a diverse and inclusive community.

The Museum contains over 10 million artifacts and specimens in a 198,000-square-foot facility. It houses notable collections in archeology, ethnology, linguistics and linguistic anthropology, herpetology, ichthyology, invertebrates, mammalogy, ornithology, genomic resources, invertebrate paleontology, paleobotany and micropaleontology, and vertebrate paleontology. The Museum has received a total of four national and international awards, including the prestigious National Medal from the Institute of Museum and Library Services, for its commitment to collection stewardship, outreach and education activities, and public programs. Visit the SNOMNH web site at: www.samnoblemuseum.ou.edu . For more information or to apply see here: https:/-/apply.interfolio.com/73214 Applications received by March 23 will receive full consideration.

Richard E Broughton Professor and Chair Department of Biology University of Oklahoma

"Broughton, Richard E." <rbroughton@ou.edu>

UOslo 3 eDNA VertebrateZoo SystMycology

Job Oslo: Associate Professor in environmental DNA

https://www.jobbnorge.no/en/available-jobs/job/-184311/associate-professor-in-environmental-dna The Natural History Museum is recruiting an Associate Professor in environmental DNA. The appointment is a fulltime, permanent position with a starting date no later than 1 January 2021.

The Natural History Museum (NHM) at the University of Oslo holds Norway's most extensive collections of animals, plants, and fungi. These natural history collections are invaluable repositories because they enable the scientific community to answer key questions about geographical and temporal variation in biodiversity. As a museum, we seek to be at the forefront of developments in biology and adapt our infrastructure to the needs of science and society today. To develop our position at the cutting edge of modern biodiversity research, we are recruiting an associate professor in eDNA. This person enters a vibrant research environment in which five out of eight research groups at the museum apply and develop metabarcoding and metagenomics approaches for various research questions. These include molecular biodiversity assessments, applied work on the authentication of food and medicine, as well as ecological or evolutionary questions using aquatic environmental DNA, trophic material, bulk invertebrate and plant samples, soil DNA, and sedimentary ancient DNA. Traditionally, the museumÂs strategy emphasizes the use and collection of individual specimens for morphological or molecular research. The collection infrastructure requirements of environmental samples calls for a reassessment of our workflows, including physical sample storage, DNA bank storage, in-silico repositories, and reproducibility of analysis pipelines.

The appointed associate professor will lead the development of the museumÂs capacity in the field of environmental DNA. This capacity includes the initiation of new research programs, teaching and supervising students, and curating and developing scientific collections of eDNA samples based on the applicant's taxonomic expertise.

We seek an active researcher with a relevant and strong publication record, and with a clear vision for developing an independent museum-based research program in eDNA. The successful candidate should be on an upward trajectory and is expected to have strong potential to execute competitive research projects at a high international level. He or she should have the ability to create an attractive research environment and perform research that inspires synergistic interactions with current research at the museum. The ideal candidate would focus on using environmental DNA to study fundamental questions in biology, rather than applying or developing methods for monitoring purposes.

An attractive start-up package is available. However, the successful applicant will be expected to obtain extramural research funding, and a proven record of acquiring such funding is essential.

NHM has a collaborative agreement with the Department of Biological Sciences about teaching and supervision of students at the bachelor and master's level, and with the Faculty of Mathematics and Natural Sciences for supervision of doctoral candidates. NHM also hosts an international research school in biosystematics (ForBio). The successful candidate is expected to participate in teaching at all levels and be a capable and enthusiastic supervisor of master's and PhD students. Relevant background in working with museum collections will be an advantage in building up a physical infrastructure for eDNA samples. Up to 50% of the working time will be devoted to curating collections (main activity), teaching and supervision of students, outreach and administrative tasks at NHM. Lectures and tuition are given in Norwegian and English. Foreign language speakers are expected to be able to teach in a Scandinavian language within two years after being hired.

Qualification requirements

The successful applicant must have

- A PhD or an equivalent doctoral degree in biology - A postdoctoral research profile with relevant experience in environmental DNA, e.g., biodiversity assessments using molecular approaches - Experience with relevant sample types, e.g., bulk samples, aquatic eDNA, faecal DNA, soil DNA, sedimentary ancient DNA and the analytical challenges associated with these samples - Experience with bioinformatic analyses of high-throughput sequence data, statistical analyses and visualization of results of metabarcoding/metagenomics data - Actively publishing scientific papers of high quality - Excellent English language skills (written and spoken)

The successful applicant should have

- Coherent taxonomic expertise relevant to their eDNA research - Proven ability to attract external research funding

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UppsalaU ResAssist EvolutionaryGenetics

Research assistant in Evolutionary Genetics at Uppsala University

A position as a Research assistant in Evolutionary Genetics is available at the Department of Ecology and Genetics, Evolutionary Biology Program, Uppsala University.

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our mission is to pursue top-quality research and education and to interact constructively with society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has 44.000 students, 7.100 employees and a turnover of SEK 7 billion. The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see www.ieg.uu.se. The Evolutionary Biology Program excels in many aspects of genetics and evolution and offers an inspiring international atmosphere. There are ample opportunities for interaction with researchers working on related topics. We are tightly linked to the Science for Life Laboratory (https://www.scilifelab.se/) and have access to advanced laboratory infrastructure, high performance computing resources and bioinformatics support.

Project description: The research at the program of Evolutionary Biology revolves around core questions in the fields of evolutionary genetics, including genomics, molecular ecology, molecular evolution and population genetics. The position will be focused on development and preparation of cells for ATACseq from frozen and fresh tissues of birds, insects and fungi. Our final aim is to identify transcriptionally active regions of the genome in these organisms and several downstream analyses will be done to investigate the molecular mechanisms and evolutionary processes associated with transcription activity. Depending on the progress of the method development, other techniques in molecular biology and genetics might be included in the work description. For any further questions, please visit the program website (http://www.ieg.uu.se/evolutionary-biology) or contact Niclas Backström (contact information below).

Application: The application should include 1) a letter of intent describing yourself, your research interests, potential previous experience with relevant methods and why you want this position, 2) a short description of your education, 3) a CV and 4) the names and contact information to at least two reference persons (e-mail address and phone no.). The application should be written in English.

For further information about the position please contact: Niclas Backström, niclas.backstrom[at]ebc.uu.se, +46-18-471 6415.

You are welcome to submit your application no later than March 23, 2020, UFV-PA 2020/299. Formal applications should be made using our online application form available vi link here: https://www.uu.se/en/about-uu/join-us/details/?positionId=316567 Niclas Backström Evolutionary Biology Program Department of Ecology and Genetics Uppsala University, Sweden Email: niclas.backstrom[at]ebc.uu.se

När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here:

http://www.uu.se/en/about-uu/data-protection-policy
niclas.backstrom[at]ebc.uu.se

USaoPaulo EvolutionaryVertZoology

University of Sao Paulo - Brazil: Faculty Position - Vertebrate Zoology

The Department of Zoology of the Institute of Biosciences of the University of Sao Paulo (Brazil) is seeking applications for one tenure-track Assistant Professor faculty position in Vertebrate Zoology (including theory and methods in phylogenetics, biogeography and comparative phylogenetic methods; evolution, phylogeny, diversity, natural history and biology of major vertebrate groups; and comparative anatomy and organogenesis of the different systems in vertebrates). Applicants must hold a Ph.D. degree in a field related to the position and a demonstrated record of research productivity. The successful candidate will be expected to maintain a rigorous research program and contribute to undergraduate and graduate teaching. Applications must be submitted by April 23, 2020.

Further information (including information for foreign applicants and/or holders of a foreign Ph.D.) can be obtained from: Dr. Ricardo Pinto da Rocha, Head of the Department of Zoology, ricrocha@usp.br.

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Silvio Shigueo Nihei Professor Associado / Associate Professor Departamento de Zoologia Instituto de Biociências - Universidade de Sāo Paulo Rua do Matāo, Trav. 14, n.101 05508-090 - Sāo Paulo/SP - Brasil Phone +55 11 30917511 E-mail: silvionihei@gmail.com, silvionihei@ib.usp.br

URL: http://www.ib.usp.br/ ˜ silvionihei https://usp-br.academia.edu/SilvioNihei https://www.researchgate.net/profile/Silvio_Nihei XXXIII Congresso Brasileiro de Zoologia Ãguas de Lindoia-SP, 01-06 de março de 2020 www.cbzoo.com.br Editor, Zootaxa (Diptera: Muscoidea) http://www.mapress.com/j/zt/pages/view/Diptera Editor, Manual of South American Diptera http://msadiptera.wix.com/manual "La duda es uno de los nombres de la inteligencia." (Jorge Luis Borges)

Silvio Nihei <silvionihei@gmail.com>

Vienna BiologicalAdaptation

Announcement of a professorship according to ç 99 (5) UG 2002 for "Global Change Biology" The University of Veterinary Medicine, Vienna (Vetmeduni Vienna) is an internationally renowned competence centre for teaching and research in veterinary medicine, as well as a sought-after partner for cooperation. The modern campus accommodates teaching and research facilities and the only veterinary teaching and research hospital in Austria. Furthermore, it is the working place of around 2300 students and 1400 staff members. The Vetmeduni Vienna distinguishes itself through its striving for excellence in teaching, research and the service units, as well as through continuous dialogue with society. A professorship for "Global Change Biology" according to ç 99 (5) UG 2002 is announced at the Vetmeduni Vienna.

Field: We are seeking an individual to represent the area of Global Change Biology at the Vetmeduni Vienna covering research and teaching aspects. The assistant professorship has access to advanced teaching and research facilities of Vetmeduni Vienna. The position of the assistant professor is regulated by a performance agreement (according to ç 27 of the collective contract (Kollektivvertrag) for university employees). The contract is initially limited to a duration of 4 years with the potential for a permanent contract at the level of associate professor after a positive evaluation of the performance agreement goals.

Main tasks: The successful candidate is expected to expand the research focus of the Vetmeduni Vienna by developing a research profile encompassing the Sustainable Development Goals of the Vetmeduni Vienna. Global Change Biology in connection with Veterinary Medicine can include the following areas: interaction with the ecological system, biodiversity, adaption to new environmental conditions, invasive und invading species - new animal species, urbanization. The applicant is expected to develop an internationally recognized line of research predominantly by acquiring third-party funds. Close integration within the Vetmeduni Vienna as well as cooperation with national and international institutions is expected. The tasks of the successful applicant include independent curricular teaching at the Vetmeduni Vienna.

Responsibilities: - Supervision and implementation of independent research activities with a strong focus on intra- and extramural collaboration - Preparation of research grants and recruitment of third- party funding - Establishment and management of a research group - Supervision of under- and postgraduates - Development of new teaching material including e-learning material, teaching and examination duties - Participation in management activities - Active contribution to the strategic goals of the Vetmeduni Vienna - Research activities involving Sustainable Development Goals (in particular SDG 2, 3, 15)

Required training, qualifications and skills: - University degree in natural science studies and further PhD study or doctoral thesis - Research activity in the area of Global Change Biology according to the career status - Knowledge in conception of third-party funded grants - Teaching experience - Very good knowledge of spoken and written English (C1 level)

Further desired qualifications and skills: - Ability to work in a team - Interdisciplinary collaboration experience - Outstanding social and communication skills - Good command of German (non-German-speaking applicants are expected to reach at least level B1 within 2-3 years)

Grade: A2 according to ç 49 (2) of collective contract for university employees Level of employment: 40 hours Length of employment: 4 years (with potential for a permanent position after positive evaluation)

Minimum salary: The minimum salary for university staff is regulated by the Universities collective contract (Kollektivvertrag) and at the A2 level amounts to 64.394,40 gross/year (14 monthly salaries). In case the performance agreement cannot be finalized at the job start, the salary will be 54.453,00 gross/year until the performance agreement can be signed.

The minimum salary may be increased when previous employment and other salary components are taken into account.

Application deadline: 24.05.2020 Reference no.: Q_GCB_2020 To apply for this position, please send your documents in English to the Office of the Senate at the University of Veterinary Medicine, per e-mail to senat@vetmeduni.ac.at

The application documents should comprise: - Application letter including a brief description of: - Current research interests and research plans for the immediate future - Previous and planed focuses in academic teaching and supervision of young researchers - Curriculum vitae including:

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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

YaleU BiodiversitySoftware

Map of Life (MOL) and the Yale Center for Biodiversity and Global Change are seeking a Software Engineer who is interested in developing new technologies to support effective global biodiversity education, monitoring, research and decision-making. The successful candidate will assemble and integrate a wide range of knowledge about species distributions and their dynamics over time. Map of Life is built on a scalable web platform geared for large biodiversity and environmental data and provides best-possible species distribution information together with a range of information and biodiversity indicator products. Map of Life leads the data integration and mapping efforts of the Half-Earth Project that aims to identify and prioritize target areas for global biodiversity conservation. Responsibilities and tasks for this position will include:

Developing responsive web applications using HTML5 and CSS3 on modern JavaScript frameworks and Python, documenting through GitHub and workflow optimization, working in Unix-based systems. Supporting and building backend API services. Supporting and building frontend interfaces with frameworks like Angular, React, etc. Receiving and providing feedback on code, incorporating user feedback directly into products. Assessing and meeting technical and stakeholder needs. Conducting written and oral presentations that summarize the analysis of data, interpret findings, and provide conclusions and recommendations. Solving problems in an organized and logical manner.

The Max Planck Yale Center supports research and training around the use of new technologies such as GPS tracking and remote sensing to address questions in ecology, behavior, and global change. Flagship Center projects include the Icarus initiative, a space station-based near-global GPS animal movement observation system, Movebank, which supports the management and integration of movement data, and Map of Life.

Diversity, equity, and inclusion are core values in our group. We aim to promote the success of traditionally underrepresented groups in science because we believe not only in the importance of increasing equity across academia, but also that a diverse team will enable a broader perspective and enhance creativity.

The position will be based at Yale University, with close collaborative links to our partners worldwide. Yale University offers researchers and staff competitive salaries and a generous package of benefits. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the School of Forestry and Environmental Studies.

For more information about this position go here:— https://sjobs.brassring.com/TGnewUI/Search/Home/Home?partnerid=25053&siteid=5248#jobDetails=1412308_5248 or contact Anna Schuerkmann at <anna.schuerkmann@yale.edu>

For more information about benefits go here:— https://your.yale.edu/work-yale/benefits/my-benefits-job-classification "Anderson, Robert" <robert.anderson.ra685@yale.edu>

Other

Australopithecus Skull Measurements

Dear friends, I am teaching Evolution and also Statistics for Biology students and I would like to use Australopithecus skull measurements in my courses. Does anybody knows about some source to obtain an Excel file with these data?

Thanks for any help!

Prof. Dr. JÃºlio Cesar Voltolini Departamento de Biologia Universidade de Taubaté

VOLTOLINI <jcvoltol@uol.com.br>

BinghamtonU REU PacificNW HostParasitoid

REU summer internship in host-parasitoid interactions and global change in the Pacific Northwest(Binghamton University SUNY)

Overview:The Prior Lab at Binghamton University SUNY is seeking one undergraduate student for a Research Experience for Undergraduate (REU) internship this summer. The successful applicant will develop an independent project that contributes to NSF-funded research investigating how insect host parasitoid communities are altered under global change in the Pacific Northwest. Please see the Prior Lab website for the type of research projects that we work on (www.priorecologylab.com).

We seek a highly motivated and enthusiastic undergraduate student for a 10-week full-time, paid internship. The majority of the time (˜ 8 weeks) will be spent conducting field research in the Pacific Northwest (northern Oregon, Washington State, and Vancouver Island, British Columbia), with the remaining (˜ 2 weeks) in the lab at Binghamton University, NY analyzing results and writing a report. Dates are somewhat flexible, between mid-May and mid-August 2020.

The selected students will conduct independent research, mentored by Dr. Kirsten Prior, in conjunction with an NSF-funded research project: Uncovering the role of altered cryptic interactions in driving the demographic success of a range-expanding species.? This project focuses on how insect communities (oak gall wasps and parasitoids) are altered under range expansions. One gall wasp species recently expanded its range from mainland western North America to Vancouver Island, British Columbia, where it's outbreaking and has become a tree pest. We're investigating how interactions with other gall wasps (competitors), parasitoids (enemies), and the host plant (oak) are altered when this species' expands its range, and how these altered interactions facilitate outbreaks. We combine field surveys and experiments in the species' native and expanded ranges, along with molecular tools to understand how interactions are altered and contribute to outbreaks. There are several independent research project ideas that the selected student could develop within this study system, and will work with Dr. Prior to develop a project.

Benefits:The selected student will receive a $5000 stipend and housing during the 10-week program. Additionally, up to $700 will be provided to travel to the Pacific Northwest. There are also modest funds for supplies. The student will live in a shared residence with Ph.D. students and field technicians. The student will pay for their own food with the use of a field vehicle that can be used to get groceries and a kitchen to prepare food.

Eligibility:Applicants must be rising sophomore, junior, or senior undergraduate students currently enrolled in a degree program. Due to NSF funding restrictions, only U.S. citizens, nationals, or permanent residents are eligible. Students must have a valid passport and driver's license. Applicants should be willing and able to work under sometimes strenuous field conditions, work and live will with others, and be able to adapt to flexible and irregular hours that are needed when conducting field research.

To Apply:Applications should be submitted to Dr. Kirsten Prior by email (kprior@binghamton.edu). Applications are being considered now, and will be considered up to?March 27, 2020. Applications should include the following documents: (1) letter of interest that describes your educational background, career goals, and how this internship will contribute towards those goals (4 paragraphs maximum), (2) current curriculum vitae/resume, and (3) unofficial transcripts. We strongly encourage undergraduates in underrepresented groups in STEM to apply.

Kirsten M. Prior, PhD Assistant Professor Binghamton University (SUNY) Department of Biological Sciences Science III, Rm. 106 (607) 777-4448 priorecologylab.com

"Kirsten M. Prior" <kprior@binghamton.edu>

Brisbane QuantGenetics Jun14-19 TravelFunds

We have received funding for graduate students and postdocs who are US citizens or permanent residents to attend the 6th International Conference on Quantitative Genetics in Brisbane, Australia, June 14-19, 2020. Conference details are available at https://icqg6.org and scholarship applications at https://forms.gle/krvrLjsC831SyVxH6 We are especially interested in reaching students from historically underrepresented groups.

We also hope to have scholarship funding for the 25th

Anniversary edition of the Summer Institute in Statistical Genetics at the University of Washington in Seattle, July 13-31, 2020. Details are available at www.biostat.washington.edu/suminst/sisg Bruce Weir bsweir@uw.edu

Bruce S Weir <bsweir@uw.edu>

Looking For 16s MicrobiomeSequence DataSets

Dear List:

I am teaching a research course this semester that was to generate 16S sequence data to characterize the gut, oral, and skin microbiomes of wild frogs and turtles. It now seems likely that this lab class will not meet again in person this semester, leaving us without sequence data to analyze. I am therefore looking for any 16S sequence data sets out there that I could use to continue this course online. This would preferably be from herps but not necessarily. One aim of this course is to expose students to authentic research so unpublished data would be preferred. Depending on the data and analyses, we aim to publish at least one manuscript from these data; data contributors would also be included as authors. Please contact me at skimble@towson.edu if you would like to contribute data.

Sincerely, Steve Kimble Clinical Assistant Professor, Towson University

Steve Kimble

Clinical Assistant Professor, Towson University

skimble@towson.edu

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

NorthDakota REU AvianPhysiologicalEvolution

Ever wondered about how stress affects the body or why some individuals are more resilient than others?

If so, join our research team and learn more about it!

Dates: 10 wks; late May/early June-early August 2020

Location: Fargo, ND

Student Benefits: Hands-on research experience, development of a diverse set of avian field research skills, and $500/week stipend plus housing and some travel costs.

Position Description:

The Heidinger lab in the Department of Biological Sciences at North Dakota State University (NDSU) in Fargo, ND, is seeking a motivated undergraduate student to participate in an REU on a project examining the long-term consequences of stress exposure in a local population of house sparrows. Duties will include manipulating stress exposure, monitoring parental behavior, checking nests, catching and re-sighting adult sparrows, and measuring offspring growth. Successful applicants must be enthusiastic and motivated. They must work well independently and as part of a research team.

Who should apply: Students in their sophomore or junior years of college, with strong credentials and majoring in wildlife ecology, biology, or conservation are encouraged to apply. Participants must be U.S. citizens or permanent residents and currently enrolled as an undergraduate student (i.e., enrolled for fall 2020). Students with backgrounds that are underrepresented in wildlife science are especially encouraged to apply. Students who have received their bachelor’s degrees and are no longer enrolled as undergraduates are not eligible to participate. A high level of responsibility, organization, and motivation are required. Applicants must be able to maintain work quality and a positive attitude during challenging field conditions that can include long field days in adverse weather conditions.

To Apply: If interested please email 1) a cover letter describing your interest in the project and previous research experience, 2) a resume or CV, and 3) the names & contact information for two references to Rebecca Young (rebecca.c.young@ndsu.edu) by April 1, 2020.

“Young, Rebecca” <rebecca.c.young@ndsu.edu>

Pandemic model

Here is a Link to a nature paper from 2006 with a model for the spread of 1918 flu in the US and Great Britain using modern travel metadata and various interventions. This is a refreshed version of that paper. It is being used to establish management strategies in the US and UK. It hasn't been peer reviewed and published in a journal, but it seems broadly accepted

https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-NPI-modelling-16-03-2020.pdf https://www.cnn.com/2020/03/17/health/coronavirus-uk-model-study/index.html The community might like to understand the policies in place.

Miriam Barlow

University of California, Merced

209.228.4174 miriam.barlow@gmail.com

Miriam Barlow <miriam.barlow@gmail.com>

RoyalSocPubl PriceEquation

Royal Society Publishing has recently published a special issue of Philosophical Transactions B entitled Fifty years of the Price equation compiled and edited by Jussi Lehtonen, Samir Okasha and Heikki Helanterä and the articles can be accessed directly at www.bit.ly/PTB1797 A print version is also available at the special price of Â£35.00 per issue from publishing@royalsociety.org

Felicity Davie Royal Society Publishing

Felicity.Davie@royalsociety.org

SMBE Nominations PresidentElect Treasurer 2Councillors

Nominations for President-elect, Treasurerand 2 Councillors due by Wednesday, March 11th, 2020

Dear SMBE Members,

I am writing to solicit nominations for SMBE President-Elect, Treasurer and 2 Councillors, whose terms will begin on January 1, 2021. All of these positions are for a duration of three years. As the society grows and thrives, council members play important roles in guiding its development and in soliciting and implementing programs that support our members, enrich opportunities for young scientists from around the world, and oversee our two excellent journals (MBE and GBE) as well as our annual meeting and satellite meetings.

Nominations will be reviewed by the Nomination Committee* who will then put forward a slate of two candidates for each position for membership vote. Past and current council members are listed athttps://www.smbe.org/smbe/ABOUT/Council.aspx Please send nominations with a brief statement in support of your suggestion (self-nominations are accepted) to: M.Mar Albà (mar.alba@upf.edu) and Nadia Singh (nsingh@uoregon.edu).

Nota bene: we ask the nominators to confirmi explicitly that the person they are nominating has already confirmed their willingness to run for office.

Please send your nominations by Wednesday, March 11, 2020.

We look forward to hearing from you.

Yours sincerely,

Nadia Singh Secretary of SMBE, on behalf of the Nomination Committee*

*The Nomination Committee is composed as follows: M.Mar Albà (Chair),Universitat Pompeu Fabra, Barcelona Maria Anisimova, Zurich University of Applied Sciences Tom Gilbert, University of Copenhagen Nancy Moran, University of Texas, Austin Yoko Satta, Graduate University for Advanced Studies in Hayama Nadia Singh (ex officio), University of Oregon

Society for Molecular Biology & Evolution smbe@allenpress.com

Society for Molecular Biology & Evolution

<smbe@allenpress.com>

Software NewRelease BAli-Phy3 5 0

Hi,

BAli-Phy version 3.5.0 is now available (http://www.bali-phy.org) for Windows, Mac, and Linux. The main new features are: - Covarion models (Tuffley-Steel '98, Galtier '01, Huelsenbeck '02, Wang et al '07) - Automatic ancestral state reconstruction. - See http://bali-phy.org/releases/3/ for more changes.

BAli-Phy is a Bayesian MCMC program for estimating alignments and phylogenies simultaneously from unaligned sequence data. BAli-Phy alignments can be 3.5 times more accurate than alignments using MAFFT and MUSCLE.

BAli-Phy can also be used to safely infer phylogenies from ambiguous regions like ITS - http://bali-phy.org/Examples/ITS/ITS12-tn93-free3/ You can download binaries for Linux, Mac, and Windows here: - http://www.bali-phy.org/download.php If you have any trouble using bali-phy, please post your questions to bali-phy-users@googlegroups.com. There is also an extensive manual at http://bali-phy.org/README.xhtml -BenRI

benjamin.redelings@gmail.com

Spain VolFieldAssist PlantEvolEcol JunJul

Nick Barton's group at the Institute of Science and Technology (IST) Austria is recruiting volunteers to assist with fieldwork on plant adaptation in the Pyrenees (Spain) this coming summer (June-July).

The project: We are studying the evolutionary processes underlying population divergence in wild Antirrhinum majus (snapdragons). We focus on natural hybrid zones between two subspecies with different flower colours. Most of the field work is contributing to a long-term pedigree project aimed at establishing a direct link from genotype to phenotype to fitness. With tens of thousands of samples collected over ten years so far, this provides an exciting and powerful system to examine many outstanding questions about adaptation and quantitative genetics in wild populations.

The work: We are seeking volunteers to assist with the field research, which involves mapping the location of individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits, and processing samples back at the field station. There may also be opportunities to be involved in other projects on plant-insect interactions. The work is highly team-orientated, typically in groups of 2-3. This is a great opportunity for anybody looking to obtain experience in fieldwork relating to evolutionary biology and plant ecology.

The field site is located near Ripoll in a beautiful part of the Pyrenees of North Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (WITHIN EUROPE) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and enthusiastic biology students/graduates with a strong interest in working outdoors with plants. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require a minimum stay of 3 weeks between May 28 and July 30. To apply, send your CV or resume by March 15. Include a few sentences about your background and why you are interested, and include the approximate date range you are available. Send any questions and your application to carina.baskett@ist.ac.at.

Carina BASKETT <carina.baskett@ist.ac.at>

Tunisia VolFieldAssist AntBehaviour

Volunteer field assistant for navigational research with desert ants in Tunisia

Navigation plays a major role in animal behaviour. The desert ant Cataglyphis fortis, inhabiting the open salt pans, has an extraordinary navigational system which guides it during its long-lasting foraging trips. The ant uses a so called path integration vector that, based on a sun compass and a step counter calculates the ant'Âs relative position to the nest. In addition, homing ants learn and use visual and olfactory cues to finally pinpoint their nest entrance.

Our group explores the role of olfaction in the behaviour of Cataglyphis fortis ants. While we could already show, that the ants use food and nest odours for pinpointing their targets, and learn olfactory landmarks to navigate between nest and food, we will now explore, whether and how olfaction regulates the high aggression between neighbouring ant colonies. The project includes fieldwork in a Tunisian saltpan where we investigate the behaviour of ants in their natural environment (from mid-June to mid-August 2020). We will stay at a fisherman'Âs town called MaharÂÂs and drive daily to a desiccated salt lake where we perform our experiments (approx. 60 km from MaharÂÂs). Based on the level of interest, the field assistance may also be expanded to a master'Âs or bachelor'Âs thesis.

These requirements should be fulfilled: Heat and sun resistant, fit enough for exhaustive days in the salt pan, interested in insects and animal behaviour. A driving license would be good but is not a necessary condition. We offer in exchange a rare possibility to gain fieldwork experience and an intense insight in the field of behavioural biology of the fascinating desert ant Cataglyphis fortis. We cover travel costs and accommodation (for a minimum of four weeks stay however, longer is desirable).

In case of interest, please contact:

Dr. Markus Knaden

Department of Evolutionary Neuroethology Max-Planck-Institut for Chemical Ecology Hans-Knoell-Strasse 8, Jena, Germany

mknaden@ice.mpg.de 03641-571421

Marilia Freire <mfreire@ice.mpg.de>

US NSF covid19

Please see below a notice from the US Nationation Science Foundation Directorate for Biological Sciences

BIO-wide Virtual Office Hours As you may have seen, Directorate for Biological Sciences (BIO) Assistant Director Joanne Tornow, PhD, wrote to the biological sciences community to share information about NSF's current operations in light of COVID-19 and provide guidance to current awardees.

In that letter < https://wordpress.com/-post/oadblog.nsfbio.com/1890 > (https://-oadblog.nsfbio.com/2020/03/26/a-letter-to-the-biological-sciences-community/) , Dr. Tornow noted that BIOstaff are interested in hearing how BIO and NSF can mitigate the longer-term harm of COVID-19 on U.S. research and training. We will be holding a series of four BIO-wide virtual office hours < https://www.nsf.gov/news/news_summ.jsp?cntn_id=-300247&org=BIO > next week during which the biological science community can share concerns, ask questions, or offer suggestions on how we can do more to address this national emergency.

Sessions dates and times are as follows and registration and log-in information will be available here < https://www.nsf.gov/news/news_summ.jsp?cntn_id=-300247&org=BIO > shortly. Please feel free to attend the session that best fits your schedule; representatives from across BIO will be in attendance during each session.

* Monday, March 30, 4-5 pm EDT * Tuesday, March 31, 3-4 pm EDT * Wednesday, April 1, 2-3 pm EDT * Thursday, April 2, 1-2 pm EDT

For more information on NSF's activities and response to COVID-19, please visit our coronavirus information page < https://www.nsf.gov/news/special_reports/-coronavirus/ >; this site is updated regularly.

Christopher Balakrishnan, Ph.D. Program Director, Evolutionary Processes Division of Environmental Biology Directorate of Biological Sciences National Science Foundation T: 703.292.2331

VisibleApeWebsite NowOpen

Visible Ape Website now open/free to anyone to interact/learn/teach

The NSF-funded Visible Ape Website has finally been launched, at www.visibleapeproject.com Details about it are given below: One of the major questions in biology is how small genotypic differences can underpin striking phenotypic differences in anatomy, physiology, development, and behavior, like those seen between humans and apes. Indeed, we share nearly 99% of our DNA with chimpanzees, our closest living ape relatives, despite having substantially different appearances and behaviors. In order to study these genotype-phenotype relationships across humans and apes, detailed phenotypic data, including anatomical data, are needed. The Visible Ape Project (VAP) includes a comprehensive, user-friendly and freely available website on ape anatomy and evolution, the Visible Ape Website.The website will serve as a valuable cross-disciplinary resource and create interdisciplinary connections between medical/veterinary education and biological anthropology, and support public interest in science, drawing further attention to and awareness of apes, whose continued existence in the wild is seriously threatened. A number of outreach activities, including US and internationally-collaborative workshops, educational, and conservation activities, will reach the public, students from the high school level through graduate levels, and researchers and medical/veterinary practitioners, around the globe,as well, crucially, rural communities living near apes.

Rui Diogo, PhD in Evol.-Funct.Morphol.& PhD in Hominid Paleobiol., Assoc. Prof. at Howard Univ. CollegeMedicine, Dep. Anat., 520 W St. NW, Numa Adams Building, room 1101, Washington DC 20059, USA.| Fellow of American Association Anatomists

Diogo's Lab Website:http://www.ruidiogolab.com Diogo's books:http://www.amazon.com/Rui-Diogo/-e/B001JS2K96 Diogo'sWikipedia page:https://-en.wikipedia.org/wiki/Rui_Diogo Diogo's research-gate:https://www.researchgate.net/profile/Rui_Diogo Diogo's Lab Twitter: @Rui_Diogo_Lab

Rui Boliqueime Martins Diogo <ruidiogo@gwmail.gwu.edu>

WestarcticaInc ConservationResScholarship Apr25

Westarctica, Inc announces the first annual Westarctica Conservation Scholarship, a $500 graduate research grant for the study of climate change. The goal of this research scholarship is to invest in early-career researchers who are pursuing a career in climate-change science. The topic is intentionally vague, and can include research into range-changes, evolution of adaptive characteristics, etc. Be creative!

Who we are: Westarctica, Inc is a non-profit organization focused on advocating for global conservation, framing conversations around Western Antarctica, an uninhabited ecosystem with no political advocates. Conserving our polar ecosystems means many things 'V reducing carbon use to halt warming and melting of polar ice, learning to talk to people who deny the problem, and researching better alternatives to virtually every aspect of modern living.

Qualification: This research scholarship is available to anyone who meets the following criteria: * pursuing a graduate (Master'Âs or PhD) in any nationally-accredited university or organization (i.e. zoo, field station) in the world. * researching a topic aligned with climate-change or global conservation issues. * planning a research project for the summer of 2020.

Application Procedure: Please fill out the form here (https://www.westarctica.info/scholarship). You will be asked to answer five questions, each in 200 words or less (unless otherwise specified): * In 20 words or less, describe the research question you are addressing. * What is the broad problem this question is addressing? * Why should the public care about your question/the problem/your research? * What possible solutions to climate-change might your work propose? * How will this money improve your research or the proposed solutions?

These applications will be reviewed by a panel of scientifically trained people from a variety of research and conservation backgrounds, as well as Westarctica, Inc board members. Finalists will be chosen, and the above answers will be submitted to the active members of the organization for a final vote.

Important Dates: April 25, 2020 (5pm EST): Applications Close May 4-8, 2020: Finalists responses will be shared with the Members May 9-13, 2020: Member Voting May 15, 2020 Winner Announced

Requirements: In accepting the award, you agree to do one follow-up interview at the end of the research period, and complete one online short-course on talking about climate change to non-believers.

If there are any questions, please feel free to email conserve@westarctica.info

Sheri Sanders Director of Conservation Westarctica, Inc. conserve@westarctica.info

Duchess of Eights <conserve@westarctica.info>

PostDocs

ArizonaStateU PopulationGenetics

The Jensen Lab is hiring a postdoc on an NIH-funded project involving theoretical and computational population genetics and large-scale data analysis. The start date is flexible. For primary research areas, current and former lab members, and recent publications, please see the lab webpage at jjensenlab.org. Interested candidates should send a brief statement of research interests and a CV to jeffrey.d.jensen@asu.edu by March 31.

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

Berlin EvolutionaryBiology

Postdoc in evolutionary and theoretical biology (4 years, salary scale: 13 TV-L FU)

Collaboration with members of the research consortium 'Integrating insect immunity, microbiota and pathogens' funded by the German Research Council (DFG). This reserch groups studies the interaction of different insect species and their microbiotas and how this interplay shapes pathogen virulence. The theoretical project is an essential component for the integration of the six empirical projects and jointly supervised by Roland Regoes (https://tb.ethz.ch/people/person-detail.html?persid=88149), who is also visiting fellow integrated into this consortium.. Specifically, the position entails

- Modelling of infections and microbiota and their interactions with the host immune system - Collaboration with all empirical projects in the group - Collaboration with a bioinformatician - Based at FU Berlin - Own research and publication of research. - Contribution to existing and fostering of new collaboration.

Required for the job are a PhD in biology or related disciplines (e.g. physics, mathematics) with a focus on evolution

Desirable: - PhD on mathematical modelling of host-pathogen interactions, virulence, epidemiology - Publication track record - Strong interest in interdisciplinary work - To be able to communicate well in English

Please submit applications (Subject header: WiMi_BIT_InsectInfect_AG Rolff) by April 6 to:

Prof. Jens Rolff Jens.rolff@fu-berlin.de Fachbereich Biologie, Chemie, Pharmazie Institute for Biology Evolutionary Biology Königin-Luise Str. 1-3 14195 Berlin Germany

Jens Rolff <jens.rolff@fu-berlin.de>

BielefeldU TheoreticalEvolution

Job announcement

Bielefeld University, Department of Evolutionary Biology

Postdoc position in Theoretical Evolutionary Ecology

Application deadline: 25.03.2020

The Faculty of Biology offers a full-time research position in Theoretical Evolutionary Ecology

The position can start as soon as possible and is funded until the end of the year 2021 by the German Research Foundation (DFG) within the collaborative research centre(SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3). The aim of the Postdoc project is to develop ecological and evolutionary theory to contribute towards a better understanding of intra-specific niche variation. The project is entitled "Modelling adaptive individualised niches in behaviour" (sub-project D04 of the collaborative research centre, with Klaus Reinhold). This theoretical project will explore the conditions that favour the evolution of between-individual variation in behavioural niches. The aim is to focus on mate choice and exploration and examine to which extent phenotypic variation can be maintained based on genetic differences and variation in adaptive phenotypic plasticity.

The collaborative research centre: The postdoc will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators and more than 20 postdoc and PhD students based at Bielefeld University, the University of MÂÂ¹nster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programs. Full details of the SFB can be found at www.uni-bielefeld.de/biologie/crc212. For further information on the projects and the involved departments, please contact Klaus Reinhold (klaus.reinhold@uni-bielefeld.de) with any informal inquiries.

Main responsibilities: research tasks (90 %): - Development of eco-evolutionary models, including - mathematical analysis of models - implementation in a programming language, e. g. in R, C++, Python - simulation studies - collaboration with other research groups in the collaborative research centre - writing scientific publications for international journals - teaching obligation in the field of Evolutionary Biologyto the extent of 1 LVS (5 %) - organizational tasks in the research group and collaborative research centre(5 %)

Your Profile We expect - university degree in a relevant discipline, e. g. biology, mathematics, physics or bioinformatics - completed PhD in a relevant field - experience with mathematical modeling of evolutionary processes - programming skills in at least one programming language (e. g. R, C++, Python) - interest in biological and mathematical questions - ability to work both independently and as part of a team - very good oral and written communication skills in English

Preferable qualifications - main focus of PhD in theoretical ecology, population genetics, behavioral ecology or evolutionary ecology - papers in peer-reviewed international journals - experience in collaborations between empiricists and theoreticians - experience with high-performance computing

Remuneration Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L). As stipulated in 2 (1) sentence 2 of the WissZeitVG(fixed-term employment), the contract will end on December 31, 2021. In accordance with the provisions of the WissZeitVGand the Agreement on Satisfactory Conditions of Employment, the length of contract may differ in individual cases. The employment is designed to encourage further academic qualification. In principle, this full-time position may be changed into a part-time position, as long as this does not conflict with official needs. Bielefeld University is particularly committed to equal opportunities and the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees. Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities. Application Procedure: For full consideration, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position; (ii) a

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Bilbao Spain DiseaseGenomics

Postdoc position available at the Integrative Genomics lab

The recently created Integrative Genomics lab led by Urko M. Marigorta at the CIC bioGUNE in Bilbao (Basque Country, Spain) seeks a motivated candidate to join as a postdoctoral researcher to work in the area of complex disease genomics.

About your position and the project You will apply statistical and bioinformatics expertise to spearhead a project exploring the genetic architecture of complex disease, with a focus on the molecular mechanisms that drive heterogeneity in symptoms as well as on developing new predictors for longitudinal tracking of disease. This work involves dealing with large omic datasets generated in-house (e.g. we are generating genomic and longitudinal transcriptomic profiles of patients to investigate the underpinnings of drug response in CrohnÂs disease), and/or gathered from large-scale public biobank databases. The specifics of the project should remain within the focus areas of the lab (https://www.cicbiogune.es/people/umartinez), but can be adapted according to your research goals and expertise (including experience in other disease domains). Financial support for this position is available for up to three years (32.3k euro /year gross salary). Start date is negotiable, but the position is immediately available.

The requirements This postdoctoral position suits best a researcher with a background in complex trait genetics, including experience with statistical genetics and genetic epidemiology, being acquainted with the analysis of large omic datasets. Candidates coming from a quantitative field (with a PhD in areas such as statistics or computer science) and that have a demonstrated interest in disease genomics are also welcomed to apply. Strong bioinformatic skills, with fluency in R, Python or similar languages, and an ability to work independently and an inquisitive mind are a must. Experience in immunology, and/or other areas in computational biology, are desirable but not essential.

The lab Our lab addresses emerging questions in disease biology and tackles them using a combination of statistical genomics and medical transcriptomics. This integrative approach, based on analyses of multilayer -omic profiles from clinical cohorts, improves our understanding of complex disease etiology and permits to refine the estimation of disease risk. Our long-term goal is to gear this knowledge towards development of new precision medicine-based solutions that can improve disease and patient management. More details about our research are available at https://www.cicbiogune.es/people/umartinez . How to Motivated candidates should apply with a package that includes (i) a detailed CV, (ii) a 2-3 page cover letter discussing your research experience (including statistical and computational skills) and productivity, motivations, areas of interest and goals for your postdoc training, and (iii) contact details of three references, using our form (https://www.cicbiogune.es/careers/job-offers) and indicating 44622 as reference

Urko M. Marigorta umartinez@cicbiogune.es

[ASOCIACION CENTRO DE INVESTIGACION COOPERATIVA EN BIOCIENCIAS] [Center of Excellence Severo Ochoa]

Center of Excellence Severo Ochoa (2017-2021)

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Please consider the environment before printing this email

Urko Martínez Marigorta <umartinez@cicbiogune.es>

BowdoinC Maine MarineEvolution

Doherty Marine Biology Postdoctoral Scholar Position number - F00147JP

Bowdoin College invites applications for appointment as Doherty Marine Biology Postdoctoral Scholar based at the Schiller Coastal Studies Center (SCSC). TheSCSCis a 118-acre coastal property on Orr's Island in Harpswell, Maine, a 20-minute drive from the Bowdoin main campusand offers outstanding access to nearshore habitats of Casco Bay. Over the last six years, theSCSChas expanded Bowdoin's research strengths on the impacts of climate change on coastal systems, including new buildings for teaching, research and residential life, anNSFfundedexperimental seawater laboratory and coastal monitoring platform, a dry laboratory and an expanded boat fleet. Applicants who take an interdisciplinary approach to studying the impacts of climate change on coastal marine organisms and ecosystems are particularly encouraged toapply. The postdoc will maintain an active research program. The teaching component includes a course module in the fall Marine Science Semester (https://www.bowdoin.edu/coastal-studies-center/marine-science-semester/index.html) and the supervision of undergraduate research inthe applicants specialty during the summer and academic year. Applicants must possess a demonstrated commitment to excellence in teaching and research, and a commitment to the liberal arts. This is a two-year appointment, starting as soon as July 1, 2020, and renewable for a thirdyear. The annual stipend for this benefits-eligible position is $55,000. Applicants must have received, or anticipate receiving, their PhD between July 1, 2014 and July 1, 2020, and those who expect to receive their PhD by June 30, 2020 should provide documentation from their homeinstitution confirming this schedule. Bowdoin is a community that warmly welcomes people of all backgrounds. We encourage applications from candidates committed to the instruction and support of a diverse student population and from those who will enrich and contribute to the College's multifaceted diversity. In yourapplication materials, please address how your teaching, scholarship, and/or mentoring would support our commitment to diversity and inclusion. Bowdoin College accepts only electronic submissions. Please submit a letter of application, curriculum vitae, statement of research and teaching interests, and the names and contact information for three references who have agreed to provide a recommendation. Review of applications will begin immediately and continue until the position is filled. Founded in 1794 on the Maine coast, Bowdoin is one of the oldest and most selective coeducational, residential liberal arts colleges in the country. Located in Brunswick, a 30-minute drive north of Portland, the College is in an area rich with natural beauty and year-round outdooractivities. Bowdoin's reputation rests on the excellence of its faculty and students, intimate size, strong sense of community, and commitment to diversity (32.7% students of color, 6% international students and approximately 15% first generation college students). Bowdoin Collegecomplies with applicable provisions of federal and state laws that prohibit unlawful discrimination in employment, admission, or access to its educational or extracurricular programs, activities, or facilities based on race, color, ethnicity, ancestry and national origin, religion, sex, sexualorientation, gender identity and/or expression, age, marital status, place of birth, genetic predisposition, veteran status, or against qualified individuals with physical or mental disabilities on the basis of disability, or any other legally protected statuses. For further information about theCollege and our department, please visit our website: http://www.bowdoin.edu . Applicants can apply at: https://careers.bowdoin.edu/postings/6671
David Carlon <dcarlon@bowdoin.edu>

CarnegieStanford ComputationalQuantGenetics

Postdoc position in Computational Quantitative Genetics

Carnegie Institution for Science, Department of Plant Biology, Stanford, CA 94305

Rhee Lab - https://dpb.carnegiescience.edu/-labs/rhee-lab Moi Exposito-Alonso Lab - www.moisesexpositoalonso.org Starting: immediate start possible; Deadline: until filled

The Rhee and Moi Labs aim to recruit a highly motivated and creative person with strong training in bioinformatics / quantitative genetics / evolutionary biology / computer science.

This project seeks to develop predictive models of causal genes of plant traits, particularly in the model C4 grass Setaria and bioenergy crop Sorghum. This project has opportunities to work with leaders and trainees in plant biology ranging from evolutionary biology, genetics, genomics, phenomics, physiology, and synthetic biology (www.foxmillet.org). The successful candidate will use machine learning models and genome-wide associations of plant functional and genomic data (RNAseq, sequence polymorphisms, evolutionary signatures, and functional annotations), both publicly available and newly generated in our consortium for Setaria and Sorghum, to discover and predict the causal effect of genes controlling metabolic, developmental, and fitness traits in stressful drought and high-density planting conditions.

This position involves conducting research independently, being involved in collaborative projects, preparing publications, and presenting research in scientific meetings. The candidate will also work with computational postdocs in the consortium who have built baseline algorithms using different frameworks, and experimental postdocs who will test the predicted causal genes using genome editing and physiological measurements. We prefer candidates interested in strengthening connections between molecular ecological genetics, sustainable breeding, and computational biology, who will be active members of the research community at the Carnegie Plant Biology and the Stanford Biology departments.

This is a full-time position with competitive salary and benefits. The labs are located at the Carnegie Institution on Stanford campus. Carnegie Postdocs have access to most Stanford facilities. Stanford campus is a vibrant community embedded in the San Francisco Bay area, with opportunities for extensive social and scientific interactions. The initial position will be for one year with potential renewal of up to three years depending on performance.

Qualifications: 1) a Ph.D. or equivalent in Computer Science, Biology, Bioinformatics, Mathematics, Engineering or related field; 2) expertise or fluency in large-scale data analysis, statistics, genomics, machine learning, and/or related field; and 3) proficient in programming. Candidates with experience in developing machine learning algorithms and/or trained in quantitative genetics are especially encouraged to apply. The successful candidate should have a demonstrated ability for independent and critical thinking, ability and initiative to learn new things, excellent communication and teamwork skills and passion for biological research.

About Carnegie: Carnegie Institution for Science is a U.S.-based non-profit, private endowment. Andrew Carnegie founded the Carnegie Institution of Washington in 1902 as an organization for scientific discovery to serve as a home to exceptional individuals - women and men - with imagination and extraordinary dedication capable of working at the cutting edge of their fields. investigators are leaders in the fields of plant biology, developmental biology, Earth and planetary sciences, astronomy, and global ecology. The Department of Plant Biology engages in basic research on the mechanisms involved in plant and algae growth, development, and evolution (https://dpb.carnegiescience.edu). Carnegie is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, religion, color, national origin, sex, sexual orientation, gender identity, age, veteran status, disability or any other protected status in accordance with applicable laws.

Please apply online including a cover letter and CV at:

https://jobs.carnegiescience.edu/jobs/postdoc-position-in-computational-quantitative-genetics/ Moisés Expósito Alonso <mexpositoalonso@carnegiescience.edu>

CharlesU PlantGenomeDuplication

***ERC-funded postdoctoral position in the evolutionary genomics of whole genome duplication

*Start (negotiable): autumn 2020 *Duration: 2 years (with possibility for an extension) *Place: Department of Botany, Charles University, Prague, Czech Republic, EU

We seek a highly motivated, independent early career researcher interested in leading a research program within the context of an ERC-funded project focused on the evolutionary consequences of whole genome duplication (for details see below). The successful candidate will join the team of Ecological Genomics lead by Filip Koláø (https://botany.natur.cuni.cz/ecolgen). This project will involve close collaboration with other labs focused on ecological and evolutionary genomics of polyploidy, Levi Yant (University of Nottingham, UK) and Christian Parisod (University of Bern, Switzerland).

**Requirements - innovative thinking, enthusiasm for evolutionary biology - keen interest in leading an independent research program and collaborating both within the group and internationally - a strong background in structural, statistical, and/or population genomics - PhD in evolutionary biology, genetics, bioinformatics, or related fields

**We offer - competitive monthly salary of 2,400 EUR (note that average gross salary in the Czech Republic was ~1,350 EUR monthly in 2019 and living expenses are generally lower in CZ) - work in a young, dynamic and international environment, situated in an inspiring city centre - co-supervision of a PhD student in the same project - involvement in international collaboration including stays in collaborating labs

**Optional - further possibilities for strengthening academic career - take part in teaching relevant courses - supervision of master project(s) in the Bioinformatics or Evolutionary Biology program - participate in fieldwork in Europe or North America - opportunity to develop independent research follow-up project - support for seeking additional self-funded projects in national (e.g. Junior Researcher projects within The Czech Science Foundation) and international funding schemes (e.g. Marie Curie, EMBO fellowship)

***Project details Whole genome duplication (WGD, polyploidization) is a dramatic genome-wide mutation whose ubiquity across eukaryotes suggests an adaptive benefit, although the underlying mechanism remains unknown. In the project, the successful applicant will test the hypothesis that WGD promotes formation and/or later accumulation of structural changes in a genome (gene duplications, inversions, repetitive DNA proliferation), potentially providing adaptive benefits when facing novel environmental challenges. The project will build on our research in Arabidopsis arenosa that demonstrated that WGD can increase the capacity of its natural populations to accumulate adaptive variation, but the candidate will extend well-beyond this system to additional species to discern the generality of initial findings from the A. arenosa system. The core work will focus on analysis of population genomic data from field surveys of ploidy-variable systems (diploid-autotetraploid), providing replicates of the WGD process in natural conditions. There will be possibility to expand to analyses of variation in experimental populations involving newly synthesized polyploids. General conclusions will be drawn taking advantage from replicated ploidy-variable plant species, which are partly already sampled and sequenced. Alongside the head - start with available data, the candidate is expected to be fully involved in the overall project design and lead the analytical part of the project. For overall info on the Starting ERC project see https://botany.natur.cuni.cz/-ecolgen/node/48 . **Please send your CV, contact details for two referees and a half-page motivation letter to Filip Koláø (filip.kolar@natur.cuni.cz). Review of the applications will begin on March 20th 2020 and will continue until the position has been filled.

– Filip Kolar Department of Botany Faculty of Science, Charles University Benatska 2, CZ - 128 01, Prague, Czech Republic *https://botany.natur.cuni.cz/ecolgen/ < https://botany.natur.cuni.cz/ecolgen/ >*

Filip Kolar <filip.kolar@gmail.com>

ChicagoBotanicGardens PlantConservation

Dear colleagues,

Plants of Concern < https://plantsofconcern.org/ > a citizen science rare plant monitoring program is hiring a postdoc to ideally start sometime in the fall (~ Sept). Anyone interested in rare plant population ecology and conservation is encouraged to apply, especially if they have experience analyzing population dynamics. The position is for 2 years. Here is a link to the posting: https://www.chicagobotanic.org/jobs/-postdoctoral_researcher_plants_concern Please share with your networks!

Any further inquries please contact Amy Iler <ailer@chicagobotanic.org>

Genetics Lab <Lab@chicagobotanic.org>

CPING network InvasivePlantGenomics

The Consortium of Plant Invasion Genomics (CPING) invites applications for its postdoctoral researcher fellowship competition. CPING is an NSF-funded project spanning five universities with the joint missions to determine how and why certain plant species become invasive and to train the next generation of botanists to use modern genomic and bioinformatic tools. Specifically, we are reconstructing genomic time series for five focal invasive plant species using herbarium specimens to investigate the roles of colonization history, admixture and adaptation in the invasion process. We also will be hosting genomics bootcamps for professors from EPSCoR regional universities and colleges. This training network will both promote genomics/bioinformatics expertise and create the opportunity for participants to contribute to CPING research projects.

Applicants may apply to work with any Co-PI in the network (see https://www.invasiongenomics.com/-participants.html) and can be based at any of the CPING hub institutions including University of Louisiana at Lafayette, West Virginia University, University of Alabama, South Dakota State University and Wichita State University. The successful applicant will focus his/her research efforts on one of the CPING focal invasive species, while having latitude to pursue independent research interests related to CPING projects. The successful applicant will collaborate with other CPING labs to leverage the strength of the network to their advantage. Opportunities for outreach through participation in genomics and bioinformatics bootcamps will also be available.

The optimal candidate would possess:

- PhD in invasion biology, botany, evolutionary biology, ecology, computational biology, or a related field - Experience constructing genomic libraries - Experience working with herbaria or other natural history collections - Experience in bioinformatics (working in a Unix environment, genome assembly, phylogenomic or population genomic analyses) - Experience coding in R, python, Perl, or another computing language - Experience researching polyploid species - Desire and propensity to teach genomics and bioinformatics to all levels of trainee - Excellent communication and organization skills.

The initial appointment is for one year with the opportunity to extend up to three years. Support includes a competitive salary and a benefits package including retirement and health care. A stipend for independent research ($5,000/year) is also included.

Informal inquiries about the position can be sent to any hub co-PI, and we encourage applicants to contact potential mentors prior to applying. Formal applications can be filled out at The active link is here: https://louisiana.csod.com/ats/careersite/-JobDetails.aspx?site=1&id=50 .Please include your CV, contact information for 3 references, and a 2-3 page research statement that outlines previous and current research, as well as a brief statement about future directions. References will only be contacted for applicants on the short list. Review of applications begins on April 1 and continues until the position is filled. Start date is flexible, but funding is available immediately.

Both CPING and University of Louisiana at Lafayette are Equal Opportunity Employers and all qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity or expression, national origin, disability status, protected veteran status, or any other characteristic protected by law.

Brittany Sutherland <blsutherland@gmail.com>

FloridaStateU EvolutionaryGenetics

Postdoctoral Scholar position in evolutionary genetics of development

The Houle lab in the Department of Biological Science at Florida State University is hiring a full-time postdoctoral scholar (PDS), starting on or after July 15, 2020.The PDS will be responsible for analysis of evolve-and-resequence and RNA expression data from artificial selection experiments, and the integration of those results with GWAS data.This an NSF-funded project on the relationship of the genotype-phenotype map to pleiotropy and evolvability, using wing and leg development in /Drosophila melanogaster/ as an experimental system. The successful applicant will have a Ph.D. in a relevant evolutionary or genetic discipline, and experience with analysis of large sequence data sets.Funding is assured for 20 months from the initial start date, and may be extendable beyond that date.Initial salary will be $50,000 USD plus health insurance.

To apply, or for more details, please contact David Houle (dhoule@bio.fsu.edu). Applications must include a cover letter that details skills and accomplishments relevant to the project, your CV, and contact information for three professional references.

David Houle <dhoule@bio.fsu.edu>

GEOMAR Kiel ComparativeGenomics

GEOMAR Helmholtz Centre for Ocean Research Kiel is a foundation of public law jointly financed by the Federal Republic of Germany (90%) and the state of Schleswig-Holstein (10%) and is one of the internationally leading institutions in the field of marine sciences. Currently GEOMAR disposes over an annual budget of approx. 80 million Euro and has approx. 1000 employees.

The research unit Evolutionary Ecology of Marine Fishes of the research division “Marine Ecology” is offering a position as

Postdoc (m/f/d) in Comparative Genomics

starting on May 1st, 2020 or upon agreement.

In the Research Group “Parental investment and immune dynamics”, we study the evolution of pregnancy focusing on syngnathids (pipefishes and seahorses) with their unique male pregnancy. This reproduction strategy evolved from carrying eggs loosely attached to the body to full pregnancy encompassing several intermediate forms. Thus, syngnathids present an ideal system to identify changes associated to the evolutionary steps from egg laying towards advanced pregnancy. Experimentally, we investigate changes in the immune system that allowed male pregnancy to evolve and assess the molecular basis associated to the evolution of syngnathids’ increasingly complex brooding structures and pregnancy. To do so, we combine a diversity of molecular and developmental biological methods, genetic engineering (CRISPR/ cas9) with comparative genomics and transcriptomics. We have recently sequenced 13 genomes of pipefishes and seahorses.

Job Description

Using comparative genomics, we aim to elucidate the coevolution of the immune system with male pregnancy. We recently determined that parts of the adaptive immune system have been lost during the evolution of male pregnancy. Comparative analyses of specific immune gene families and developmental pathways will permit to gain insight into how the immune system has been remodeled and how this relates to male pregnancy evolution. We furthermore aim to identify gene co-option accompanying the evolution of pregnancy and the establishment of new genes with subsequent neo- or sub-functionalization. To do so, transcriptomic analyses of genes that are differentially expressed during male pregnancy should be combined with genome-wide selection analyses. The project will be conducted in close collaboration with the experimental PhD students and postdocs in the laboratory that are focusing on genetic engineering of pregnancy genes, gene expression visualization and tissue transplant experiments.

Qualification The successful candidate is required to have a PhD in Natural Sciences (Biology, Bioinformatics or a related discipline). We expect a highly motivated Postdoc with a keen interest and background in comparative genomics, transcriptomics and evolutionary biology, that will allow the candidate to efficiently analyze the available data-sets and prepare manuscripts to be submitted to respected peer-reviewed international scientific journals. Knowledge of programming languages (Perl/Python/R) is thus required. Experience with gene annotation, orthologous gene identification and methods of detecting selection would be a plus. Also, familiarity with genes of the immune system, developmental pathways, and basic knowledge of fish biology would be desirable. Close interactions with the other PhD students and postdocs in the project at GEOMAR and with our collaboration partners at the Centre for Ecological and Evolutionary Synthesis (University of Oslo, Norway) will stimulate intellectual exchange and facilitate collaborations. Proficiency in spoken and written English is expected.

The position is available for a funding period of three years. The salary is up to the class E13 TVöD-Bund of the German tariff for public employees. This is a full-time position. The position can be split.

The position is embedded in a Starting Grant from the European Research Council focusing on male pregnancy (MALEPREG) and is in close collaboration with the Centre for Ecological and Evolutionary Synthesis at the University of Oslo. Several visits and longer research stays in Oslo are planned for the successful candidate. The genomes are already sequenced and assembled, the project can thus start immediately.

The GEOMAR, the University of Kiel and the Max Planck Institute for Evolutionary Biology in Plön offer a stimulating research environment with strong focus on Evolutionary Biology.

Kiel is the capital of the most Northern state of Germany, directly located at the coast of the Baltic Sea. The town offers many opportunities for leisure activities, in particular people enjoying water sports will love the environment.

GEOMAR Helmholtz Centre for Ocean Research Kiel seeks to increase the proportion of female scientists and explicitly encourages qualified female academics to apply.

GEOMAR is an equal opportunity employer and encourages scientists

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IllinoisStateU FunctionalGenomics

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

Postdoctoral Research Position (1 year)

Salary: $43,000 per year

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

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

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

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

If interested, please apply at www.jobs.ilstu.edu/applicants/Central?quickFindy471 . For informal inquiries please contact Scott Sakaluk (sksakal@ilstu.edu) or Ben Sadd (bmsadd@ilstu.edu).

Illinois State University is an Equal Opportunity/Affirmative Action Employer

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

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bmsadd@ilstu.edu

IVPP Beijing ComputationalPhylogenetics

Two Postdoc Positions in Computational Phylogenetics

Two postdoc positions are available in the lab of Dr. Chi Zhang in the Institute of Vertebrate Paleontology and Paleoanthropology (IVPP), Chinese Academy of Sciences (CAS) in Beijing, China. The position is for two years initially, with possible extension upon progress. The starting date is flexible.

Project 1: We are developing phylogenetic tools to study speciation and gene flow (hybridization or introgression) using genetic sequence data from extant and extinct species. The development is based on the BEAST2 platform (https://www.beast2.org).

Project 2: We are developing and applying tools to date species divergences using both morphological and molecular data (MrBayes and BEAST2 primarily). We will focus on morphological evolutionary models and diversification processes.

In these projects, you will be expected to contribute to the software development and/or empirical data analyses. You are also encouraged to develop an independent project where Bayesian phylogenetic computation plays a central role. Our lab has access to the high-performance computing resources in IVPP.

Requirements: You should have a doctoral degree in bioinformatics, statistics, computer science, evolutionary biology, or related major. You should be comfortable with Bayesian statistics and computation, and have prior experience in programming using Java, C/C++, Python, R, or other languages. If you focus on empirical research, the ability of applying various phylogenetic tools and understanding the outcomes is desired. You need to have good communication, scientific reading and writing skills in English.

Your salary will be covered by Dr. Zhang's research funding, and the CAS President's International Fellowship for Postdoc Researchers (PIFI, http://english.cas.cn/cooperation/fellowships, if qualified). The annual salary is about 250 thousands CNY per year (before tax). Besides, there are extra funding for research equipments and international conferences, etc.

IVPP is one of world's premiere paleontological institutions focusing on morphology, taxonomy, phylogeny, paleoecology, and many other fields. More information can be found here (http://english.ivpp.cas.cn/au/bi/). The institute is located in central Beijing, a good place to enjoy Chinese food and culture.

To apply, please email a single PDF file to Dr. Chi Zhang (zhangchi@ivpp.ac.cn), consisting – a cover letter briefly describing your research experience, skills, interests, and future plan; – a CV with contact information for at least two referees. The positions are open until fully filled.

Chi Zhang Associate Professor Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences 142 Xizhimenwai Street, Beijing, China zhangchi@ivpp.ac.cn https://scholar.google.com/citations?user=3D4othtCUAAAAJ zhangchicool@gmail.com

Lyon WaterStriderSexualConflict

Two-year Postdoctoral position in Evolution and Development

Topic: Sexual conflict in water striders Deadline: Till position is filled Contacts: abderrahman.khila@ens-lyon.fr or locke.rowe@utoronto.ca Position: 24 months. Starting date: As soon as possible. Location: Institute of Functional Genomics of Lyon, France

A position as a postdoctoral researcher is available in a collaboration between the Institute of Functional Genomics of Lyon (IGFL, France) and the Department of Ecology and Evolutionary Biology at the University of Toronto (EEB U of T, Canada). The fellow will be based in Lyon and will work in collaboration with Abderrahman Khila (IGFL) and Locke Rowe (EEB U of T).

A detailed description of IGFL can be found here: http://igfl.ens-lyon.fr/ and the Khila lab here: http://igfl.ens-lyon.fr/equipes/a.-khila-developmental-genomics-and-evolution A detailed description of the EEB U of T can be found here: http://www.eeb.utoronto.ca/ and the Rowe lab here: https://rowe.eeb.utoronto.ca/ Project description: Selection in males and females is often antagonistic where traits favoured in one sex may impose costs to the other (Arnqvist and Rowe, 2005). This project examines the development and evolution of male modified antennae in a genus of water striders called Rheumatobates (see Khila et al. Science 2012). In this genus, of about 40 species, we know of at least five independent events of male-specific modifications of the antennae into grasping traits (Rowe et al. Can. Ent. 2006). While these modifications converge functionally, there is a striking divergence in their morphology. This project includes three primary parts:

1- Behavioural analyses of how males of three Rheumatobates species use their antennae to grasp females during pre-mating struggles

2- Test, using RNA interference, the role of the gene distal-less in these modifications (Khila et al. Science 2012; Crumiere and Khila, Biology Letters 2019)

3- Analyses of sex biased gene expression based on existing RNAseq data of male and female antennae of six species, including three with modified male antennae and the other three with monomorphic antennae.

Qualifications: The successful candidate must have a PhD in evolutionary or molecular biology/genetics. Documented experience in bioinformatics and analyses of genomic/transciptomics data is strongly desired. Good communication skills, both in terms of written and spoken English. A competitive track record. We will also favour candidates with a demonstrated ability to work collaboratively in a team.

Desired qualifications: Experience with non-model organisms and EvoDevo is a plus but not a requirement for this position. These skills can be acquired in the host lab.

How to apply: Please send the following by e-mail to abderrahman.khila@ens-lyon.fr or locke.rowe@utoronto.ca

1- A letter of intent explaining how this position would fit your career plan, your fit to the position, and your research interests.

2- Your CV including your publication list and a description of your education

3- Names and contact information of three references who can write letters of recommendation on your behalf

Abderrahman Khila <abderrahman.khila@ens-lyon.fr>

MichiganStateU IntegrativeModelingRangeShifts

Postdoctoral Position, Integrative Modeling of Species Range Shifts, Department of Fisheries and Wildlife, Michigan State University

Application Review Date Extended to April 23rd!!

A postdoctoral research associate position in population genetics and demographic modeling is available in the Department of Fisheries and Wildlife at Michigan State University. The successful applicant will join an established collaborative network of researchers across five institutions (Michigan State University, the Morton Arboretum, the College of Charleston, the Missouri Botanical Garden, Mount Royal University) and contribute to an NSF-funded project focused on quantifying species' historical range shifts using multiple data types (for more information see: https://www.nsf.gov/awardsearch/-showAward?AWD_ID=1759759). Although multiple data types contain information on species' range shifts (i.e., fossil pollen data, occurrence data and ecological niche models, and population genetic data) these datasets do not always result in equivalent inferences (e.g., on the speed of range shifts). This project seeks to integrate these data types in a coherent analytical framework to infer demographic parameters (migration rates, population sizes, etc.), the location of glacial refugia, and the pace of post-glacial range movement (see Hoban et al 2019 Ecography). The statistical framework provided by Approximate Bayesian Computation (ABC) is a major component of the integrative modeling approaches we are developing. Our project team currently includes individuals with expertise in Mathematics, Statistics, Ecology, Biogeography, and Population Genetics, and we look forward to welcoming a new collaborator to the project.

Applicants must have a Ph.D. in Genetics, Ecology, Evolutionary Biology, Bioinformatics, or a similar field with demonstrated experience in population genetics and some coding experience. In particular, experience with programming (R, Python, C++), Approximate Bayesian Computation, cluster computing, and/or analysis of population genomic data is desirable. Other desired qualifications include a strong work ethic, problem-solving and time management skills, and experience communicating scientific results. Applicants should demonstrate an interest in joining an established interdisciplinary research team working at the interface of statistics and ecology, and in contributing to an open-source software development project. This position includes opportunities (and funding) to engage in a wide variety of professional development activities (depending on areas of interest) and to participate in planned outreach efforts associated with this project.

Interested applicants should submit a cover letter, statement of research interests, and contact information for three references via the Careers @ MSU website (job posting #632351): https://careers.msu.edu/en-us/job/-503149/research-associatefixed-term .In addition to the materials above, code (e.g., link to a GitHub repository) and writing samples (i.e., one or more recent publications) are also strongly encouraged, and will be considered during review. Questions about the position can be directed to Dr. John Robinson, jdrob@msu.edu. The initial appointment for this position is for a period of one year, with the possibility of renewal for a second year pending satisfactory performance. The preferred start date for this position is Summer 2020, but the start date is flexible given current events. Review of applications will begin April 23, 2020 and will continue until the position is filled

jdrob@msu.edu

MNH Stockholm Phylogenomics

Postdoctoral position in phylogenomics

A two-year postdoctoral position is available in the Department of Zoology, Swedish Museum of Natural History, Stockholm. The position is supervised by Prof. Ulf Jondelius, as a part of the project "Evolution of Xenacoelomorpha, an ancient animal group " funded by the Swedish Reseach Council. The goal of this project is to perform an analysis of phylogeny, evolutionary rates and gene content of the marine animal group Xenacoelomorpha using transcriptomic and genomic data. The successful candidate will manage and analyse transcriptome and genome sequencing data, perform phylogenomic analyses and write papers. There will be opportunities to participate in undergraduate teaching and supervision of students.

Qualifications Postdoctoral positions are appointed primarily for purposes of research. Applicants are expected to hold a Swedish doctoral degree or an equivalent degree from another country. The degree should have been completed no more than three years before the deadline for applications. In the appointment process, special attention will be given to research skills. We are looking for candidates with primarily dry-lab skills in the fields of genomics, transcriptomics and phylogenomics including experience with managing, processing and analysing next-generation sequencing data. Specific experience with metazoan evolution and microscopic invertebrates constitutes an advantage, but is not strictly necessary. The candidate must be highly motivated, creatively thinking with a collaborative attitude, have strong writing skills and a record of high-quality scientific publications. Excellent English language skills both written and spoken, are a requisite.

Terms of employment The position involves full-time employment for a maximum of two years, Start date 2020-06-01 or as per agreement. The Swedish Museum of Natural History strives to be a workplace free from discrimination and with equal opportunities for all.

Application deadline 1 April 2020

Informal queries may be directed to ulf.jondelius@nrm.se

FURTHER INFORMATION AND HOW TO APPLY (in English): https://www.nrm.se/en/-ommuseet/jobbahososs/ledigatjanster.9005019.html Ulf.Jondelius@nrm.se

NHM UOslo Phylogenomics

For the following PostDoc (Jobbnorge ID:184791) please apply at https://www.jobbnorge.no/en/available-jobs/-job/184799/postdoc-in-phylogenomics The deadline for the deadline is at 14.04.2020.

About the position A 3-year PostDoc position is available at the Natural History Museum (NHM), University of Oslo. The subject of the PostDoc position will be part of the recently founded RCN-project "InvertOmics - Phylogeny and evolution of lophotrochozoan invertebrates based on genomic data". The origin and evolution of Bilateria is controversially discussed in several biological disciplines such as systematics or evolutionary developmental biology. In one hypothesis, evolution in Bilateria advances from a simple body organization similar to flatworms towards more complex forms several times independently. In the other one, the evolution progresses in the opposite direction from a complex ancestor more like an annelid to simple organizations by several separate reductions. Support for one or the other depends on the phylogeny and evolution of Lophotrochozoa, one of the major bilaterian taxa, but a robust phylogeny is still lacking despite recent phylogenomic studies. This is due to both low coverage by genomic data and misleading biases in data of lophotrochozoan taxa. In this project, high-quality reference genomes shall be generated and new procedures to both ameliorate negative effects of biases and establish a new support measurement, which is entirely different from all recent support measurements. Due to both the large genomic dataset and these thorough analyses, a robust phylogeny of Lophotrochozoa shall be provided allowing contributions to discussions about the origin and evolution of Bilateria as well as of lophotrochozoan taxa and character traits. The aim of this PostDoc project is to concentrate on the methodological problems of the reconstruction of the phylogeny of Lophotrochozoa. Thegoal is to develop a new approach to assess the support for specific phylogenetic hypotheses and determine a priori the best procedure to ameliorate the effect of misleading biases. Therefore, the effects of misleading biases shall be simulated in a phylogenomic setting based on parameter spaces derived from empirical data and also include confounding effects of reticulate evolution, adaptive radiations and incomplete lineage sorting. Based on these simulated data both a best-practice procedure and new support measurement on how likely a reconstructed relationship is true shall be derived. These approaches will be used to address possible biases in the dataset compiled from genomic data to reconstruct the phylogeny of Lophotrochozoa (see the accompanying advertisement for a PhD position). The Natural History Museum has a modern DNA laboratory as well as access to the Norwegian Supercomputer facilities. The postdoc will be associated with the research group “Frontiers in Evolutionary Zoology”, specifically Torsten Struck (Professor of Evolutionary Genomics).

Qualification requirements - We seek a person with strong motivation for research in phylogenomics. - The candidate must be skilled in phylogenetic reconstruction methods. - Experience with the development of new tools for phylogenetics is required and with the generation of huge numbers of simulated datasets is preferable. - Computing skills in either Deep Learning, Neural Networks or Machine Learning Algorithms are advantageous. - Communication skills (including written and spoken English) - A strong academic track record - Team-working and networking skills

A degree equivalent to a Norwegian doctoral degree in biology, bioinformatics or equivalent. For candidates not having finished their doctoral degree the doctoral dissertation must be submitted for evaluation by the closing date of the call. An appointment is dependent on the defense of the doctoral thesis being approved.

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

How to apply The application must include - cover letter (statement of motivation, summarizing scientific work and research interest) - CV (summarizing education, positions, pedagogical experience, administrative experience and other qualifying activity) - copies of educational certificates (academic transcripts only) - a complete list of publications

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Norway Bioinformatics

#Postdoc #research #position in my lab :) Postdoc position in rapid diagnostics of #AntimicrobialResistance : #Bioinformatics and #MachineLearning https:/-/www.jobbnorge.no/en/available-jobs/job/185050/-postdoc-position-in-rapid-diagnostics-of-antimicrobial-resistance-bioinformatics-and-machine-learning?fbclid=-IwAR1hpG7fpEO2rb26X_XDA3r1aVZpW4n52FNo5Xn5Z6iNKqG2Cv_
yusuf.zhc@gmail.com

PasteurInst Paris PopulationGenetics

Two post-doctoral positions in Population Genetics and Quantitative Genetics at Institut Pasteur in Paris

The Quintana-Murci laboratory (Unit of Human Evolutionary Genetics, CNRS UMR2000) is recruiting two post-doctoral researchers in population genetics and computational biology at Institut Pasteur, Paris. Our research is focused on how natural selection, human demography and lifestyle have shaped the patterns of diversity of the human genome, to understand how this may impact phenotype variation and disease. Specifically, our projects aim to increase our understanding of (i) the demography history of human populations, with a focus on Africa and the Pacific, (ii) the occurrence of natural selection, in its different forms, and the relationship between population demography and the burden of deleterious alleles; (iii) the genetic and epigenetic determinants of immunity-related traits, with an emphasis on molecular phenotypes; and (iv) the relationship between genetic diversity, epigenetic patterns and changes in lifestyle and habitat of human populations.

The current postdoc projects will focus on:

(i) Population genetics. Dissecting the genetic and epigenetic history of human populations, with a focus on demographic inference, admixture patterns, different forms of genetic adaptation (polygenic adaptation and adaptive admixture) and interactions between genetic variation and DNA methylation. The project aims to delineate evolutionary mechanisms that affect genetic diversity, to obtain insight into phenotypes having participated in human adaptation and maladaptation, thereby affecting human health. This proposal, which combines population genetics, computational modelling and development of statistical frameworks, will shed light into the genetic history of neglected populations, such as the Yakut from Siberia and Polynesian islanders.

(ii) Quantitative genetics. Dissecting the contribution of rare/common variants, together with other non-genetic factors (including sex, age, lifestyle habits, latent infections, etc.) to variation in molecular phenotypes (gene expression, alternative splicing and DNA methylation) related to infection and immune stimulation. It aims to define the genetic architecture of expression phenotypes in the context of GxE interactions, and explore the (causal) relationships between genetic, epigenetic, and environmental factors accounting for immune response heterogeneity, in a cohort of 1,000 healthy individuals.

Requirements: - Ph.D. in population genetics, quantitative genomics, statistical genomics, bioinformatics, or computational biology - Strong programming and bioinformatics skills (R and Bash scripting, cluster computing) - Proficiency in English.

Duration: 2 years funding are available, and support will be provided to become self-financed through competitive fellowship applications.

Application Procedure: E-mail a CV, motivation letter and three reference names (in a single pdf file) to quintana@pasteur.fr by **April 30, 2020**.

Please put “Postdoc Population Genetics” or “Postdoc Quantitative Genetics” (depending on the topic of your choice) in the subject line of your email. Interviews, via Skype, will be held soon after this date. The starting date can be any time but not later than October 2020 (negotiable).

Lluis QUINTANA-MURCI <lluis.quintana-murci@pasteur.fr>

RoyalHolloway GenomicConflict

Royal Holloway University of London Department of Biological Sciences Postdoctoral Research Assistant Full-time Fixed-Term Contract (2 years)

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 intra-genomic conflict as an evolutionary force, and the successful candidate will work on a NSF-NERC funded research project which focuses on the evolution of meiosis and recombination via intra-genomic conflict in general and sperm parasitism in particular. The project will involve formulating mathematical 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 how intra-genomic conflict can transform genomic architectures.

You will be responsible for the formulation and analysis of mathematical models, in addition to the preparation for publication and presentation of the models. You will work alongside the project’s Principal Investigator.

The successful candidate will have a PhD in Biology, Mathematical Biology or Evolution.

This is a full time, fixed-contract post, available for 2 years from the 1st of May 2020 (although we can accommodate any starting date until 1st of Sep 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, 3 April 2020 Interview Date: TBC (Mid-late April 2020 at Royal Holloway)

The College is committed to equality and diversity, and encourages applications from all sections of the community.

"Ubeda, Francisco" <f.ubeda@rhul.ac.uk>

SmithColl Genomics MicroEuks

The Department of Biological Sciences at Smith College invites applications for a postdoctoral research position focusing on the biodiversity of lineages within Arcellinida (testate amoebae), to

begin July 2020. The position is in Laura Katz's lab: http://www.science.smith.edu/katz-lab/research. The initial appointment is for one year, with the possibility of extending for additional years. Candidates with experience involving genomics, bioinformatics and/or target lineages are encouraged to apply. Ph.D. in evolution, microbiology, genomics or related field is expected by time of appointment.

The goals of the project are to characterize the biodiversity of lineages within Arcellinida through a combination of community and genome analyses, including: high-throughput sequencing of communities, genomes and transcriptomes; bioinformatic analyses of resulting data; and some microscopy of target lineages. There is also some opportunity for field work.

More details and application instructions can be found here:

http://apply.interfolio.com/74216. Review of applications will begin March 15, 2020.

Laura Katz <lkatz@smith.edu>

TempleU TreeOfLife

Postdoctoral position, Tree of Life, Temple University, Philadelphia, USA

A postdoctoral position is available at Temple University in Philadelphia for conducting research on the tree of life and its timescale. This is part of the TimeTree project and database (www.timetree.org) of S. Blair Hedges (Center for Biodiversity, www.biodiversitycenter.org) and Sudhir Kumar (iGEM, Institute for Genomics and Evolutionary Medicine, igem.temple.edu). The research involves a diversity of topics in evolutionary biology including speciation, extinction, and diversification. Temple has exceptional research strength in these and related fields of biodiversity, bioinformatics, ecology, and evolutionary genomics.

We are seeking a person with training in evolutionary biology and phylogenetics and skilled in bioinformatics. Some programming knowledge, preferably R, is required. An ideal candidate will have experience with the literature and questions in this area, experience with species-rich analyses, and a general working knowledge of taxonomy.—

The Center for Biodiversity and iGEM are both located within Temple's Science, Education, and Research Center (SERC) on the main campus. They are affiliated with the Department of Biology and College of Science and Technology. Temple University is located in the heart of historic Philadelphia and is home to many academic and research institutions as well as numerous cultural attractions.

Interested persons should send an e-mail to postdoc@timetree.org, stating their interest in this position, and attach a curriculum vitae that also contains contact information for three references. Review of applications will begin on March 23rd (extended) and continue until the position is filled.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community (AA, EOE, m/f/d/v).

sbh@temple.edu

UBirmingham ComparativeGenomics

Exciting Postdoctoral Position in comparative genomics of Antarctic and sub-Antarctic insects

Location: University of Birmingham (UoB) and British Antarctic Survey (BAS), UK (with collaborators in USA: University of Kentucky and Ohio State University; Chile: Magallanes University; France: Rennes University).

Closing Date for applications: 1st of May 2020

Start date: As soon as feasible post interview, ideally before end of August 2020 in order to undertake pre-field season training with BAS.

Duration: 2 years

Job description: We are seeking a postdoctoral researcher with both bioinformatics and field biology experience. Applicants must hold a PhD-degree and evidence of bioinformatics experience is critical, ideally at postdoc level. The candidate will be required to (i)understand theoretical underpinnings of sequence alignment algorithms for next generation sequencing (NGS) data; (ii) have proven experience in NGS analysis and comparative genomics (experience of RNA-seq, Chip-seq or metabolomics data also useful); (iii) have knowledge of data visualization methods and of bioinformatics resources such as annotation tools and databases; (iv) have knowledge of methods and approaches for data integration; and a strong statistical genetics background.

The position will also offer an opportunity for Antarctic field research to acquire samples from different locations. Consequently, experience of working independently in field setting, ideally insect biology related, is highly desirable. This element will mainly be supported by our project partners at BAS with the collection sites on Bird Island/South Georgia in the sub-Antarctic. However, there is also scope to undertake field research with our collaborators in the USA/Palmer Station Antarctica, Chile/Puerto Williams or France/Crozet Island.

Facilities: The Hayward "Insect Molecular physiology" lab is based within the School of Biosciences at UoB. This lab is next door to the state of the art Functional Genomics Facility, which is part of a large recent investment in Next Generation Sequencing (NGS) at UoB. The University also has a high performance computing cluster (BlueBEAR, http://www.bear.bham.ac.uk), which is powered by approx. 2000 cores with 100Gb EDR Infiniband interconnect; all tightly coupled with the wider BEAR including the Research Data Store (RDS). The position with be co-supervised by Prof Pete Convey at BAS, offering access to specialist research facilities and the extensive polar library at BAS HQ in Cambridge.

The project: This is an NSF-NERC funded project investigating mechanisms of adaptation to terrestrial Antarctica through comparative physiology and genomics of Antarctic and sub-Antarctic Insects. We have recently sequenced the genome of the sub-Antarctic midge, Eretmoptera murphyi and the postdoc will begin by undertaking a detailed analysis of this genome, and then comparing it with a previously sequenced Antarctic sister-species, Belgica antarctica, as well as other species being collected as part of the project.

The project also emphasizes outreach and education, and the postdoc will be required to contribute to these activities.

For more information on the position please contact Dr Scott Hayward: s.a.hayward@bham.ac.uk To download the full job description and details of this position and submit an electronic application online please click on the Apply Online button below or visit our careers website; https://bham.taleo.net/careersection/external/-jobsearch.ftl?lang=en&portal=101430 233, please quote Job Ref 95184

"Teets, Nicholas M." <n.teets@uky.edu>

UCalifornia Irvine EvolutionaryEpigenomics

Postdoctoral Fellow in Evolutionary Epigenomics 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/epigenome evolution. 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 evolutionary epigenomics. Candidates will ideally have interests broadly relevant to these topics, but will also 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. Experience with high-throughput sequencing and/or strong quantitative skills are especially desired.

The expected start date is July 2020, but flexible.

To apply, email the following to Grace Lee (grylee@uci.edu) with the subject line "Postdoc application: [Your full name]." - curriculum vitae - 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>

UCalifornia Riverside InsectGenomics

Insect Genomics Postdoc Opportunity at University of California, Riverside

A Postdoctoral Scientist position is available in the Nabity lab at the University of California, Riverside. The Nabity lab seeks a post-doctoral scholar with strong experience in genome sequencing, annotation, and visualization. The applicant will work alongside team members to assess how genome architecture differs among related species with novel phenotypes and in the context of compatible/incompatible interactions with plant hosts. The research goals are to 1) annotate existing genomes and sequence additional genomes for comparative evolutionary analyses, and 2) resequence select populations of variable phenotypes to identify genes linked to phenotypes and host plant resistance. The expectations of the position include the quasi-independent execution of bioinformatics analyses, willingness to learn new analyses, and active engagement in mentoring students and disseminating science.

The ideal candidate will have experience in genomics, a strong publication record, and a PhD in a Biology-related discipline. Preference will be given to individuals with experience with comparative analyses and/or insects.

The University of California, Riverside is a highly diverse and rapidly growing campus located in the historic city of Riverside, California. UCR is a world-class research university with an exceptionally diverse undergraduate student body. Its mission is explicitly linked to providing routes to educational success for underrepresented and first generation college students. A commitment to this mission is a preferred Qualification, and we especially encourage applications from individuals that are members of groups historically underrepresented in higher education. The campus is located within one hour of downtown Los Angeles, a city that provides world-class cultural opportunities. Riverside also provides easy access to numerous outdoor recreational areas, including forest, alpine, ocean, and desert environments.

The position is available starting immediately (exact start date is negotiable). Evaluation of applications will begin immediately and priority will be given to applications that are complete by April 11. The position will remain open until a suitable candidate is found. Initial support is for two years with additional time contingent upon performance.. Applications must include a CV, a cover letter describing research interests and career goals (2 pages max), and the names and emails of 3 references. Application materials should be emailed to Dr. Paul Nabity (pauln@ucr.edu) with the subject line "Genomics Postdoc."

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, disability, protected veteran status, or any other characteristic protected by law.

Dr. Paul D. Nabity, Assistant Professor of Plant-Insect Ecology Department of Botany and Plant Sciences University of California, Riverside http://www.nabitylab.org Paul Nabity <pauln@ucr.edu>

UCollege London PlantProteomeGenetics

Want to help find out how protein abundance is controlled in plants?

We are seeking an exceptionally talented post-doctoral computational biologist to join Richard Mott's group in the UCL Genetics Institute.

A fundamental question is how the control of protein expression in plants differs from that of gene expression, and under what circumstances is variation in protein abundance a more relevant driver of phenotype. To this end, we will resequence the genomes of a large Arabidopsis population, and then measure the epigenomes (DNA methylation and open chromatin), transcriptomes and proteomes in the same individuals. Your role will be to interpret the data and answer these questions.

You will be expert in bioinformatics, quantitative genetics, and in the analysis of different types of sequence data, with a proven track-record from publications. The post is a key part of a major 5-year BBSRC programme BB/T002182/1 to understand the relative impacts of genetic, sequence, epigenetic, transcriptomic and proteomic variation on phenotype in the plant Arabidopsis thaliana. The project is a collaboration between UCL, Rothamsted Research and the University of Cambridge.

Full details and the online application form are available at

https://tinyurl.com/s9r4f38 Closing date for applications is 5th April 2020.

Project Description is here: https://tinyurl.com/sskvdhl Contact Richard Mott r.mott@ucl.ac.uk for informal enquiries.

"r.mott@ucl.ac.uk" <r.mott@ucl.ac.uk>

UConnecticut HostMicrobiomeEvolution

University of Connecticut: Postdoctoral researcher studying microbiota / host gut interactions and coevolution.

A postdoctoral researcher position is available in Dr. Daniel Bolnick's research group (https://-bolnicklab.wordpress.com), in the Department of Ecology and Evolution at the University of Connecticut. We seek a successful researcher with experience in cell/tissue culture or mechanistic study of host-microbiome interactions.

Tasks: Thanks to funding from the Gordon and Betty Moore Foundation's Symbiosis in Aquatic Systems Initiative, the Bolnick lab is embarking on a collaboration with Dr. Rebecca Carrier and Dr. Sam Scarpino at Northeastern University, Dr. Natalie Steinel at the Univesity of Massachusetts Lowell, and Dr. Katherine Milligan-Myhre at the University of Alaska Anchorarge. We will develop a microfluidics gut-on-a-chip system to enable mechanistic study of the interactions between a small fish, threespine stickleback (Gasterosteus aculeatus), and its native gut microbiota. The postdoc will work primarily in the Bolnick Lab at the University of Connecticut, but will frequently collaborate with and visit the other research groups on the team, and work closely with a second postdoc based at the University of Massachusetts Lowell. The postdoc will work on improving methods to maintain primary cell cultures of stickleback gut epithelium and immune cells, kept alive on microfluidic gut-on-a-chip system developed in the Carrier Lab. These cells will be observed during interaction with sticklebacks' gut microbiota (form the Milligan-Myhre lab), and assayed for cell activity using methods developed with the Steinel Lab, and statistical approaches developed in the Scarpino Lab. This platform for experimental study of host-microbiome interactions can ultimately facilitate studies of host-microbiome coevolution. The postdoc's tasks will include experiments to evaluate cell culture methods, manuscript preparation, presentations at scientific conferences, and some limited animal care.

Duration: The position is available for 27 months with current funding, with possible extensions contingent on additional grant support. The postdoc should be able to start in late summer or early fall 2020, exact dates to be negotiated with the PI.

Compensation: Starting salary will be $52,700 plus health benefits.

Minimum Qualifications: Applicants should have a PhD in evolution, genetics, immunology, cell biology, or a closely related field. Prior experience with cell or tissue culture is strongly preferred. Previous research experience and publications should demonstrated a commitment to basic research, good work ethic, lab skills, organizational ability, and publication productivity.

Preferred Qualifications: Expertise in molecular genetics (particularly RNAseq), CRISPR/cas9 gene editing, RNAi, or other experimental genetic manipulations is a strong plus, as is experience with flow cytometry.

Applications should electronically submit a single pdf file containing the following, in order: 1) A statement of past research achievements, including relevant skills. This should not exceed two single-spaced pages.

2) A statement of what you can contribute to the Bolnick Lab's research, and how this fits into your career goals. This should not exceed one single-spaced page.

3) CV 4) A copy of two publications or submitted manuscripts.

3) A list of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

The application file should be submitted by applying online at https://hr.uconn.edy/jobs, Staff Positions, Search # 494463. You may independently contact Dr. Daniel Bolnick (daniel.bolnick@uconn.edu). Include the subject line "Fish-on-Chips Postdoc: <YOUR NAME>". Applications must be received by May 1, 2020 for full consideration, though the position is open until filled.

For questions about this position, please email Dr. Bolnick (daniel.bolnick@uconn.edu). For information about the Bolnick Lab visit the lab website (https://bolnicklab.wordpress.com), lab photostream (https://www.flickr.com/photos/98765823@N08/-albums), and Dr. Bolnick's Google Scholar page (https://scholar.google.com/citations?user=-cfwxm0AAAAAJ&hl=en).

The University of Connecticut is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Texas Disability Services Office (http://-sites.utexas.edu/disability/).

Dr. Daniel I. Bolnick

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UCopenhagen GutMicrobiomeEvolution

Postdoc in Ecological Hologenomics at The GLOBE Institute We are looking for a highly motivated and dynamic researcher for a 3-year position to work on studying the relationship between ecological niches and gut microbiomes of vertebrates integrating field work, spatial and molecular analyses at the Centre for Evolutionary Hologenomics, GLOBE Institute, University of Copenhagen.

The continuous interaction between hosts and microorganisms associated with them is known to shape and even drive many biological processes of complex organisms, including vertebrates. The capacity to host different microbial communities (metagenomic space) as well as to enable or promote community variation (metagenomic plasticity) can shape multiple biological features of complex organisms. Current molecular and spatial methods enable nuanced analyses of microbiota composition and variation across physical, ecological and phylogenetic spaces, which could contribute to cast further light into the relationship between gut microorganisms and ecological features of their hosts.

In this regard, your position would be working alongside the research groups of Assoc Prof Antton Alberdi, and Prof Tom Gilbert on studying how metagenomic space varies among vertebrate individuals/populations/species/clades, by estimating the metagenomic spaces of 10 closely related species pairs in light of their ecological and genomic features. Metagenomic space and plasticity of host-associated microorganisms will be measured through extensive fieldwork across animals' full distribution ranges. In a second phase, captivity experiments in which environmental factors will be modified will be conducted with selected species to better approximate species' metagenomic spaces, and directly measure metagenomic plasticity. This project is embedded within the Earth HoloGenome Initiative, which you will also contribute to by managing sampling logistics, sample processing and data analysis.

Your tasks would therefore be research, including publication/scientific communication of research results, project management, as well as research-based teaching.

For further details: https://employment.ku.dk/all-vacancies/?show=151406 Thank you very much Antton

Antton Alberdi, PhD

Associate Professor

Center for Evolutionary Hologenomics

GLOBE Institute,University of Copenhagen H2020 HoloFood project Scientific Manager, Earth HoloGenome Initiative Coordinator E-mail: antton.alberdi@sund.ku.dk Skype: anttoniou Phone: 0045 53840119 (DK), 0034 667498730 (ES)

Antton Alberdi Estibaritz <antton.alberdi@sund.ku.dk>

UExeter InsectVirusInteractions

Full time Postdoctoral Research Fellow to conduct research on host-pathogen interactions working with Wellcome Trust Sir Henry Dale research fellow Dr Ben Longdon, at the University of Exeter, Penryn campus.

This full time post is available on a two year fixed term contract, with the possibility of extension. Apply here https://-jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/-ETREC107GF.open?VACANCY_ID%3d472746SGEX%1BUSESSION=F734DF9523454CFE9CAE09B647684C58&WVID=-3817591jNg&LANG=USA About the role

Host-parasite interactions offer fascinating opportunities to study coevolution, local adaptation and rapid evolutionary change. Our work uses a unique experimental system of up to 50 species of Drosophila and naturally occurring RNA viruses to ask fundamental questions about pathogen host shifts 'V where a pathogen jumps from one host species to another. Host shifts are a major source of emerging infectious diseases, with HIV, Ebola virus and SARS coronavirus having all jumped into humans from other host species. By taking a comparative approach, with a strong set of hypotheses from ecological and evolutionary theory, we can provide insights into the factors underlying host shifts that will be generally applicable to any group of hosts or viruses.

Understanding pathogen host shifts is critical, especially in light of environmental change. Our model system has provided key insights into host shifts, namely the importance of genetic similarity between hosts. Based on work in Drosophila melanogaster, we know the interactions between host antiviral immunity and the ability of the virus to supress this immune response, can play a role in explaining differences in susceptibility. The initial aim of the postdoc is to examine why viruses can infect some hosts and not others by looking at how the viral suppressor of immunity functions in different host species, and how this influences patterns of susceptibility across the host phylogeny, but there are many opportunities to develop new projects to explore the ecology and evolution of pathogen host shifts.

Applicants will possess a relevant PhD or equivalent qualification/experience in a related field of study.

The successful applicant will be responsible for leading experimental work, data collection and analysis, working closely with the PI and collaborators. The post will be based at the University of Exeter in the internationally excellent Centre for Conservation and Ecology

https://www.exeter.ac.uk/cornwall/research/-facilitiesandcentres/cec/. The centre has a huge number of researchers working in ecology and evolution, including a large group of researchers working on host-parasite interactions (including Prof Angus Buckling, Prof Camille Bonneaud, Prof Edze Westra, Prof Robbie McDonald, Dr Alex Hayward and Dr Stineke Van Houte) and provides an exciting and stimulating research environment.

Please highlight in your cover letter why you would like to work in our group (www.benlongdon.com), why you are interested in this project, and how your skillset/experience is relevant. If you think you might be a great fit for this position but are unsure on whether you have relevant experience, please get in touch before applying, happy to consider applicants from different backgrounds.

Informal enquiries strongly encouraged to Dr Ben Longdon, e-mail b.longdon2@exeter.ac.uk.

The University of Exeter is an equal opportunity employer. We are officially recognised as a Disability Confident employer and an Athena Swan accredited institution. Whilst all applicants will be judged on merit alone, we particularly welcome applications from groups currently underrepresented in the workforce.

"Longdon, Ben" <B.Longdon2@exeter.ac.uk>

UKansas Inversions

A postdoctoral research fellowship is available to work with John Kelly on an NSF funded project titled "Chromosomal inversions and gene expression in Mimulus." Our aim is to estimate the quantitative importance of inversions to differences among individuals within populations, to differences among populations, and to differences among species within the M. guttatus complex. The first part of the project will use comparative genomics to determine the roles of purifying versus positive selection acting on inversions. Second, we will employ genetic mapping to determine the nature of inversion effects on genome-wide transcription and how these effects evolve. The postdoctoral researcher will collect new data from greenhouse experiments, perform genomic analyses, and apply statistical and evolutionary models to the resulting data.

The postdoctoral researcher will have substantial opportunity to develop and work on related projects in evolutionary genomics and quantitative genetics. Researchers with a PhD in evolutionary biology, computational biology, genomics, population/statistical genetics, or a related field are encouraged to apply. Programming experience and previous success with basic genetic laboratory methods are favorable qualifications.

The ideal start date is Fall 2020, but this is flexible. A complete online application includes a cover letter, a vitae, a brief description of your research interests and contact information for three professional references. Application deadline is 3/18/2020. For first consideration, please apply before that date. To apply and for more details, please go to https://employment.ku.edu/staff/-16689BR. Also, feel free to write if you have any questions about the position to John Kelly at jkk@ku.edu.

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

"Kelly, John K" <jkk@ku.edu>

Ulm BeeVirusEvolution

University of Ulm, Germany Institute of Evolutionary Ecology and Conservation Genomics

Wilfert group

We would like to recruit a Postdoctoral Research Fellow as part of an ERC consolidator project to study the evolution of bee viruses in nature following the introduction of a vector, the ectoparasitic Varroa mite. The project will be based on initial field work (Islands in the Irish Sea and Channel). The project will focus on reconstructing transmission networks between bee species as well on understanding patterns of evolution in viruses following the introduction of vector-born transmission. The ERC-funded post is for 3.5 years (salary scale TV-L 13, 100%) , with a preferred starting date in spring 2020 to allow for fieldwork from mid-June.

The post will include population genetics, phylogenetic modelling, new sequencing approaches and bioinformatics as well as field work and associated lab work focussing on RNA virus detection. Expert dedicated technical support is available for field and lab work. The successful applicant will be able to develop research objectives, projects and proposals; identify sources of research funding and contribute to the process of securing funds and make presentations at conferences and other events.

Applicants will possess a relevant PhD in a related field of study. The successful applicant will have expertise in the fields of phylodynamics, disease ecology or molecular ecology. The successful applicant will also be able to work collaboratively, supervise the work of others and act as team leader as required. Applicants should have expertise in population genetics, phylogenetics and/or bioinformatics. Ideally, the candidate will have experience in phylogenetic modelling of viral transmission and/or molecular ecology of RNA viruses. Experience in fieldwork and wet lab molecular ecology and evolution would be advantageous.

The position will be based at the University of Ulm, at the Institute of Evolutionary Ecology and Conservation Genomics. Ulm is a delightful historic city on the Danube in Southwestern Germany; it is one hour from the Alps, Lake Constance, Munich and Stuttgart.

For further information, please contact Prof. Dr. Lena Wilfert lena.wilfert@uni-ulm.de. The closing date is the 20th of March 2020. The job advert with detailed information on profile and responsibilities, as well as the link to the online application system can be found here https://stellenangebote.uni-ulm.de/jobposting/ed1df97395fcae29bbaebb5898360cba32e14b7c < https://stellenangebote.uni-ulm.de/jobposting/38f94282a8360ea97a2d2587b7bf6516625c0e4b > Please note that applications have to be processed online!

Prof. Dr. Lena Wilfert University of Ulm Institute of Evolutionary Ecology and Conservation Genomics Albert-Einstein Allee 11 D-89069 Ulm Germany Tel.: 0049-731-5030615 Fax: 0049-731-5022683

email: lena.wilfert@uni-ulm.de Website: https://www.uni-ulm.de/en/nawi/bio3/prof-dr-lena-wilfert/ Lena Wilfert Ulm <lena.wilfert@uni-ulm.de>

UMelbourne MalariaParasiteEvolution

Postdoc Job posting : Malaria Parasite Evolution Research at University of Melbourne

We are seeking a highly motivated post-doctoral researcher with experience in molecular epidemiology/genomics/bioinformatics to join the group of Prof Karen Day within the Department of Microbiology and Immunology, in her laboratory located at the Bio 21 Institute, University of Melbourne.

The successful applicant will undertake molecular evolution research on the malaria parasite Plasmodium falciparum sampled during various malaria interventions in a longitudinal field study in Northern Ghana funded by the NIH NIAID as part of the NSF Ecology and Evolution of Infectious Diseases Program.

They will join a multidisciplinary team including malaria modelling colleagues from University of Chicago and malaria epidemiologists from Institutions in Ghana. Details of the position and application process can be found : http://jobs.unimelb.edu.au/caw/en/job/902428/research-officer Contact karen.day@unimelb.edu.au if you have any queries Professor Karen Day AM Professor Population Biology and Redmond Barry Distinguished Professor

Department of Microbiology and Immunology and Bio21 Institute The University of Melbourne 30 Flemington Road, Victoria 3010 AUSTRALIA

Telephone 61 8344 7644 Email : karen.day@unimelb.edu.au

karen.day@unimelb.edu.au

UOklahoma FishGenomics

Postdoctoral Scientist

The fish labs of R. Broughton, R. Betancur, and D. Arcila in the Department of Biology and Sam Noble Museum of Natural History at the University of Oklahoma are jointly recruiting a highly motivated postdoctoral fellow to work on research projects on fish genomics and evolution. One of these projects aims to investigate the genomics of hybridization and diversification in fishes in the genus Cyprinella across their range in central and southwestern North America. This will include generating a chromosome-level reference genome along with genome resequencing and transcriptomic data from multiple individuals and populations. Other genomic methods to assess evolutionary parameters of populations and taxa may also be used.

The ideal candidate will have experience or a strong interest in fishes with broad training in population genetics, genomics, comparative biology, and/or phylogenetics. Desired skills include the ability to collect fishes in the field by seining in creeks and rivers, big data management and statistical analyses, proficiency with Unix/Linux, use of R, Python, etc., or other computational skills.

For inquiries about the position interested candidates can contact R. Broughton, R. Betancur or D. Arcila with a cover letter, CV, and contact information for up to three references. The anticipated start date is flexible, but the position can start as early as March, 2020. The position may be available for up to 3 years, pending satisfactory performance. Review of candidates is ongoing and will continue until the position is filled.

Richard Broughton <rbroughton@ou.edu> http://www.ou.edu/cas/biology/people/faculty/richard-broughton R. Betancur & D. Arcila < ricardo.betancur@ou.edu, dahiana.arcila@ou.edu> http://www.fishphylogeny.org "Santaquiteria Gil, Aintzane" <a.santaquiteria@ou.edu>

UppsalaU 2 EvolutionaryGenomicsButterflies

Two PostDoc positions in Butterfly Evolutionary Genomics at Uppsala University

Two PostDoc positions in Butterfly Evolutionary Genomics are available at the Department of Ecology and Genetics, Evolutionary Biology Program, Uppsala University.

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our mission is to pursue top-quality research and education and to interact constructively with society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has 44.000 students, 7.100 employees and a turnover of SEK 7 billion. The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see www.ieg.uu.se. The Evolutionary Biology Program excels in many aspects of genetics and evolution and offers an inspiring international atmosphere. There are ample opportunities for interaction with researchers working on related topics. We are tightly linked to the Science for Life Laboratory (https://www.scilifelab.se/) and have access to advanced laboratory infrastructure, high performance computing resources and bioinformatics support.

Project descriptions in brief:

Project 1. Despite the importance of recombination in determining the faith of novel mutations and segregating alleles, our understanding of the mechanisms determining where in the genome recombination occurs, and the evolutionary consequences of regional variation in recombination rate, is limited to a small set of model organisms. The proposed project aim is therefore to characterize the fine-scale recombination landscape in wood white (Leptidea sp.) butterfly populations with dramatic karyotype variation. The data will be used to assess:

1) the conservation/turnover rate of the recombination landscape in holocentric organisms and if recombination is associated to any specific genomic features

2) the effect of regional recombination rate variation on maintenance/loss of genetic diversity

3) the effect of recombination on the evolutionary rates of sex chromosomes and autosomes when recombination is restricted to the male germline

4) the effect of chromosome fissions/fusions on the global recombination landscape and the adaptive potential of populations

Project 2. Migration is a widespread phenomenon in animals. It is a behavior that allows organisms to adapt to variation in resource availability throughout the year, but migration can also be associated with high risks. The study of evolutionary advantages of migration and the cost-benefit balance associated with this behavior is specially needed in insects, for which our knowledge to date is very limited. A fundamental difference exists between vertebrate and insect migrations. As opposed to vertebrates, insect migrations are often multigenerational, meaning that not the same individuals, but their offspring complete migratory circuits. Migratory strategies vary significantly and may include long and/or short distances, seasonal diapause or year-round migrations, and different numbers of generations can be involved. In this project, the aim is to develop a theoretical modelling approach to characterize the impact of migratory behavior on maintenance/loss/gain of genetic diversity for a variety of migratory strategies found in butterflies. The modelling will be combined with analysis of large-scale population genomic data with particular focus on the painted lady (Vanessa cardui), a nearly cosmopolitan species with complex migratory patterns.

For further information about the positions please contact: Niclas Backstrom, niclas.backstrom[at]ebc.uu.se, +46-18-471 6415.

You are welcome to submit your application no later than April 10, 2020 (UFV-PA 2020/800 & UFV-PA 2020/914). Formal applications should be made using our online application forms available here: https://www.uu.se/en/about-uu/join-us/details/-?positionId=320804 https://www.uu.se/en/about-uu/-join-us/details/?positionId=322491 Niclas Backstrom Evolutionary Biology Program Department of Ecology and Genetics Uppsala University, Sweden

När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. For att läsa mer om hur vi gor det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal

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UppsalaU EcoEvolutionMicrobeEukaryotes

A postdoctoral position is open in the lab of Fabien Burki at the Department of Organismal Biology, Uppsala University (Sweden).

See full description and how to apply here: https://www.uu.se/en/about-uu/join-us/details/?positionId=322255 Closing date: April 10, 2020

Project description: How have eukaryotes diversified over geological time and across large geographic regions? In this project, we aim to look at this broad and important question by combining aspects of macroevolution and macroecology to better understand patterns of microbial eukaryote diversity and the processes that led to this diversity. The focus organisms are microbial eukaryotes (protists), which represent the vast bulk of eukaryotic diversity in all environments. In the last decade, the study of protist diversity and distribution has been dramatically improved by high-throughput metabarcoding. While powerful to reveal novel diversity, this approach is typically limited by its current low phylogenetic resolution. To overtake this limitation, we have recently developed an approach that makes use of long-read sequencing (PacBio) to generate much longer sequences (~5000pb) directly from environmental samples (Jamy et al. 2019. Longread metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. Mol Ecol Resour). This approach offers the key advantage to improve the phylogenetic resolution of environmental diversity, thus allowing to efficiently address evolutionary and ecological questions especially when combined to the much wider breadth of short-read data already available. In this project, we will analyse a large dataset of long environmental reads that we have generated from a wide array of environments (marine and lake environments, tropical and boreal soils, bogs, etc).

Duties: Most of the work will be bioinformatic in nature since the main datasets are either already available. Thus, the main duties are to perform bioinformatic analyses within the broad framework of this project, compile and disseminate the results orally and in writing in scientific publications. Importantly, while the general framework is defined, we encourage participation and independence of the position's holder to develop specific lines of inquiry in consultation with the supervisor. Training of junior group members might also be involved, as well as other standard tasks related to a research group.

Requirements: To qualify for an employment as a postdoctor you must have a PhD degree or a foreign degree equivalent to a PhD degree in Biology or equivalent. The PhD degree must have been obtained no more than three years prior to the application deadline. The three year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc. Highly motivated, enthusiastic and hard-working individual with strong academic proficiency within the fields of microbial eukaryote evolution and/or ecology. We are looking for a candidate with an open-minded, cooperative attitude, who can work both independently and in a team. Documented experience in analysis of high-throughput metabarcoding datasets of environmental DNA and phylogenetics is required. Experience with biogeographical approaches and phylogeography is desired, as well as experience with Bayesian methods for character evolution. You should be proficient on the command line and with an advanced knowledge of at least one scripting language and R. Fluent in English both in spoken and written.

Additional qualifications: Although this position is centered around bioinformatic methods, visualisation techniques of environmental diversity might be desirable. Thus, experience with fluorescence in-situ hybridization (FISH) methods will be seen as an asset.

Terms of employment: The position involves full-time employment for a maximum of two years, with the possibility of extension under special circumstances. Start date: June 1, 2020, or as otherwise agreed

Contact: Further information about the position can be obtained from Dr. Fabien Burki, telephone: +46 18-471 27 79, fabien.burki@ebc.uu.se.

This project is founded by a grant from SciLifeLab (www.scilifelab.se), a Swedish national center for molecular biosciences with focus on health and environmental research. The center combines frontline technical expertise with advanced knowledge of translational medicine and molecular bioscience. SciLifeLab is hosted by four Swedish universities (Karolinska Institutet, KTH Royal Institute of Technology, Stockholm University and Uppsala University) and collaborates with several other universities.

När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. För

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UppsalaU GeneticDiversity

A postdoctoral researcher position in molecular ecology with focus on species-genetic diversity correlations in a meta community perspective is available in the group of Frank Johansson at the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Sweden. The project is funded by the Swedish Research Council, FORMAS.

Project description: We are hiring a postdoctoral researcher for the project" Species-genetic diversity correlations in a meta community perspective". The aim of the project is to understand how species and genetic diversity are correlated in general, but with and emphasize on urban environments, and how this relationship is affected by environmental variables such as habitat size, urban areas, connectivity etc. Our study system is ponds in the city of Stockholm which are studied with regard to biodiversity (invertebrates, fish, and amphibians) and environmental variables. The data set collected will be analyzed with advanced multivariate statistics.

Duties: You will use molecular methods as well as community ecology methods to analyze and summarize data. The molecular work consists of extraction DNA from already collected samples, preparation of "next generation" sequencing using ddRadseq, analyzing genetic variation and genetic structure from molecular data. The community ecology work consists of several statistical analyses and therefore you need knowledge on one or several of the following analyses: covariance decomposition, structural equation modelling (SEM), Redundancy Analysis (RDA), multivariate regression trees (MRT) och MoranÂs eigenvector maps (MEM).

Qualifications required: A doctoral degree, or a foreign degree equivalent to a doctoral degree, in the area of evolutionary ecology, ecological genetics molecular ecology or a similar field of knowledge. Vast experience with molecular genetic methods is a requirement for the position, and candidates with advanced knowledge on multivariate statistics will be given priority. Candidates must be able to express themselves fluently in spoken as well as written English. Great emphasis will be placed on personal qualities such as excellent collaboration skills and sense of initiative. To be eligible the candidate must have a PhD degree, or a foreign degree equivalent to this, completed less than three years before the application deadline. The three year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc.

Qualifications desired: We are looking for a highly independent and proficient person to drive forward the project. The ideal candidate will be a team player that has experience in the above mentioned qualifications, and proven proficiency in writing and publishing in English in scientific journals.

Application: The application should include 1) a letter of intent describing yourself, your research interests and why you want this position, 2) your CV, 3) a short description of your education, 4) a copy of your doctoral degree and course grades, 5) the names and contact information to at least two reference persons (e-mail address and phone no.), 6) a copy of your master thesis and 7) publications produced. The application should be written in English.

The environment: The Evolutionary Biology Centre is one of the world's leading research institutions in evolutionary biology and part of Uppsala University - the oldest university in Scandinavia. Uppsala University, ranked 7th in the world in evolutionary biology (CWUR 2017), attracts approximately 40.000 students from all over the world, creating an international and stimulating research environment. The research themes at the Department of Ecology and Genetics (www.ieg.uu.se) spans the scope from evolutionary ecology to genetics and metagenomics to studies of ecosystems. The city of Uppsala is a vibrant college town, conveniently situated 40 minutes by train from Stockholm (and even closer to the Arlanda International Airport), with beautiful and easy accessible surroundings.

Salary: Individual salary.

Starting date: 2020-06-01, or as agreed.

Type of employment: The position is a temporary position for 24 months

Scope of employment: 100 %.

For further information about the position please contact: Frank Johansson, frank.johansson@ebc.uu.se, +46 18 471 6488.

For more information on ongoing research in our group, see: https://katalog.uu.se/profile/?id=N11-702 Please submit your application April 13, 2020. UFV-PA 2020/778.

Please do not send offers of recruitment or advertising services.

Submit your application through Uppsala UniversityÂs recruitment system.

Login and apply : https://uu.varbi.com/en/what:login/-type:job/jobID:320626 Frank Johansson Professor in Conservation Biology

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UppsalaU TheoreticalPopulationGenetics

A position as a postdoctoral researcher/fellow in theoretical population genetics is available at the Department of Ecology and Genetics, Evolutionary Biology program.

Further information about the position and details about application are available at: https://www.uu.se/en/-about-uu/join-us/details/?positionId=3D322453 You are welcome to submit your application no later than 2020-04-30.

For inquiries please contact: Carina Farah Mugal, carina.mugal@ebc.uu.se

Project description: Stochastic models have a strong tradition in population genetics. Diffusion and branching processes are frequently used to describe evolution forward-in-time. At the same time, birth-death processes such as the coalescent are used to track evolution backward-in-time. Duality relationships between forward-in-time and backward-in-time models have been established and analysed. Together, such mathematical treatment has led to a large body of theoretical population genetics and promoted our general understanding of evolution.

Building on concepts of theoretical population genetics, we have formulated a time-dependent Poisson random field model that permits describing allele frequency trajectories in nonstationary populations (doi: 10.1016/j.tpb.2016.06.003). This has, for example, enabled us to formulate an analytical description of the joint allele frequency spectrum of two populations during the process of speciation, and investigate the impact of incomplete lineage sorting on genomic signatures of natural selection.

The project profits from an interdisciplinary collaboration between the Department of Ecology and Genetics and the Department of Mathematics at Uppsala University.

Duties: Several extensions of the basic model of allele frequency evolution are of interest, such as dependence among allele frequency trajectories due to physical linkage and recombination. A relevant body of population genetics models that address recombination exists the sequential Markovian coalescent, the ancestral recombination graph and diverse branching process models. The Postdoc project will start by investigating possibilities of integrating such models of recombination into the forward-in-time model of allele frequency evolution, which has been formulated by our group. In particular, analytical results on the allele frequency spectrum (AFS) in the presence of physical linkage are of interest. Ultimately, the derivation of such an AFS shall form the basis to analytically investigate the relationship between the recombination rate and measures of natural selection, which is a central question in evolutionary biology.

Qualifications required: For this position, the candidate must hold a PhD degree within mathematics, evolutionary biology, bioinformatics or another relevant field. The Postdoc candidate must have experience in mathematical biology and interest in population genetics. The candidate must be able to express themselves fluently in spoken as well as written English. In addition, the applicant must be able to work independently, have good collaborative skills and be able to communicate (both spoken as well as written). The applicant must have integrity and personal maturity, be able to take initiative and to handle setbacks.

To be eligible the candidate must have a PhD degree, or a foreign degree equivalent to this, completed less than three years before the application deadline. The three year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc.

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

http://katalog.uu.se/profile/?id=3DN8-1504 När du har kontakt med oss pÃ¥ Uppsala universitet med

e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. For att läsa mer om hur vi gor det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy
"carina.mugal@ebc.uu.se" <carina.mugal@ebc.uu.se>

USaoPaulo Brazil EndangeredSpecies

I would appreciate your help for announcing a Postdoc position for Generation of iPS from Endangered Species at Sāo Paulo and Sāo Paulo State Universities, Brazil as follow:

PD fellowship opportunity in Generation of induced pluripotent cells from Endangered Animal Species.

The Deer Research and Conservation Center (NUPECCE) under coordination of professor Jose Mauricio Barbanti Duarte from the Animal Science Department of the Sāo Paulo State University, and the Research Group for Bird Propagation (GEMA) under coordination of professor Ricardo José Garcia Pereira from the Department of Animal Reproduction of the Sāo Paulo University, participate in the FAPESP Thematic Project "Evaluation, recovering and conservation of the endangered fauna of the Pernambuco Endemism Center (CEP)", which is coordinated by Luis Fabio Silveira (MZUSP, Sāo Paulo), and 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 develop activities of "Use of fibroblast cryobanks for conserving endangered animal species of the CEP", which has as specific objectives:

- To develop media for animal cell cryopreservation;
- Rescue e culture frozen cells from a variety of biological materials (skin, feathers, fur, etc);
- To implement protocols for the production of induced pluripotent cells from these cell cultures;
- To perform different pluripotency tests including gene and protein expression, and cellular differentiation.

This opportunity is open to highly qualified Brazilians and foreigners. The candidate should preferably have training in the area either of Biomedicine, Biochemistry, Genetic, Biology or Veterinary Medicine, satisfactory CV and scientific knowledge in the research area of the scholarship. It is essential the candidate to be fluent in English, to have a satisfactory knowledge of Portuguese, to exhibit the ability to write scientific articles, and readiness to reside in Jaboticabal during the first year and in Sāo Paulo for the second and third years (both cities are located in Sāo Paulo State, Brazil). 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. The professional should be familiar with bibliographic search tools, know how to plan and conduct experiments independently. Among the knowledge and techniques necessary for the development of this project we emphasize:

1. Large practice in cell freezing and culturing;

2. Wide knowledge and capability in cellular biology (immunofluorescence, immunohistochemistry, cell cytometry, etc);

3. Recognized experience in molecular biology (PCR, RT-PCR, qRT-PCR, oligonucleotide design and molecular cloning).

Contract period and start of work: The scholarship lasts until 24 months, with the possibility of extension for another 12 months). The forecast is to begin in June 2020.

Values and conditions: 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; 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 more details, go to: http://www.fapesp.br/270 . How to apply: The submission deadline is April 30, 2020. Registration exclusively by email (ricpereira@usp.br). Include the subject "Postdoctoral ARCA project", followed by your name, and send the following files in PDF format:

1. An English text with a maximum of 2 pages explain-

ing your motivations to work on this project;

2. Summarized CV (maximum 3 pages), including published papers attesting to the capacity to carry out the project;

3. Two letters of recommendation from researchers who should send them directly to the email above.

Selection: The selection will be made based on the candidate's CV (experience in the research area of the project and quality of the publications) and in the letters of motivation and recommendation. Applicants may be invited to a personal interview or

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UToronto 2 EcologicalPopulationGenomics

Two post-doctoral fellowships are available to work with John Stinchcombe in the general area of ecological genetics and plant population genomics. I am looking for people with bold ideas on how they can push their research, and my lab's, forward.

The full ad with the application details, how to apply, etc is here:

https://t.co/cL7aQtplpd?amp=1 Potential topics include validating novel candidate genes underlying flowering time variation, genomic and transcriptomic approaches to plant-microbe interactions, and empirical work at the intersection of quantitative and population genetics.

Job Requirements: The candidate(s) must have a recent PhD in evolutionary biology, genomics, population/statistical/ quantitative genetics or a related field, with strong evidence of published research productivity. The ideal candidate would have some combination of extensive experience with data analysis and statistical skills, experience working next-generation sequencing or transcriptome data, and/or facility implementing greenhouse or field experiments with large numbers of plants. A burning desire to test evolutionary hypotheses with genetic and ecological data in plants would be favorable.

To apply: All individuals interested in this position must submit the following documents to Professor John Stinchcombe (john.stinchcombe@utoronto.ca) by the closing date. 1. A cover letter indicating the intersection of their research interests and expertise with recent work in the lab, including how both will be extended; 2. A current C.V.; 3. Three (3) relevant publications or preprints; and 4. Contact information for three (3) references by the closing date (June 1, 2020). Review of complete applications will begin March 30, 2020.

Cheers, and stay safe and socially-distant, John

John Stinchcombe <john.stinchcombe@utoronto.ca>

UTubingenGermany InvasionGenomics

The Plant Evolutionary Ecology group at the University of TÂÂ¹bingen is seeking a motivated

Postdoc in ecological genomics of invasive plants

to perform molecular work on invasive knotweeds (Reynoutria ssp) collected from field surveys and ecological experiments. The postdoc will contribute to the project "Genomics and Epigenomics of Plant Invasion" and the closely associated DFG-funded project "Evolution of plant defenses during a plant invasion". These projects aim to understand (epi)genomic mechanisms associated with large-scale variation and adaptation in native vs. introduced populations of knotweeds. The postdoc will use molecular approaches, including reduced-representation bisulfite sequencing (epiGBS) and RNA-Seq, and work closely with other members of the lab to associate (epi)genomics data with phenotypic and environmental data.

The project is part of the "Make Our Planet Great Again" initiative (www.daad.de/mopga-gri/) and is in close collaboration with the University of Rennes in France, Fudan University in Shanghai and other groups in China who will be examining complementary ecological, chemical and other genomic aspects, so there will be excellent opportunities for collaborations and learning outside of one'Âs own project. We are looking for someone who likes to ask big questions using large genomics data sets, and who is interested in spending time in China.

Applicants should have a PhD in ecology, evolution, genetics, bioinformatics, or a related field. Expertise in ecological genomics and statistics is required. Previous experience with bisulfite sequencing, reduced-representation approaches and/or polyploidy will be ideal. Strong candidates will also possess: (1) creativity, independence, and a desire to learn new things, (2) excellent oral/written communication skills, and (3) proficiency in R.

The position is full-time and for 2 years. It will be based at University of TÂÂ^{1}bingen. The start date is flexible, but ideally in spring/summer 2020. Payment will be at German payscale level TV-L E13. To apply, please email a cover letter, CV and the names and contact details of three references as single PDF document until 21 March to Christina Richards (christina.richards@uni-tuebingen.de).

TÂÂ^{1}bingen is a beautiful university town with a high quality of life and one of the oldest universities in Germany. The Plant Evolutionary Ecology group (uni-tuebingen.de/plantevoeco) at TÂÂ^{1}bingen, including Christina Richards (ecologicalepigenetics.com) as MOPGA group leader, studies a broad range of questions on plant variation and adaptation in changing environments.

The University of TÂÂ^{1}bingen is committed to increase the proportion of women in science, and qualified women are therefore particularly encouraged to apply. Equally qualified applicants with disabilities will be given preference.

– Christina Richards, Ph.D. MOPGA-GRI scholar University of TÂÂ^{1}bingen Plant Evolutionary Ecology group Auf der Morgenstelle 5 D-72076 TÂÂ^{1}bingen

Associate professor University of South Florida Department of Integrative Biology 4202 East Fowler Avenue SCA 127 NES 107 (shipping) Tampa, FL 33620 (813)974-5090 (813)974-3263 FAX http://www.ecologicalepigenetics.com Twitter: @EcolEpig Facebook: Ecological Epigenetics

Christina Richards <christina.richards@uni-tuebingen.de>

UWisconsin Madison EvolutionaryAndSyntheticBiology

We are recruiting a postdoctoral associate in yeast evolutionary and synthetic biology. Apply by 31st March for full consideration. Please see the full ad: https://hittinger.genetics.wisc.edu/Images/postdocAd2020mar.pdf .

Chris Todd Hittinger, Associate Professor of Genetics University of Wisconsin-Madison 1552 University Avenue, Wisconsin Energy Institute 4129 Madison, WI 53726-4084, USA http://hittinger.genetics.wisc.edu, cthittinger@wisc.edu

cthjunk@hotmail.com

UWisconsinMadison PopulationGenomics

The research group of John Pool at the University of Wisconsin - Madison invites applications for a postdoctoral research position. There are multiple potential project areas, with an overarching theme of addressing big questions in population/evolutionary genetics. I'd like to give the successful candidate for this position a strong voice in shaping their research direction in the lab.

Potential research areas could include (but are not limited to):

* Model Inference for the Genetic Architecture of Adaptive Evolution When traits evolve in nature, we'd like to understand things like how many genes are involved, whether selection acts on standing variation or new mutations, whether it ultimately fixes the causative variants. We focus on local adaptation among Drosophila melanogaster populations from contrasting natural environments, which provides a powerful and efficient system for investigating these questions. One particular opportunity is to make statistical inferences about the genetic architecture of adaptation, in part from existing QTL mapping data.

* Fundamental Population Genetics We are interested in leveraging big data (such the >1000 genomes from our Drosophila Genome Nexus) to ask basic population genetic questions. Our lab is especially interested in leveraging genetic differentiation between populations to address classic but unresolved questions about the influence of natural selection on genomic diversity.

* Quantifying Adaptive Potential It is widely recognized that genetic diversity is a primary determinant of whether populations can rapidly adapt to new challenges. Yet in spite of its relevance to basic evolutionary biology and conservation, our understanding of adaptive potential is still quite lacking. Our lab is interested in which types of genetic diversity are most important for adaptive potential (e.g. within vs. between population) and how best to quantitatively estimate adaptive

potential within and among populations.

Our research group was founded 8 years ago and currently includes 1 postdoc and 6 graduate students. I have also advised 5 former postdocs, and the publication records of Amir Yassin and Justin Lack show what a productive environment our lab can be. I also welcome postdocs taking important components of our research with them when they found their own labs. Further lab info: http://www.johnpool.net UW-Madison offers a superb scientific environment with a supportive, collaborative, and egalitarian culture. Many labs focus on population genetics, evolutionary genomics, and Drosophila research: https://evolution.wisc.edu/-people/faculty/ https://genetics.wisc.edu/drosophila-and-other-insects/ Madison offers an exceptional quality of life in a beautiful landscape, and has been ranked as the best US city for young adults. Downtown and campus are bordered by lakes, and Madison features diverse art, music, cultural, and culinary offerings. http:/-/www.visitmadison.com/media/rankings/ To apply, send a a statement of research interests (up to 1 page) addressing the intersection between your own scientific interests and the Pool lab's research in terms of potential projects, along with a CV and contact info for 3 references.

I am interested in adding to the diversity of our lab in a broad sense, including gender balance, cultural perspectives, and intellectual backgrounds and skill sets.

Start dates are flexible. Salary follows the NIH scale. Individual or family health insurance is offered.

Applications are due May 1. However, earlier applications are welcome, and later applications may still be considered. Informal pre-application inquiries (e.g. to discuss potential research topics) are also welcome at any time.

John Pool Associate Professor Laboratory of Genetics University of Wisconsin - Madison

“jpool@wisc.edu” <jpool@wisc.edu>

UWisconsin Madison YeastEvolution

We are recruiting a postdoctoral associate in yeast evolutionary and synthetic biology. Apply by 31st March for full consideration. Please see the full ad: https://hittinger.genetics.wisc.edu/Images/-postdocAd2020mar.pdf .

Chris Todd Hittinger, Associate Professor of Genetics University of Wisconsin-Madison 1552 University Avenue, Wisconsin Energy Institute 4129 Madison, WI 53726-4084, USA http://hittinger.genetics.wisc.edu, cthittinger@wisc.edu

cthittinger@wisc.edu

UZurich 2PDF PhD eDNA

University of Zurich (UZH) and Eawag, the Swiss Federal Institute of Aquatic Science and Technology (Duebendorf, Switzerland), are internationally recognized institutes that are committed to the ecological, economical and social management of water. They offer excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, and long-term research programs and data sets. These institutions share common goals towards education, research, and technology transfer at the highest international level. University of Zurich (UZH) and Eawag, the Swiss Federal Institute of Aquatic Science and Technology (Duebendorf, Switzerland), are internationally recognized institutes that are committed to the ecological, economical and social management of water. They offer excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, and long-term research programs and data sets. These institutions share common goals towards education, research, and technology transfer at the highest international level.

The Altermatt lab at the Department of Evolutionary Biology and Environmental studies (UZH) and the Department of Aquatic Ecology (Eawag) has a vacancy for a –> Postdoc position (3+1 years) ???eDNA metabarcoding to assess distribution, diversity and indicator status of groundwater amphipods in Swiss drinking water wells (AmphiWell)???

Amphipods are among the most common invertebrates in streams, rivers and lakes. They play a key role in the functioning of these ecosystems and are regularly used for monitoring and bioindication. While the diversity and distribution of the epigean (above ground) amphipods is well documented, there is a significant and largely unknown diversity of amphipods in hypogean (below ground) habitats. The project AmphiWell will establish scientific baseline data about the diversity and distribution of amphipods (especially genus Niphargus) in Swiss groundwaters. The Postdoc project will establish eDNA metabarcoding methods to monitor groundwater from a biological perspective. The tools will be developed in close collaboration with respective stakeholders, such that they can be directly used and implemented by water providers. The project is aligned with a parallel PhD project that focuses on biogeography and species diversity of amphipods in groundwater. Goals of the Postdoc project are: 1) Establish environmental DNA (eDNA) techniques as a monitoring tool for groundwater amphipods to fit into existing drinking water monitoring frameworks. 2) Using a metabarcoding eDNA approach to describe whole communities of groundwater habitats (e.g. including molluscs, isopods, possibly bacteria). 3) Analyse the occurrence of groundwater amphipods with respect to chemical parameters/descriptors of the groundwater.

The postdoctoral fellow will use our established collection of groundwater amphipods (genus Niphargus sp.) to build a reference barcode library, develop appropriate primers for eDNA analyses, and plan, conduct and analyse an eDNA sampling campaign in collaboration with drinking water providers to assess biodiversity of groundwater amphipods. The project builds on existing data from an ongoing project (www.amphipod.ch). The project is co-funded by the Swiss Federal Office for the Environment (BAFU/FOEN) and some interest in stakeholder interactions would be wanted. Competitive applicants have previous experience in eDNA analyses, metabarcoding and bioinformatics. Strong expertise in spatial ecology, biodiversity sciences and statistics is desired. Applicants will be highly motivated, enthusiastic and independent scientists. They must have a good conceptual understanding of ecological theory and strong laboratory skills. Excellent communicational and writing skills in English, experiences with publishing scientific articles, good work ethics, and creative thinking are a must. A PhD in Ecology or related subject is necessary for admission.

To apply, you must have a PhD degree in Ecology, Molecular Ecology or a closely related science field and should have a valid driver licence. The successful applicant will be based in the group of Prof. Dr. Florian Altermatt (www.altermattlab.ch) at Eawag and UZH in Duebendorf/Zurich. Dr. Roman Alther (Eawag/UZH) and Prof. Dr. Cene Fi??er (University of Ljubljana) are further project partners. The position is for a period of 3 years with a 1 year extension option, and should start in summer 2020.

We are looking for a highly motivated, enthusiastic and independent person with a passion for science to join our highly international team. Zurich hosts many other research groups in ecology and biodiversity research, and is among the world???s leading cities in terms of science, culture and quality of life. Applications from women are especially welcome.

For further information about the position please consult

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Vienna InsectGenomics

Subject: PostDoc_Insect_Genomics_Vienna

Boku, University of Natural Resources and Life Sciences, Vienna Postdoctoral Research Fellow Fixed-term contract 3 years Full-time 40 h/week Application deadline: 31 March 2020

A Postdoctoral position is available at the Department of Forest and Soil Sciences, Boku, Vienna in the lab of Christian Stauffer.

The project is on apple proliferation, a disease caused by a phytoplasma. These bacteria are transmitted by different insect species. While several phloem feeders occur on apple, only a small number is able to acquire and transmit phytoplasma. The project aims to address the question of the phytoplasma transmission efficiency of different insect species. Whole genome sequencing of different insects will be performed to study the interaction between the phytoplasma and of various vector populations.

We are looking for an enthusiastic candidate with a strong background in whole genome sequencing and bioinformatics of insects. To investigate factors affecting transmission efficiency the candidate will perform genomic analyses of the insects.

The project is in close collaboration with Hannes Schuler (University of Bolzano). Other partners in the project are Katrin Janik (Research Centre Laimburg), Rosemarie Tedeschi (University of Turin) and Omar Rota-Stabelli (Fondazione Edmund Mach).

The salary is according to the standard personnel costs of the FWF https://www.fwf.ac.at/en/research-funding/personnel-costs/ General requirements for the position: The candidate should hold a PhD degree in Entomology, Bioinformatics, Biotechnology, Biology or Evolutionary Biology with a multidisciplinary profile. The candidate should have excellent communication skills and should be fluent in English. German skills, although helpful, are not essential.

Please send applications to christian.stauffer@boku.ac.at within 31 March as a single pdf containing CV, list of publications, a statement of research interests, and the names of two references with contact details. Please indicate "Insect Genomics" as subject of the mail.

Christian Stauffer, Institute of Forest Entomology, Forest Pathology and Forest Protection; Department of Forest and Soil Sciences, Boku, University of Natural Resources and Life Sciences, Vienna, Peter Jordanstrasse 82-I, SCHW 01/124 1190-Austria

Tel: +43 1 47654-91631 http://www.wabo.boku.ac.at/ifff/ E-mail: christian.stauffer@boku.ac.at

Christian Stauffer <christian.stauffer@boku.ac.at>

WorkshopsCourses

AMUPoznan Poland PlantBioinformatics Jul6-10

Category: Course Topic: AMUPoznan.Poland.Bioinformatics.PlantResearch.July6-10

Dear colleagues,

We are extremely happy to announce 13th edition of Poznan Summer School of Bioinformatics that will take place on 6-10 July 2020. This year the course will cover high-throughput data analysis in plant biology, including subjects like differential gene expression, miRNA analysis, genome variants calling, proteomics or metabolomics. The course is suitable both for beginners and for those who already have some basic knowledge in bioinformatics and find it necessary and interesting to learn more about bioinformatics applications in omics-related studies.

The deadline for REGISTRATION is 22nd June 2020.

The course consists of lectures and hands-on. This combination should fit best your needs as you have a chance to try out the discussed methods yourself.

For further information please visit our website: http://bioinformatics-school.pl Please forward this announcement to anyone who might be interested. Best regards, PSSB Organizing Committe Contact: genomics@amu.edu.pl

Joanna Ciomborowska-Basheer, PhD Institute of Human Biology and Evolution Faculty of Biology Adam Mickiewicz University Poznan Uniwersytetu Poznanskiego 6, 61-614 Poznan e-mail: joannac@amu.edu.pl tel. +48 61 829 58 36

Joanna Ciomborowska-Basheer <joannac@amu.edu.pl>

Berlin Metagenomics Jun1-5

Dear all,

there are still a few places left on the 3rd edition of the course “Metagenomics, metatranscriptomics, and multi’omics for microbial community studies”: (https://www.physalia-courses.org/courses-workshops/-course33/)

Where: Free University Berlin (Germany)

When: 1-5 June 2020

Instructors: Dr. Curtis Huttenhower, Dr. Jeremy E. Wilkinson, Dr. Kelsey N Thompson, Dr. Eric Franzosa (Department of Biostatistics, Harvard T.H. Chan School of Public Health)

This course will provide a thorough introduction to microbial community data analysis (metagenomics, metatranscriptomics, and other culture-independent molecular data) through a balanced approach of lectures and hands-on lab sessions. Course participants will learn how to process data from raw meta’omic sequencing files through appropriate bioinformatic methods and approaches for subsequent integrative statistical analyses. Participants are invited to bring their own data to the practical session on the final day or can use publicly available data from the Integrative Human Microbiome Project (HMP2).

Program: (https://www.physalia-courses.org/courses-workshops/course33/curriculum-33/)

For the full list of our courses and Workshops, please see: (https://www.physalia-courses.org/courses-workshops/)

Should you have any questions, please contact us at (mailto:info@physalia-courses.org)

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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Berlin PopulationGenomics May18-22

Dear all,

last 5 places left on the 5th edition of the Physalia course on Population Genomics!

After the great success in both Europe and Canada, we are very happy to bring this course back in Berlin in May (18-22): (https://www.physalia-courses.org/-courses-workshops/course9/)

The instructors of this course are: Dr. Lewis Spurgin and Dr. Martin Taylor from the University of East Anglia (UK).

The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

For the full programma, please see: (https://-www.physalia-courses.org/courses-workshops/course9/-curriculum9/)

For the full list of our courses and Workshops, please see: (https://www.physalia-courses.org/courses-workshops/-course9/)

Should you have any question, please feel free to contact us at (mailto:info@physalia-courses.org)

Best regards, Carlo

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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

BielefeldU EnvironmentalChange

Dear evoldir community,

Understanding and managing the ecological consequences of global environmental change is a key challenge for the 21st century. Starting in fall 2020, Bielefeld University is offering a new Master programme Ecology and Environmental Change. The Master programme brings together different fields of ecology (animal and plant ecology, chemical ecology, conservation ecology and theoretical evolutionary ecology) to explore how individuals, populations, communities and ecosystems respond and adapt to environmental change.

Over the course of the Master programme, students learn to design and conduct laboratory and field experiments, acquire chemical-analytical methods, learn how to build eco-evolutionary models, and strengthen their statistical analysis and scientific communication skills. In the first year, students take classes including Ecosystem Wadden Sea (with excursion), Environmental change and chemical communication, Models in conservation biology, Animal Ecology in a changing world, Effects of environmental change on plant chemistry, Plant ecology in a changing environment, Nature conservation and environmental protection (with excursion). The second year consists of individual research modules and the Master thesis.

All classes are taught in English and international applicants are very welcome! German skills are not required, but free German classes are offered for students at Bielefeld University.

The application deadline is July 15, 2020.

For more information and how to apply, visit https://www.uni-bielefeld.de/fakultaeten/biologie/studium/studiengaenge/master/eec It would be great if you could share this information with prospective Master students at your institution.

Many thanks,

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

Meike Wittmann <meike.wittmann@googlemail.com>

Boston PlantDiversity Jun8-19

Submission deadline approaching!

This two-week short course (June 8 ’V 19, 2020) will be taught by experts from around the world as an intense lecture, laboratory, and living collections learning experience. The course will be based at the Weld Hill Research Building at the Arnold Arboretum in Boston (Massachusetts), which offers a state-of-the-art microscopy laboratory for teaching and sits amid the 15,000+ living specimens of more than 2,200 species at the Arnold Arboretum.

This course will provide a working knowledge of concepts that are central to understanding the developmental basis for the remarkable structural and functional diversity of plants. Topics include developmental dynamics, evolutionary diversification, and ecological and physiological function. Ultimately, this course aims to provide the skills necessary to interpret the vast array of morphologies that exist among plants. Each day will consist of lecture and laboratory sessions, with ample opportunity to explore the Arnold Arboretum.

There are no course fees, room and board are provided, and funds are available to help defray costs of participant travel.

Course Instructors: Pamela Diggle (University of Connecticut), Peter Endress (University of Zurich), William (Ned) Friedman (Harvard University), Cynthia Jones (University of Connecticut).

Application Deadline: Applications must be submitted by 11:30 pm March 15th, 2020. Application instructions are available on the course website: https://www.arboretum.harvard.edu/education/summer-short-course/ Eligibility: Summer short courses are open to postdoctoral researchers, graduate students, and undergraduates in their final year of study (who have been admitted to a graduate or professional program for the fall of 2018). Non-US-citizens are welcome to apply (but are responsible for obtaining the appropriate visa to be able to attend the course).

How to Apply: For full application instructions (including list of required documents) and to submit applications, please visit the course website (https://www.arboretum.harvard.edu/education/summer-short-course/).

Questions or Comments? Contact Pamela Diggle at pamela.diggle@uconn.edu

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788 <tel:860-486-4788>

pamela.diggle@uconn.edu

Crete MappingTraitEvolution Aug3-7

Dear colleagues,

Registration is open for the third edition of the course "Mapping Trait Evolution", August 3rd 'V 7th, 2020

Instructor: Dr. Jeroen Smaers (Stony Brook University, USA).

PROGRAM:

Monday. (R packages: ape, Geiger).

Morning: Phylogenetic data.

What is the basic structure of phylogenetic data? How to visualize and manipulate phylogenetic data?

Afternoon: Models of evolution.

What are models of evolution? What are the assumptions of the different models of evolution? How are models of evolution utilized?

Tuesday. (R packages: ape, nlme, caper, evomap).

Morning: Phylogenetic regression.

Assumptions, properties, and applications of the phylogenetic regression.

Afternoon: Phylogenetic ancova.

Testing for grade shifts using the phylogenetic regression.

Wednesday. (R packages: phytools, motmot, geiger, ape, evomap, BayesTraits).

Morning: Ancestral estimation.

Using models of evolution to estimate values of ancestral nodes.

Afternoon: Analysis of rates of evolution.

Estimation of rates of evolution. Testing hypothesis about rates of evolution.

Thursday. (R packages: bayou, phylolm, surface, OUwie, mvMORPH).

Morning: Inferring the structure of a macroevolutionary landscape.

Using Ornstein-Uhlenbeck models to map macroevolutionary patterns.

Afternoon: Testing the structure of a macroevolutionary landscape.

Applications and assumptions of OU models. Using OU models to test macroevolutionary hypotheses.

Friday. (R packages: geomorph).

Morning: Modularity and integration.

What is 'Â¥phylogenetic'Â modularity and integration? Applications and assumptions.

Afternoon: Case study.

MORE INFO: https://www.transmittingscience.org/-courses/evolution/mapping-trait-evolution/or writing to courses@transmittingscience.org

Best wishes

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Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org

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Glasgow CompSciSkills MayJun

Advanced Python for biologists (APYB04)

https://www.prinformatics.com/course/advanced-python-biologists-apyb04/ This course will be delivered by Dr Martin Jones from the 29th June - 3rd Julyin Glasgow City Centre.

Course overview:Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The course will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

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Python for data science, machine learning, and scientific computing (PDMS02)

https://www.prinformatics.com/course/python-for-data-science-machine-learning-and-scientific-computing-pdms02/ This course will be delivered by Dr Mark Andrews from the4th - 8th May in Glasgow City Centre.

Course Overview:Python is one of the most widely used and highly valued programming languages in the world, and is especially widely used in data science, machine learning, and in other scientific computing applications. This course provides both a general introduction to programming with Python and a comprehensive introduction to using Python for data science, machine learning, and scientific computing. The major topics that we will cover include the following: the fundamentals of general purpose programming in Python; using Jupyter notebooks as a reproducible interactive Python programming environment; numerical computing using numpy; data processing and manipulations using pandas; data visualization using matplotlib, seaborn, ggplot, bokeh, altair, etc; symbolic mathematics using sympy; data science and machine learning using scikit-learn, keras, and tensorflow; Bayesian modelling using PyMC3 and PyStan; high performance computing with Cython, Numba, IPyParallel, Dask. Overall, this course aims to provide a solid introduction to Python generally as a programming language, and to its principal tools for doing data science, machine learning, and scientific computing. (Note that this course will focus on Python 3 exclusively given that Python 2 has now reached it end of life).

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Bioinformatics with Linux and Python (BILP01)

https://www.prinformatics.com/course/bioinformatics-with-linux-and-python-bilp01/ This course will be delivered by Dr Martin Jones from the11th-15th May in Glasgow City

CentreCourse Overview:A fundamental part of bioinformatics (in contrast to simply computational biology) is the idea of scaling and automation. We want to arrange our tools into pipelines which can be executed with minimal supervision. Reliable automation of this type is key to many of the things that we want from our analyses; chiefly the ability to reproduce our results, and to extend them to other datasets.In this course we will examine two different systems for automating bioinformatic analyses. For situations where we are mostly running existing command line tools, bash scripting will allow us to build pipelines with minimal overhead. We'll start with simple command lines and see how the Linux environment ' though not designed with biology in mind ' is well suited to the type of automation we need.For situations where we don't have an existing tool available, and hence need to implement our own logic, bash quickly becomes unwieldy ' it's theoretically possible to write complex programs in bash, but the experience is painful! It's much better to use a more modern programming language, and for most biological tasks Python fits the bill.

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Landscape genetic data analysis using R (LNDG04)

https://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg04/ Please feel free to share

This course will be delivered by Prof. Rodney Dyer form 1st - 5th June in Glasgow City Centre.

Course Overview: The term 'landscape genetics' has been applied studies that integrate ecological context and intervening landscape into population genetic analyses of contemporary processes such as gene flow and migration. This course will cover the basics of both quantitative landscape

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KlosterLehnin Germany EvolutionResistance Aug24-28

Ecological immunology workshop 2020: evolution of resistance, tolerance & symbionts, 24-28 Aug 2020

ABSTRACT SUBMISSION DEADLINE EXTENDED TO 25th March 2020

Update due to COVID-19: We are currently still planning to go ahead with the workshop. In mid-June we will make a final decision, based on how the situation develops.

Abstract submission is now open for the above meeting, to be held at Kloster Lehnin, close to Berlin, Germany. For more information and abstract submission please see here: https://fu-berlin.de/xmed313 The meeting is the next installment in a loose series of workshops on ecological & evolutionary immunology / insect immunity, that started in 2001 in Sheffield, the most recent one being in Blossin (close to Berlin) in 2017. These meetings bring together researchers with different backgrounds but with a shared interest in immunity and host-microbe interactions, and where we encourage the presentation of unpublished results.

The hallmark of these workshops is the open atmosphere, fostering free exchange by keeping it an affordable, small meeting (˜85 participants). The format consists of invited speakers, contributed talks and a dedicated poster session. Long breaks provide plenty of opportunity for informal exchange. Past workshops have initiated new collaborations and ideas focusing on frontier research.

The premises are basic but in a beautiful location conducive to the success of the meeting. We will be located at a lakeside, which during August offers great swimming and canoeing, and a small café on the lakeside.

Our invited speakers are: Alex Best (University of Sheffield, UK) Nicholas Buchon (Cornell University, USA) Delphine Destoumieux-Garzon (University of Montpellier, France) Laura Flórez (University of Mainz, Germany) Andrea Graham (Princeton University, USA) Bruno Lemaitre (EPFL Lausanne, Switzerland) Jessica Metcalf (Princeton University, USA) Charlotte Rafaluk-Mohr (Freie Universität Berlin, Germany) Roland Regoes (ETH Zürich, Switzerland) Mike Strand (University of Georgia, USA) Ãlio Sucena (Gulbenkian Institute, Portugal) Pedro Vale (University of Edinburgh, UK) Heiko Vogel (Max-Planck Institute for Chemical Ecology, Jena, Germany) Bregje Wertheim (Groningen University, The Netherlands) Anna Zaidman-Rémy (Insitute National de Sciences Appliquées, Lyon, France) Important dates: 25th March - Abstract submission deadline 8th April - Decisions on abstracts 30th April - Registration deadline and payment of fees

Cost: Includes registration fee, accommodation and food 350— Student 440— Non-student

We look forward to receiving your abstracts!

Best wishes from the organisers

Sophie Armitage, Lea Otte & Jens Rolff (FU Berlin)

– Sophie Armitage

Heisenberg Fellow Freie Universität Berlin Institute of Biology Königin-Luise-Str. 1-3 14195 Berlin https://armitagelab.com/ Sophie Armitage <saoarmitage@zedat.fu-berlin.de>

LakeheadU DNASkills Apr14-24

DNA Skills Training Course:

The DNA Skills Training Course is designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation. This non-credit course is now offered in two formats: a hands-on laboratory course or an online virtual course.

This training course is offered at various times throughout the year and we will work with you to find a suitable time for training. The cost of the onsite training course is $2500.00 and the online virtual training course is $600.00.

The next scheduled times for the onsite DNA Skills Training Course are: April 14-24, 2020 May 5-15, 2020 May 26 - June 5, 2020 June 15-25, 2020 July 6-16, 2020

The online DNA Skills Training Course starts May 4, 2020.

For more information please contact us at 807-343-8877 or email paleodna@lakeheadu.ca or visit our website at www.ancientdna.com and click on 'Training Courses'.

Thank you.

Karen.

Karen Maa Administrative Assistant

Mailing Address: Paleo-DNA Laboratory 955 Oliver Road Thunder Bay, ON P7B 5E1

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Telephone: 1-866-DNA-LABS

Karen Maa <kmaa@lakeheadu.ca>

Montpellier EvolutionInfectiousDisease Jun12-14

We would like to announce that applications are still open for the workshop 'Opportunities for Collaborative Projects on the Ecology and Evolution of Infectious Diseases' 12 -14 June, just before the EEID2020 meeting in Montpellier.

You can apply and find more information about the event online at https://pre-eeid2020.sciencesconf.org/ The aim of the workshop is to promote international collaborations on 'hot topics' in Ecology and Evolution of Infectious Diseases. Promotion of new collaborative projects will be in the form of organising ideas for large research grant applications, but also for early career scientists (PhD students, postdocs) looking for laboratories to apply for Post-doctoral research grants, or later career scientists identifying sabbatical locations.

The meeting will be held at a residential centre, Le Hameau d'Etoile, near the village of St Martin de Londres in the foothills of the Cevennes mountains, 25 km north of Montpellier. Coaches will transport people to and from the venue (departure from Montpellier on the afternoon of Friday June 12th and return to Montpellier from Hameau de l'Etoile on June 14th in the afternoon). Please note attendees are expected to participate for the duration of the meeting. Attendance at the meeting is 150 Â, plus 250 Â for accommodation and food (400 Â in total).

As the meeting is organised with the support of national research agencies (NSF, BBSRC, NSFC and CNRS), we are very pleased that we will be able to cover partial/all costs for most attendees at the meeting. Travel costs will also be covered for some attendees from the US and Britain.

We hope to see you there and/or at the EEID2020 meeting (www.eeidconference2020.org),

Eric Harvill (UGA), Alison Duncan (ISEM/CNRS) & Thierry Boulinier (CEFE/CNRS) Sponsors: NSF (USA), BBSRC (UK), NSFC (China), CNRS (France)

alison duncan <Alison.Duncan@umontpellier.fr>

Online 2 BiologicalStatistics May25-29

ONLINE COURSE ' Generalised Linear (MIXED) (GLMM), Nonlinear (NLGLM) And General Additive Models (MIXED) (GAMM) (GNAM02) This course will be delivered live

https://www.psstatistics.com/course/generalised-linear-glm-nonlinear-nlglm-and-general-additive-models-gam-gnam02/ This course will be delivered via video link from the 25th-29th May

In light of travel restrictions due to the COVID-19 (Coronavirus) outbreak this course will now be delivered live by video link.

This is a 'LIVE COURSE' the instructor will be delivering lectures and coaching attendees through the accompanying computer practical's via video link, a good internet connection is essential.

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Please note we will also be offering the following online;

1) Introduction to Bayesian hierarchical modelling using R (IBHM04) 21st-24th April > www.psstatistics.com/-course/introduction-to-bayesian-hierarchical-modelling-using-r-ibhm04/ 2) Python for data science, machine learning, and scientific computing (PDMS02) 4th-8th May > www.psstatistics.com/course/python-for-data-science-machine-learning-and-scientific-computing-pdms02/ 3) Reproducible Data Science and R Package Design (RDRP01) 29th June - 3rd July > www.psstatistics.com/course/reproducible-data-science-and-r-package-design-rdrp01/ —

Course Overview: This course provides a general introduction to nonlinear regression analysis, covering major topics including, but not limited to, general and generalized linear models, generalized additive models, spline and radial basis function regression, and Gaussian process regression. All of these methods are encountered frequently in the analysis of evolutionary/biological data.

We approach the general topic of nonlinear regression by showing how the powerful and flexible statistical modelling framework of general and generalized linear models, and their multilevel counterparts, can be extended to handle nonlinear relationships between predictor and outcome variables. We begin by providing a comprehensive practical and theoretical overview of regression, including multilevel regression, using general and generalized linear models. Here, we pay particular attention to the many variants of general and generalized linear models, and how these provide a very widely applicable set of tools for statistical modeling. After this introduction, we then proceed to cover practically and conceptually simple extensions to the general and generalized linear models framework using parametric nonlinear models and polynomial regression. We will then cover more powerful and flexible extensions of this modeling. framework by way of the general concept of basis functions. We'll begin our coverage of basis function regression with the major topic of spline regression, and then proceed to cover radial basis functions and the multilayer perceptron, both of which are types of artificial neural networks. We then move on to the major topic of generalized additive models (GAMs) and generalized additive mixed models (GAMMs), which can be viewed as the generalization of all the basis function regression topics, but cover a wider range of topic including nonlinear spatial and temporal models and interaction models. Finally, we will cover the powerful Bayesian nonlinear regression method of Gaussian process regression.

Monday 25th ’ Classes from 09:30 to 17:30 Module 1: General and generalized linear models, including multilevel models. In order to provide a solid foundation for the remainder of the course, we begin by providing a comprehensive practical and theoretical overview of the principles of general and generalized linear models, also covering their multilevel (or hierarchical) counterparts. General and generalized linear models provide a powerful set of tools for statistical modeling., which are extremely widely used and widely applicable. Their underlying theoretical principles are quite simple and elegant, and once understood, it becomes clear how these models can be extended in many different ways to handle different statistical modeling. situations.

For this module, we will use the very commonly used R tools such as lm, glm, lme4::lmer, lme4::glmer. In addition, we will also use the R based brms package, which uses the Stan probabilistic programming language. This package allows us to perform all the same analyses that are provided by lm, glm, lmer, glmer, etc., using an almost identical syntax, but also us to perform a much wider range of general and

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

Online BayesianModellingUsingR Apr21-24

ONLINE COURSE ’V Introduction to Bayesian hierarchical modelling using R (IBHM04) This course will be delivered live

This course will be delivered via video link from the 21st-24th April

In light of travel restrictions due to the COVID-19 (Coronavirus) outbreak this course will now be delivered live by video link.

This is a ’Â¥LIVE COURSE’Â ’V the instructor will be delivering lectures and coaching attendees through the accompanying computer practical’Âs via video link, a good internet connection is essential.

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Please not we will also be offering the following online;

1) Python for data science, machine learning, and scientific computing (PDMS02) 4th-8th May > www.psstatistics.com/course/python-for-data-science-machine-learning-and-scientific-computing- pdms02/

2) Generalised Linear (MIXED) (GLMM), Nonlinear (NLGLM) And General Additive Models (MIXED) (GAMM) (GNAM01) 25th-29th May > www.psstatistics.com/course/generalised-linear-glm-nonlinear-nlglm-and-general-additive-models-gam-gnam02/

3) Reproducible Data Science and R Package Design (RDRP01) 29th June - 3rd July > www.psstatistics.com/course/reproducible-data-science-and-r-package-design-rdrp01/ —–

Course Overview: This course will cover introductory hierarchical modelling for real-world data sets from a Bayesian perspective. These methods lie at the forefront of statistics research and are a vital tool in the scientist’Âs toolbox. The course focuses on introducing concepts and demonstrating good practice in hierarchical models. All methods are demonstrated with data sets which participants can run themselves. Participants will be taught how to fit hierarchical models using the Bayesian modelling software Jags and Stan through the R software interface. The course covers the full gamut from simple regression models through to full generalised multivariate hierarchical structures. A Bayesian approach is taken throughout, meaning that participants can include all available information in their models and estimates all unknown quantities with uncertainty. Participants are encouraged to bring their own data sets for discussion with the course tutors.

Course Programme Tuesday 21st ’V Classes from 09:00 to 17:00

Module 1: Introduction to Bayesian Statistics Module 2: Linear and generalised linear models (GLMs) Practical: Using R, Jags and Stan for fitting GLMs

Wednesday 22nd ’V Classes from 09:00 to 17:00

Module 3: Simple hierarchical regression models Module 4: Hierarchical models for non-Gaussian data Practical: Fitting hierarchical models

Thursday 23rd ’V Classes from 09:00 to 17:00

Module 5: Hierarchical models vs mixed effects models Module 6: Multivariate and multi-layer hierarchical models Practical: Advanced examples of hierarchical models

Friday 24th 'V Classes from 09:00 to 17:00

Module 7: Shrinkage and variable selection Module 8: Hierarchical models and partial pooling Practical: Shrinkage modelling

Please email oliverhooker@psstatistics.com with any questions.

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Oliver Hooker PhD. PR statistics

2019 publications;

A way forward with eco evo devo: an extended theory of resource polymorphism with postglacial fishes as model systems. Biological Reviews (2019).

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53 Morrison Street Glasgow G5 8LB +44 (0) 7966500340

Oliver Hooker <oliverhooker@prstatistics.com>

Online LandscapeGenomics Jun8-12

Dear all,

due to the current COVID-19 outbreak, we decided to move the Landscape Genomics online: (https://www.physalia-courses.org/courses-workshops/course17/)

When: 8-12 June 2020

Instructors: Dr. Stéphane Joost and Dr. Elia Vajana (EPFL, Lausanne, CH)

The course will provide an overview of the type of dataset that can be used for a landscape genomics analysis. Firstly, students will learn how to obtain environmental data from publicly available databases, how to process it with Geographic Information Systems (GIS) and how to use the latter to produce indicators able to describe the characteristics of the landscape. Next, the course will discuss the different approaches to obtain genetic data and subsequently show how to study genetic variation and population structure across space in the R environment. Students will be given an overview of the different statistical approaches to study local adaptation, and will be trained in using two of them, Sambada and LFMM. The course will also cover the critical task of the interpretation and validation of the results. Finally, the workshop will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

If interested, please have a look at: (https://www.physalia-courses.org/courses-workshops/course17/)

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 PopulationGenomics May18-22

Dear all,

the 5th edition of the Population Genomics course will be held online: https://www.physalia-courses.org/courses-workshops/course9/ Instructors: Dr. Martin Taylor and Dr. Lewis Spurgin (University of East Anglia, UK)

The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. The course will use a range of software including the Linux operating system and R.

This course is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an underpinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and FST are desirable.

Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Programme: (https://www.physalia-courses.org/-courses-workshops/course9/curriculum9/)

Other upcoming Physalia courses will be also held online: 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/=0A=0ATwitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/-#!forum/physalia-courses info@physalia-courses.org

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ONLINE RNAseqBioconductor Jun15-19

Dear all,

registrations are now open for the 2nd edition of the course "Analysis of RNA sequencing data with R/Bioconductor" which has been moved ONLINE: (https://www.physalia-courses.org/courses-workshops/-course19/)

When: 15-19 June 2020

Instructor: Dr. Ludwig Geistlinger (City University of New York School of Public Health, USA)

This course will provide biologists and bioinformaticians with practical statistical analysis skills to perform rigorous analysis of RNAseq data with R and Bioconductor. The course assumes basic familiarity with genomics, but does not assume prior statistical training. It covers the statistical concepts necessary to design experiments and analyze high-throughput data generated by next-generation sequencing, including: exploratory data analysis, principal components analysis, clustering, differential expression, and gene set analysis.

Program: (https://www.physalia-courses.org/courses-workshops/course19/curriculum-19/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

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>

QuebecCity SeascapeGenomics Oct12-16

Course: Seascape Genomics

Where: Laval University, Quebec City (Canada)

When: 12-16 October 2020

Instructors: Dr. Laura Benestan (University of Montpellier, FR) and Oliver Selmoni (EPFL, CH)

In this course , students will learn the basics of this approach and train using state of the art methods. Firstly, students will learn how to extract environmental data from publicly available databases and how to use it to characterize the seascape structure and conditions. For instance, students will learn how to use remote sensing data to describe sea water temperature oscillations or sea water movements. Next, the course will bring its focus on genomic analyses: students will learn how to evaluate genetic structures in the marine environment and how to calculate and display connectivity between populations. The combination of environmental and genomic data will also lead to the study of local adaptation. Students will learn different methods to discover genetic/genomic signatures potentially involved in adaptation against specific environmental constraints. The course will also cover the critical task of the interpretation and validation of the results, particularly in an applied conservation and management context. Finally, the workshop will consider the crucial aspects and good habits to account for designing a seascape genomics experiment (e.g. sampling design) from a relevant scientific question.

Course website: (https://www.physalia-courses.org/-courses-workshops/course70/)

For the full list of our courses and workshops, please see: (https://www.physalia-courses.org/courses-workshops)

Should you have any questions, please feel free to contact us at (info@physalia-courses.org)

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org 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>

Raleigh NC EvolutionaryMedicine May17-22

Reminder - applications for the Evolutionary Medicine Summer Institute are due in 2 weeks, on March 20th!

The Triangle Center for Evolutionary Medicine (TriCEM) is now accepting applications for the 2020 Evolutionary Medicine Summer Institute (EMSI), held May 17-22 at NC State in Raleigh, NC. EMSI introduces core evolutionary concepts to a wide range of topics in human, animal, and plant health, and trains students, researchers, and health practitioners in computational methods used in evolutionary and ecological research. EMSI brings together internationally recognized experts in evolutionary biology with participants who want to apply these perspectives to cancer, infectious disease, evolution of microbial resistance, neurology, autoimmune disease, the microbiome, and more. Lectures on key concepts are complimented with hands-on computational exercises. Our goal is to give participants the background on evolutionary principles and the tools necessary to apply evolutionary biology to questions of medical and veterinary importance.

For more information (including last year's schedule) and to apply, please visit the EMSI website at https://-sites.duke.edu/emsi/. Application deadline is March 20, 2020.

If you have any questions, please feel free to reach out to Meredith Spence Beaulieu (meredith.spence.beaulieu@duke.edu) or Courtni France (cnf12@duke.edu).

Meredith R. Spence Beaulieu, PhD, BCE-Intern Pronouns: she/her/hers Assistant Director, Triangle Center for Evolutionary Medicine (TriCEM) 103A Biological Sciences, Duke University (919) 684-9681 www.tricem.org "Meredith Spence Beaulieu, Ph.D." <meredith.spence.beaulieu@duke.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ... plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.